

GAM-NAME GAM-SEQ GAM-SEQ-ID DICER-SEQ DICER-ID GAM-DRAW

GAM24

GAGGCAGGAGAATTGCTTGAACCCAGGAAGTGGAGGCTTCAGTGAGCTGAGAACACGCCACTGCACTCCAGTCC
TGGGCAACAGAGCAAGACTCTGTCTC 1 AACACGCCACTGCACTCCAGTCCT 2

G AA GAA-- AG GCTT A - AGAA

GAGGCAG AG TTGCTT CCCAGGA TGGAG CAGTG GC TG
CTCTGTC TC AACGAG GGGTCCT ACCTC GTCAC CG AC

- AG ACAAC G- AC-- - C ----

GAM25 TCAGAGTGAACAGGCAACCTACAAAATGGGAGAAAATTTTCGCAACCTACTCATCTGA 11
TGAACAGGCAACCTACAAAATGGG 12

G AC CAA----- CA

TCAGA TGA AGG CCTA A

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AGTCT ACT TCC GGGT /

- CA AACGCTTTTAAAAGA AA

GAM26

TGTAAATTTGTTTAAGTTCCTTGTAGATGCTGGATATTAGACCTTTGTCAGATGGATAGAGTGCAAAAATTTTCTCC
CATTCTGTAGGTTGTCTGGTTTACTCTGTTGATAGGTTCTTAATGCTGTGCA 36
TATTAGACCTTTGTCAGATGGATA 37

AATTT - TT TG-- TGC ATTA TTGT T-- T GC

TGTA GTTTAAG CCT TAGA TGGAT GACCT CAGA GGA AGAGT A

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ACGT CGAATTC GGA GTCT ATTTG TTGGA GTCT CCTTTTA A

GT-- T TT TAGTT C-- GCTG T-- TAC C AA

GAM27 AAAAAAGACTGAATTTCTGGCTTACTTGCATATACAGACTGGGATTTTTTTTTTTTTTTT 46
GACTGGGATTTTTTTTTTTTTTTTTT 47

CT TT TG - TACTTG

AAAAAAGA GAA TCC G CT C

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TTTTTTTT TTT AGG C GA /

TT TT GT A CATATA

GAM28 AAACATCTCCAGGCTTTGATTTTTGTACCATGGAAATTGTATTTAACCATACAGGGTTTTGGTATGTTT 54
TATTTAACCATACAGGGTTTTGGT 55

CT - - -- TT C G

AAACAT CCAGG CTTTG AT TT GTAC AT G

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TTTGTA GGTTT GGGAC TA AA TATG TA A

T- T A CC TT T A

GAM29 AAAGAACCTCGTCGTGACATTTCTCAGAAGCCATGACATGTCCCTGCGGCTGGAGGCCTTT 67
TGTCCTGCGGCTGGAGGCCTTT 68

AA -- --- T TCAGA

AAAG CCTC GTCGT GACAT TC A

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TTTC GGAG CGGCG CTGTA AG /

C- GT TCC C TACCG

GAM30

AAAGTCCTACGTGACTGATTTTAAACATTGTGATAAAATTAATTTTCAGTATAATAGTTGAATGTGTTAAGATAGGAT
TTT 97 TAATAGTTGAATGTGTTAAGATAG 98

CG- TGAT AC ATA TT

AAAGTCCTA TGAC TTAA ATTGTG AAA A

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 TTTTAGGAT ATTG AAGTT TAATAT TTT /
 AGA TGT- GA GAC TA
 GAM31 AAATATGCGCGAGAACCGCCGCGGTGTGACAAAAACCGCGCCGCGGGGCTCTTATTATATTT 119
 TATGCGCGAGAACCGCCGCGGTGT 120
 CGC- AA CC ACA
 AAATATG GAG CCG GCGGTGTG A
 ||||| ||| ||| |||||
 TTTATAT CTC GGC CGCCGCGC A
 TATT GG -- CAA
 GAM32 AAATCACATTTCTTTTATCATGTAACTTGTACCAAAGACTTATGAATAGATTTATGAATT 134
 TCACATTTCTTTTATCATGTAAA 135
 A CATT TTTTA TAAA GT
 AA TCA TCT TCATG CTT A
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 TTAGT AGA AGTAT GAA C
 A ATTT TA--- TCA- AC
 GAM33
 AAGAAATAGTTTTAAGTAACTTTTTATAGCAAGATGATACAATGGTATGAGTGTAATCTAAACTTCCTTGTTGTATTA
 CCTTGATGCTGTTACTTTTATTTTATTCCTT 160 TAGCAAGATGATACAATGGTATGA 161
 A TTTT- TTTT G A TG TAT GTAA
 AAG AATAG AAGTAAC TATA CAAG TGATACAA G GAGT T
 ||||| ||||| ||| ||| ||||| | |||
 TTC TTATT TTCATTG GTAT GTTC ATTATGTT T TTCA /
 C TTATT TC-- - C GT CC- AATC
 GAM34 AAGAAGGTGATGCCGAAGCTGAGGTGCGAAATTACGAAGATCAGCTATCAAACCTTGGAATCATGTCTT
 177 TCAGCTATCAAACCTTGGAATCAT 178
 AG G- ----- GG- GAA
 AAGA GTGAT CCGA AGCTGA TCG A
 ||||| ||||| ||| ||||| |||
 TTCT TACTA GGTT TCGACT AGC /
 G- AA CAACTA AGA ATT
 GAM35
 AAGATGCTACCCAGCATCTTTAAACCAGCTTGGTGCGGATAGTCTGACTAGTTTAAGGAGACTGGCGAAGCGTCT
 T 188 GACTAGTTTAAGGAGACTGGCGAA 189
 AC- CA C C TG T GG
 AAGATGCT CCAG TCTTTAAAC AG T G GC A
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 TTCTGCGA GGTC AGGAATTTG TC A C TG /
 AGC AG A -GT - AT
 GAM36 AAGATGTAGCGGGTTTTCTGGTGGTGGATCCGAAGATGGGCCACAGAGATTCCACTTTCCTCTT 208
 TAGCGGGTTTTCTGGTGGTGGATC 209
 TGT- C GT G GG C
 AAGA AG GG TTTCTG TGGT ATC G
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 TTCT TC CC AGAGAC ACCG TAG A
 CCTT A TT - GG A
 GAM37
 AAGGCGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACCTCCTGACCTCAAGTGGATATGCCTGCCTT 214
 TGACCTCAAGTGGATATGCCTGCC 215

GT-- CA TT C CT CT
 AAGGCGGG TTCAC TG GG CAGG GGT C
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 TTCCGTCC AGGTG AC CC GTCC TCA /
 GTAT A- T- A -- AA
 GAM38 AAGGGGATCTGAAAACCAGAGCGTCCCCGGCGCTCCCTTCTGTGCCGCCCGCTTAGGCAGGTTCCCTT
 235 TCTGAAAACCAGAGCGTCCCCGGC 236
 AAAA A TCCC TCC
 AAGGGGATCTG CC GAGCG CGGCGC C
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 TTCCCTTGGAC GG TTCGC GCCGTG T
 --- A CC-- TCT
 GAM39
 AAGGTGTCCAGGCCACAGTCTCAAGGGCTTTCTAGCAGCTTGGGGCTCCTGAAAGTCTGGCTGACTCTGCTTCT
 CTCGGACACCTT 245 TGAAAGTCTGGCTGACTCTGCTTC 246
 ----- CAC TCAA T C TT
 AAGGTGTCC AGGC AGTC GGGCTTTC AG AGC G
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 TTCCACAGG TTCG TCAG TCTGAAAG TC TCG /
 CTCTC TC- TCGG - C GG
 GAM40
 AATAAAAAGCTAACCTGGTTCAAAATGCTGATTAAGTTTCTACAAGCAAACACAAAACAGTGTTTTTTTTTATT 259
 TAAAAAGCTAACCTGGTTCAAAAT 260
 CT - GTTCAAAA- GATTAAG
 AATAAAAAG AAC CTG TGCT T
 ||||| ||| ||| |||
 TTATTTTTT TTG GAC ACGA /
 -- T AAAACACAA ACATCTT
 GAM41 AATAAAATTTCTCAAACCTATATCAATATCTAAAGTGCATATATTTTTTAAGAAAGATTATT 263
 TAAAATTTCTCAAACCTATATCAAT 264
 AA C CT CAA CT
 AATAA TTTCT AAA ATAT TAT A
 |||| |||| ||| ||| |||
 TTATT AAAGA TTT TATA GTG /
 AG A TT TAC AA
 GAM42
 AATCCCATTTTGGGGTTTTCCATCCGGAATTTTGTTTTAATAAGGGTTCAGTTTCTTTTTCCCCAGGGATT 283
 TAAGGGTTCAGTTTCTTTTTCCCC 284
 ATTT TTTTCCATCCG T
 AATCCC TGGGG GAATTTTGT T
 |||| ||| |||||
 TTAGGG ACCCC CTTGGAATAA /
 --- TTTTCTTTGA T
 GAM43 AATGACACCGTTGATTGAGCTTGTGAGCAGAGCTGAAAGAGACAGTCGACGGATGTGCATT 300
 TGACACCGTTGATTGAGCTTGTCA 301
 - - AG- G A
 AATG ACA CCGTTGATTG CTT TCAGC G
 |||| ||| ||||| ||| |||
 TTAC TGT GGCAGCTGAC GAA AGTCG /
 G A AGA - A

GAM44 AATGAGTTTCTTACTCGGGAGCTGGCTGAAGATGGCTACTCTGGAGTTGAGGTGCGAGTT 309
TGAGTTTCTTACTCGGGAGCTGGC 310

GA T - G C GA
AAT GT TCTTA CTC GGAG TGGCT A
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TTG CG GGAGT GAG TCTC ATCGG G
AG T T G - TA

GAM45 AATTCTCAAAGGTGCTAGAACAAATCGTCCACTTCTACAGTGTTCTCGTATCCAACAGAGTT 337
TCAAAGGTGCTAGAACAAATCGTC 338

CAAA T AATC CCA
AATTCT GGTGC AGAACA GT C
||||| ||||| ||||| |||
TTGAGA CTATG TCTTGT CA T
CAAC C GA-- TCT

GAM46
ACAAGGGGATGACTGGTGGGTCTCTCTTGGCCCCGTGGTGGCGGTCCGGGGGGGGGCTTCTTCCTTACGTCCCTC
TGT 365 TGA CTGGTGGGTCTCTCTTGGCCC 366

AG ACT T-- C G
ACA GGGATG GG GGGTCTCTCTTGG CCGT G
||| ||||| || ||||| ||||| |||||
TGT CCCTGC CC TTCGGGGGGGGGCC GGCG T
CT ATT TTC T G

GAM47 ACAGGCATGAGCCACTGCGCCCAGCCTGGAAGTTAATTTTTATGGTTGTGTATGTGTTGCTTGT 387
CATGAGCCACTGCGCCCAGCCTGG 388

TGAGC - CC - T
ACAGGCA CAC TGC GC AGCC TGGAAG T
||||| ||| ||||| ||| |||||
TGTTTCGT GTG ATGTG TTGG ATTTTT A
T--- T -- T A

GAM48 ACATGTGGTGTGTTTGGTTTCCTGCTCCTCTGTAAGTTTGCTGAGGATAATGGCTTCCAGCTTCATCCATGT
422 TGTGGTGTGTTTGGTTTCCTGCTCCT 423

T T-- TTT TGC- T A
ACATG GGTG TTGG CC TCCTC GTA G
||||| ||||| ||||| ||| ||||| |||||
TGTAC CTAC GACC GG AGGAG CGT T
- TTC TTC TAAT T T

GAM49
ACCCTAGCTAACATCCTACAGAATGGTGAAAGACTGAGTGTTTTTCCCCTATAATAGGAAACAAGCAAGGGT 429
TAACATCCTACAGAATGGTGAAAG 430

A AACA CAGAAT T TG
ACCCT GCT TCCTA GG GAAAGAC A
||||| ||| ||||| || ||||| |||||
TGGGA CGA AGGAT CC CTTTTTG /
A ACAA AATAT- C TG

GAM50 ACTAGAATGTTGACCTCGAGCCGAGGCCTACTTGCAGCGCACCGGAGGAGAGGTCTCTAGT 453
TAGAATGTTGACCTCGAGCCGAGG 454

ATGTT GAG- AG - AC
ACTAGA GACCTC CCG GC CT T
||||| ||||| ||| |||||
TGATCT CTGGAG GGC CG GA T

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----- AGGA CA C CG
GAM51 ACTATTATGATCAAGGATATGGAAATTACAATAGTGCCTATGGTGGTGATCAAACTATAGT 459
TATTATGATCAAGGATATGGAAAT 460
TA--- AGGA AA C
ACTAT TGATCA TATGG ATTA A
||||| ||||| ||||| |||||
TGATA ACTAGT GTATC TGAT /
TCAAA GGTG CG A
GAM52 AGAGCCGGCTGGGAGAGGCGGCGTCAGGGTGGGTCTGCGCCTGCCCTTTCCGCGCCGGCTTT 480
TGCGCCTGCCCTTTCCGCGCCGGC 481
- A - T T
AGAGCCGGC TGGGAG GGC GGCG CAGGG G
||||||| ||||| || ||||| |||||
TTTCGGCCG GCCTTT CCG CCGC GTCCT G
C C T - G
GAM53
AGAGGAAGCGGGAGGAGCTGAGCAACGTA CTGGCCGCCATGAGGAAAGCTGCTGCCAATGAAAGACTGAGCCC
CTCCCCCTGCCCTCT 522 GAAAGACTGAGCCCCTCCCCCTGCC 523
A- C A G CAACG C C CATGAG
AGAGG AG GGGAGG GCT AG TA TGGC GC G
||||| || ||||| || || || ||||| ||
TCTCC TC CCCTCC CGA TC GT ACCG CG /
CG - C G AGAAA A T TCGAAA
GAM54 AGATAAAAGGTTTCTAAAACATGACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTT
531 TAAAAGGTTTCTAAAACATGACGG 532
AAAGG C AAA C GAG
AGATA TTT TA CATGA GGAGGTT A
||||| || || ||||| |||||
TTTAT AAA AT GTACT TCTTCGA /
GTA-- A GAG - AGT
GAM55 AGATACCATACACATGATGAAGTTGCTGTTTGAAAGTACTGTTGAAGCACTGTACAAGTTTGTGGTTCT
545 TACCATACACATGATGAAGTTGCT 546
T C A A A T GTTTGAAA
AGA ACCATA AC TG TG AGT GCT G
||| ||||| || || || |||||
TCT TGGTGT TG AC AT TCA CGA T
- T A - G - AGTTGTCA
GAM56 AGATCAGATGGTCGTAGTTGTGTGGCTTTATTTCTGAGTTCTCTTAACTGTTCCATTGGTCT 556
TCAGATGGTCGTAGTTGTGTGGCT 557
A TCG TGT- TAT
AGATCAG TGG TAGTTG GGCTT T
||||||| || ||||| |||||
TCTGGTT ACC GTCAAT TTGAG /
- TT- TCTC TCT
GAM57 AGATGACGTTTATGATCGTATGCTGCTAGACTACTTCTTTTCTTATCATCAGTTCATCCATCT 561
TGACGTTTATGATCGTATGCTGCT 562
ACGTTTA C TGCTGCT CT
AGATG TGAT GTA AGA A
||||| ||||| ||||| |||||
TCTAC ACTA TAT TCT /

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CTACTTG C TCTTT-- TC
GAM58 AGATGAGGTCTCAGATGCGAGATCAACTCTAATACGAAATCCATCTGCAATCTGGGCCCCATTT 573
TGAGGTCTCAGATGCGAGATCAAC 574
A T - G CAAC- TA
AGATG GGTG CAGAT GC AGAT TC A
||||| ||||| || |||| ||
TTTAC CCGG GTCTA CG TCTA AG T
C - A - CCTAA CA
GAM59 AGCAATCAAAGGTTTTTCGCAATTCTCCAGTGGGAGTAAACCACAGACTACGAGGGAGTTTGACAGCT
588 TCAAAGGTTTTTCGCAATTCTCCAG 589
AA GG CAAT CCA GAG
AGC TCAAA TTTTCG TCT GTGG T
||| ||||| ||||| ||| |||||
TCG AGTTT GGGAGC AGA CACC /
AC GA ATC- --- AAA
GAM60
AGCATGACTGACACGTCTGACCCCTGAGAAGGTGGTCTCTGCCTTCCTAAAGGTGTCATCTGTGTTCAAGGACGA
AGCT 604 TGACACGTCTGACCCCTGAGAAGG 605
ATGA-- -- TC C GA-- TG T
AGC CT GACACG TGAC CCT GAAGG G C
||| || ||||| ||||| ||| ||||| |
TCG GA TTGTGT ACTG GGA CTTCC C /
AAGCAG AC CT T AATC GT T
GAM61 AGCATTCCAACAAAGGGTTTTAATGTAGATTTTTTTTTTTTTTGACCCCATGCTGTTGATTGCT 617
TTCCAACAAAGGGTTTTAATGTAG 618
TTC AA-- TTTTAA TTTT
AGCA CAACA GGG TGTAGA T
||||| ||||| ||| |||||
TCGT GTTGT CCC ACGTTT /
TA- CGTA C----- TTTT
GAM62 AGCCAGTCATTCTAAGGGGCTTTGTATTGGTGCTATAAAGTCAACCTCAATTCCTTACAGTGGTCTGGTT
630 TAAAGTCAACCTCAATTCCTTACA 631
- C ----- TTG
AGCCAG TCATT TAAGG GGCTTTGTA G
||||| ||||| ||||| |||||
TTGGTC GGTGA ATTCC CTGAAATAT /
T C TTAACCTCAA CGT
GAM63
AGCCCTCGATGAGAACAAGGTCACGGTCAGCTGATTTACTTGAGCGTTTCGGCTTACTCTGACCTGACACACTCCA
CAGAGCACTGGCT 652 TGAGAACAAGGTCACGGTCAGCTG 653
--- GAT- AACA-- C C TTTACT
AGCC CTC GAG AGGTCA GGT AGCTGA T
||||| ||| ||| ||||| ||| |||||
TCGG GAG CTC TCCAGT TCA TCGGCT /
TCAC ACAC ACACAG C T TGCGAG
GAM64 AGCCGGGTTGCGCCAGGCTGTCATAGTCCTTCTCGTGGAACACGGCGGCGCGGTCACCCAGGCT 673
ACACGGCGGCGCGGTCACCCAGGC 674
- --- AG CATAG TTC
AGCC GGGT TGCGCC GCTGT TCC T
||||| ||||| ||||| ||||| |||

TCGG CCCA GCGCGG CGGCA AGG /
A CTG -- CA--- TGC
GAM65 AGCCTCACAGCTCAGGTCTCTCTTTGCCTGTCACAGTGGAAGTCCCGTGCTGAGCCCAGGTT 697
TCACAGCTCAGGTCTCTCTTTGCC 698
CACA GTCTCT- GC T
AGCCT GCTCAG CTTT CTG C
||||| ||||| ||| |||
TTGGA CGAGTC GAAG GAC /
CC-- GTGCCCT GT A
GAM66 AGCCTGAGACTAGTTTCGGACTCCCCTTCGGCAAGGTCTGAAGGGGGTTTCGGCTGGTCTCTGCT 721
TGAGACTAGTTTCGGACTCCCCTTC 722
CT T T A
AGC GAGACTAGT CGGAC CCCCTTCGGC A
||| ||||| ||||| |||||
TCG CTCTGGTTCG GCTTG GGGGAAGCTG /
T- - - G
GAM67
AGCCTTTATTGGGTCAGGGCTTGCTCCAGAGCTCAGGGGCCAGGTAGGTCAGGAGCCTTGGGATGGCT 737
TATTGGGTCAGGGCTTGCTCCAGA 738
- ATT G AG CCAGA C
AGCC TTT GG TC GGCTTGCT GCT A
||||| ||| ||||| |||
TCGG AGG CC AG CTGGATGG CGG G
T GTT G GA AC--- G
GAM68
AGCGGGATCGCTTCGGGTGCTCGACTCCTGTTGCGCATGCTCAGCGCGCTGCCCGGCTGGGGACCCGCGCAC
CTGCAGCGCCCGCT 748 GCCCGGCTGGGGACCCGCGCACCT 749
AT T T A-- T C - TC
AGCGGG CGCT CGGGTGC CG CTCC GTTG GCA TGC A
||||| ||| ||||| || ||| ||| |||
TCGCCC GCGA GTCCACG GC GGGG CGGC CGT GCG /
-- C C CCA T C C CG
GAM69 AGCGGGATGGCTGCAGCCAAGGAGCTGGGGGAGGGCCGGGCTCAGGGCTAGCCCTTTCCGCT 782
TCAGGGCTAGCCCTTTCCGCT 783
T- GC AAG G GG
AGCGGGA GGCT AGCC GAGCT GG A
||||| ||| ||| ||||| ||
TCGCCTT CCGA TCGG CTCGG CC G
TC -- GA- G GG
GAM70
AGCTTCACGCTCTTTGTCATCCTGGACTTCTTCCCGCTCATCGCCCACTATTACCTCACCCTCTGGATGAGGCT
GATGAGGCAGGCAAGCGGATTTTTGGTCCCCGGGTGGGGAACGAGCTGTGCGAGGT 792
TGAGGCTGATGAGGCAGGCAAGCG 793
G - - - G T- TCTTC- CA - CAC - - AC
A CTT CAC GCTC TTT TCATCC GGACT CCGCT TC GCC TATTA CCTCA CC T
| ||| ||| ||| ||||| ||||| ||| ||| ||||| |||
T GAG GTG CGAG AAG GGTGGG CCTGG GGCGA GG CGG GTAGT GGAGT GG /
G C T C G CC TTTTA AC A A-- C A TC
GAM71
AGGAAAACTTATGGCATGTATAGTGAGGTAAAGGACTTGCATGTCCCTCGCGATGGTTTCCTTCCCCTTATTCTT
ACTGCTCAGTGTCT 818 TGGCATGTATAGTGAGGTAAAGGA 819

AGGGCGGCCCGGGGAGCACCTGGTTTTATTTCCGTGCAGTGAGGGGATATCATCCTGGTGCCCTCGTCTTGGTTT
919 ATCATCCTGGTGCCCTCGTCTTGG 920
G - C A T TTT- TT GTGC
AGG CG G CGGGG GCACC GG TAT CC A

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 TTT GT C GCTCC CGTGG CC ATA GG /
 G T T - T TACT GG AGTG
 GAM78
 AGGGGGGCACACCACATCAAAATGAGGGGTGTGTTGCTGTTGCGAAATTAAACCAATCGTTGTGTTTGTCCCC
 938 AAACCAATCGTTGTGTTTGTCCCC 939
 CAC TCAA GG GTG---- T
 AGGGGGCA CACA ATGA GGT TTGC G
 ||||| ||| ||| ||| |||
 TCCCCTGT GTGT TGCT CCA AGCG T
 TT- ---- AA AAATTAA T
 GAM79 AGGGGGGGGCTCCAAATAGTGTGGCCTTTAAATTGCTGGGAACGGGGAGGCCCAACCCT 952
 TGGGAACGGGGAGGCCCAACCCT 953
 GG - AAATA G-TG CTTT
 AGGG GGGC TCC GT T GC A
 ||| ||| ||| || | ||
 TCCC CCCG AGG CA G CG /
 AA G GG--- AG GT TTAA
 GAM80
 AGTCTCTGACCAGCCTGAACGTGTCTTATGTCACTTGTTTGGAAATGATGTGATTGAAGATTTTCAGAGAGGTCATT
 GGAGGCT 971 TGATTGAAGATTTTCAGAGAGGTCA 972
 --- AGC CGT AT -TG T
 AGTCTCT GACC CTGAA GTCTT GTCAC T TT G
 ||||| ||| |||| |||| |||| | ||
 TCGGAGG CTGG GACTT TAGAA TAGTG A AA G
 TTA AGA --- GT TGT A
 GAM81
 AGTGAGGGGCAGGATGAAATCATCTAGGGTAGGTATTTAGAGGGAGGGCGCCGTGCAAAATAAAATCCTCACT
 997 AGGGGCAGGATGAAATCATCTAGG 998
 ----- - A AAA A- GTA
 AGTGAGGG GCA GG TG TC TCTAGG G
 ||||| ||| ||| || |||||
 TCACTCCT CGT CC GC AG AGATTT /
 AAAATAAAA G - GGG GG ATG
 GAM82
 AGTGGACAATGTCATGTTTGGAGAAAGATAACAACACAAATAATGTAACCTTTCTTAAAAGGCAGAACTCAATCC
 ATT 1017 TGTCATGTTTGGAGAAAGATAACA 1018
 CAAT CA ---- A ATA ACAC
 AGTGGA GT TGTTT GG GAAAG ACA A
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 TTACCT CA ACGGA TC CTTTC TGT A
 AACT AG AAAT - CAA AATA
 GAM83 AGTTGATCAGATTTCAAGGTCTGGGGAGTATATCCACTGTGTACTGGGTCTTGAGCTCTAGAGAGCT
 1037 TCAGATTTCAAGGTCTGGGGAGTA 1038
 GA - T GT GGGG CC
 AGTT TC AGA TTCAAG CT AGTATAT A
 ||| || ||||| || |||||
 TCGA AG TCT GAGTTC GG TCATGTG /
 G- A C TG ---- TC
 GAM84 ATAGAAGTATACTGAGAGTCTAAAATACATTCTAGTAGTGCATGTCTTGGTGTGCTTTTGT 1061
 TAGAAGTATACTGAGAGTCTAAAA 1062

TG GTCTAAAA AT
 ATAGAAGTATAC AGA TAC T
 ||||| || ||
 TGTTTTCGTGTG TCT ATG C
 GT GTACGTG- AT
 GAM85
 ATATATGTTTTCTTTTTAAGCTAGCTAAAGAAAATACTCTTGATCGGGGTTAGTTCTTAAAGCAAAAAACAGAAGAA
 AAGTATGTAT 1078 TAAGCTAGCTAAAGAAAATACTCT 1079
 - TAAGCTA A- AAT TG
 ATATATG TTTTCTTTT GCT AAGAA ACTCT A
 ||||| ||||| || |||| ||||
 TATGTAT AAAAGAAGA CGA TTCTT TGGGG /
 G CAAAAA AA GAT CT
 GAM86 ATATGGTCATGTGAATCAAATTTGATGTATAAAGTACTCACACAAGTTGTCTCAAAGATGATAT 1095
 TATGGTCATGTGAATCAAATTTGA 1096
 G ATG AT A A ATAAA
 ATAT GTC TGA CAA TTTG TGT G
 |||| || || || |||| ||
 TATA TAG ACT GTT GAAC ACA /
 G AA- CT - - CTCAT
 GAM87 ATATGGTGTGAGAAATGGCTGTAGGAAACAACACTCAACGAAGTTATTCCATCATCCCGTGT 1111
 TATGGTGTGAGAAATGGCTGTAGG 1112
 TG GA- GTAG- AAC
 ATATGG TGA AATGGCT GA A
 |||| || |||| ||
 TGTGCC ACT TTATTGA CT A
 CT ACC AGCAA CAC
 GAM88
 ATCACAAGTGGGGTGTACTCCCCCTTGCATATTGGGAACAACATCACAAGTGGGGTGTACTGCCTCTGTGAT
 1124 TCACAAGTGGGGTGTACTGCCTCT 1125
 AGT - T - C- A G
 ATCACA GGGGT GTAC CCCC CTTG AT TTG G
 |||| |||| |||| |||| || ||||
 TAGTGT CTCCG CATG GGGG GAAC TA AAC A
 --- T T T AC C A
 GAM89 ATCACAGCTGTGCCAGTAATAAGGATGCTAACAATTAATTTTATCAAACCTAACTGTGACAGCTGTGAT
 1140 TCACAGCTGTGCCAGTAATAAGGA 1141
 GC AATAAG- CTAACA
 ATCACAGCTGT CAGT GATG A
 ||||| |||| ||||
 TAGTGTGACACA GTCA CTAT T
 GT ATCCAAA TTTAAT
 GAM90
 ATCGTCAATGAAAGCCCTGGGCTGCTCTCCAGGATGTCACCATTGGGGGTTTCGGCTCGTCCGGTGGCCGGGGC
 GGGTTTCCACCGGTGTGGCGCCTGGCCGCGTCCGGGGGCTTCGGGCGAT 1159
 TGTCAACCATTGGGGGTTTCGGCTCG 1160
 AA A T TCT A C - TTC - T
 ATCGTC TGAA GCCCTGGGC GC CCAGG TGTCAC ATTGG GGG GGCTCGTCC GG G
 |||| || ||||| || |||| |||| || ||||| ||
 TAGCGG GCTT CGGGGCCTG CG GGTCC GCGGTG TGGCC CCT TTGGGCGGG CC /

-- - - CC- - - A --- G G
 GAM91 ATCGTGGGGCTTGTGGGAAATGGTGGGGAGTGCCAATGGCCGTAAATTATGTGTGCGCGAT 1168
 TGGCCGTAAATTATGTGTGCGCGAT 1169
 G TT GAA GG-- A
 ATCGTGG GC GTGG ATGGT GG G
 ||||| || ||| |||| ||
 TAGCGCT TG TATT TGCCG CC T
 G -- AAA GTAA G
 GAM92 ATGAGATTTGGGAGGGGGCCAGGGGCAGAATGATATGGTTTGACTGTGTCCTCACCCAAATCTCAT 1171
 TGAGATTTGGGAGGGGGCCAGGGGC 1172
 A C G GCA GA
 ATGAGATTTGGG GGGG CA GG GAAT T
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 TACTCTAAACCC CTCC GT TC TTTG A
 A T G AG- GT
 GAM93 ATGAGGAACTCCTACAACCTCAATAGTAAACAAACAAAAACCCCTGATTCCTGGAGATCCTGAT 1196
 TGAGGAACTCCTACAACCTCAATAG 1197
 G A TACAAC ATA AAAACA
 AT AGGA CTCC TCA GT A
 || |||| ||| || ||
 TA TCCT GAGG AGT CA /
 G A TCCTT- CCC AAAACA
 GAM94 ATGCAGTATTTGGTTTCCTGTTCCCTGTGTTAATTTGCTTAGGATAATGGCCTCCAGCTGCAT 1206
 ATGCAGTATTTGGTTTCCTGTTCC 1207
 ATT TTT TGT- T TA
 ATGCAGT TGG CC TCCTG GT A
 ||||| || || |||| ||
 TACGTCG ACC GG AGGAT CG T
 --- TCC TAAT T TT
 GAM95
 ATGTGTTTCGTGACACGGATCAACCTTTTTGTGCTTATCGAGGAGCAGAAAATCGTTGTGAAAGTGTTGAAGCCAC
 GT 1220 TGACACGGATCAACCTTTTTGTGC 1221
 TTCG GGAT- CT G AT
 ATGTG TGACAC CAAC TTTT TGCTT C
 |||| |||| ||| |||| ||||
 TGCAC GTTGTG GTTG AAAA ACGAG G
 CGAA AAAGT CT G GA
 GAM96 ATTCAGAGTCCTGCACCAAGCCCCAGAGATGGTTTTGGTGGGTCTTGGTGGGGCCCAGGAAT 1227
 TCAGAGTCCTGCACCAAGCCCCAG 1228
 AGA- TG C GA TG
 ATTC GTCC CACCAAG CCA GA G
 |||| ||| ||||| |||| ||
 TAAG CGGG GTGGTTC GGGT TT /
 GACC -- T GG TT
 GAM97 ATTCTTAATCTTAGTGAAATTCTGAAATACTTGATAATTCTTTAAAAGCTGTCTGGTTAAGAAT 1259
 TAAAAGCTGTCTGGTTAAGAAT 1260
 T-- GAAATTCT A CT
 ATTCTTAATC TAGT GAA TA T
 ||||| ||| || ||
 TAAGAATTGG GTCG CTT AT /

TCT AAAATTT- A AG
 GAM98
 ATTTGTTTTTATTGGTGTAGTCGCTGCAGTTTTACCTGCCATGGTGGTGCTCAGGTATAACATAGATGGAAACAAG
 T 1276 TATTGGTGTAGTCGCTGCAGTTTT 1277
 G A CG C T TG
 ATTTGTTTTTATT GTGT GT CTG AGT TTACC C
 ||||| |||| || || ||||
 TGAACAAAGGTAG TACA TA GAC TCG GGTGG C
 A A TG - T TA
 GAM99
 CAAAGCCAGCAACGACATGTACCACAGCCGCGCGCTGCAGGTGGTGCGCGCCCGCAAGCAGATCGTAGCTGGG
 GTG 1293 ACGACATGTACCACAGCCGCGCGC 1294
 AAG A CA ACCACA C C
 CA CCAGC ACGA TGT GC GCGCGCTG A
 || |||| |||| || || ||||
 GT GGTCG TGCT ACG CG CGCGTGTT G
 GG- A AG AACGCC - G
 GAM100 CAATGGGAAGGTTGATGCTCGAAGTGACCGAACTGGGGAGGTCATCTTTAAGGACAATTTTCTTCTG
 1303 TGGGAAGGTTGATGCTCGAAGTGA 1304
 AT ATG CG - GAAC
 CA GGGAAGGTTG CT AAG TGACC T
 || |||| || || ||||
 GT TCTTTTAAAC GA TTC ACTGG G
 CT AG- AT T AGGG
 GAM101
 CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCCGGCTGATGGTGGTGGAGGAACCGATG
 TGTTTACTGTG 1315 TGAACCTTCACCTGGAACATCA 1316
 AATC - GACTA TGGAA A AC
 CACAG AGAC CAT CCTTCACC CATCA CC G
 |||| |||| || |||| ||||
 GTGTC TTTG GTA GGAGGTGG GTAGT GG C
 A--- T GCCAA TG--- C CC
 GAM102
 CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCCGGCTGATGGTGGTGGAGGAACGATGT
 GTTTACTGTG 1327 TGAACCTTCACCTGGAACATCA 1316
 AATC - GACTA TGGAA A AC
 CACAG AGAC CAT CCTTCACC CATCA CC G
 |||| |||| || |||| ||||
 GTGTC TTTG GTA GGAGGTGG GTAGT GG C
 A--- T GCAA- TG--- C CC
 GAM102
 CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCCGGCTGATGGTGGTGGAGGAACGATGT
 GTTTACTGTG 1328 TGAACCTTCACCTGGAACATCA 1316
 AATC - GACTA TGGAA A AC
 CACAG AGAC CAT CCTTCACC CATCA CC G
 |||| |||| || |||| ||||
 GTGTC TTTG GTA GGAGGTGG GTAGT GG C
 A--- T GCAA- TG--- C CC
 GAM102
 CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCCGGCTGATGGTGGTGGAGGAACGATGT
 GTTTACTGTG 1329 TGAACCTTCACCTGGAACATCA 1316

AATC - GACTA TGGAA A AC
CACAG AGAC CAT CCTTCACC CATCA CC G
|||| | ||| ||||| |||| |
GTGTC TTTG GTA GGAGGTGG GTAGT GG C
A--- T GCAA- TG--- C CC

GAM102

CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCCGGCTGATGGTGGTGGAGGAACGATGT
GTTTACTGTG 1330 TGA CTACCTTCACCTGGAACATCA 1316

AATC - GACTA TGGAA A AC
CACAG AGAC CAT CCTTCACC CATCA CC G
|||| | ||| ||||| |||| |
GTGTC TTTG GTA GGAGGTGG GTAGT GG C
A--- T GCAA- TG--- C CC

GAM102

CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCCGGCTGATGGTGGTGGAGGAACGATGT
GTTTACTGTG 1331 TGA CTACCTTCACCTGGAACATCA 1316

AATC - GACTA TGGAA A AC
CACAG AGAC CAT CCTTCACC CATCA CC G
|||| | ||| ||||| |||| |
GTGTC TTTG GTA GGAGGTGG GTAGT GG C
A--- T GCAA- TG--- C CC

GAM102

CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCCGGCTGATGGTGGTGGAGGAACGATGT
GTTTACTGTG 1332 TGA CTACCTTCACCTGGAACATCA 1316

AATC - GACTA TGGAA A AC
CACAG AGAC CAT CCTTCACC CATCA CC G
|||| | ||| ||||| |||| |
GTGTC TTTG GTA GGAGGTGG GTAGT GG C
A--- T GCAA- TG--- C CC

GAM102

CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCCGGCTGATGGTGGTGGAGGAACGATGT
GTTTACTGTG 1333 TGA CTACCTTCACCTGGAACATCA 1316

AATC - GACTA TGGAA A AC
CACAG AGAC CAT CCTTCACC CATCA CC G
|||| | ||| ||||| |||| |
GTGTC TTTG GTA GGAGGTGG GTAGT GG C
A--- T GCAA- TG--- C CC

GAM102

CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCCGGCTGATGGTGGTGGAGGAACGATGT
GTTTACTGTG 1334 TGA CTACCTTCACCTGGAACATCA 1316

AATC - GACTA TGGAA A AC
CACAG AGAC CAT CCTTCACC CATCA CC G
|||| | ||| ||||| |||| |
GTGTC TTTG GTA GGAGGTGG GTAGT GG C
A--- T GCAA- TG--- C CC

GAM102

CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCCGGCTGATGGTGGTGGAGGAACGATGT
GTTTACTGTG 1335 TGA CTACCTTCACCTGGAACATCA 1316

AATC - GACTA TGGAA A AC
CACAG AGAC CAT CCTTCACC CATCA CC G

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GTGTC TTTG GTA GGAGGTGG GTAGT GG C
A--- T GCAA- TG--- C CC
GAM103
CACAGACGAACAGGCAAGGGGCTAGGGAAGAAGAGGGGACCCATGTCTTCGGAAATACAAGGGACTTCTGCAAT
CCATGGAGAATGCCAAATAATGTG 1336 TACAAGGGACTTCTGCAATCCATG 1337
GACGAACA AGGGG G AGA- GGA A --- T
CACA GGCA CTA GGA AGAGG CCC TG TC T
||||| ||||| ||||| ||||| ||||| ||
GTGT CCGT GGT CCT TCTTC GGG AC AG C
AATAAA-- AAGA- A AACG A-- A ATAA G
GAM104 CACCTGCCCCAGCCCCTGCCTCTGCCCCAAGTGGGGCCAGCTGCCCTCACTTCTGGGGTGGATG
1347 ACCTGCCCCAGCCCCTGCCTCTGC 1348
C TG CCCCT--- CT - A
CA C CCCAG GC CTG CCC A
|| | ||||| || |||||
GT G GGGGTC CG GAC GGGG G
A GT TCACTCC TC C T
GAM105 CACTAACAACCTTCTGGCCGGGCCACGGGGCTCATGCCTTGTAATTCTCAGCCAGAGGGCGGGTG 1391
TAACAACCTTCTGGCCGGGCCACGG 1392
AACAA C CC-- T
CACT CTTCTGGC GGG ACGGGGC C
||||| ||||| ||||| |||||
GTGG GGAGACCG CTC TGTTCG A
GCG-- A TTAA T
GAM106 CACTGGCCGAACCTCTCGGTCTCGGGTCTTGAGTGGGGCCCGCAGCCGAAGAGTTGCAGGTG 1403
TGGCCGAACCTCTCGGTCTCGGGTC 1404
G CG - CT G
CACT GC AACTCT CGGT CGGGTCTT A
||||| ||||| ||||| ||||| |||||
GTGG CG TTGAGA GCCG GCCCGGGG G
A -- A AC T
GAM107 CACTTGTAATCCCCCCTGTACTTACCTACTCACATTGGAGAGTTCTGAGGCCGGAGTAACTGTG 1411
AGTTCTGAGGCCGGAGTAACTGTG 1412
TTG A CC GT-- A TACT
CAC TA TCC CCT ACTT CC C
||| ||||| ||| |||||
GTG AT AGG GGA TGAG GG A
TCA G CC GTCT A TTAC
GAM108 CAGAATGTCAGAGCTGAGTCTGGTGTTACTGACTAAGGAACAACCTGACTCAGGCTCTAGATGGCTG
1428 TGTCAGAGCTGAGTCTGGTGTTAC 1429
AAT - - T - A GA
CAG GTC AGAGC TGAGTC GGT GTT CT C
||| ||||| ||||| ||||| ||||| ||
GTC TAG TCTCG ACTCAG CCA CAA GA /
GG- A G T A G AT
GAM109
CAGAGATCAGAATACGAAGCTTCCTCTCAGCATCATGGGAGGAGATAAAATAATTCATTCTATGGTCTTTG 1443
GGAGGAGATAAAATAATTCATTCT 1444
-- AC GC----- GC

CAGAGATCA GAAT GAA TTCCTCTCA A
 ||||| ||| || |||||
 GTTTCTGGT CTTA CTT GAGGAGGGT T
 AT -- AATAAAATA AC
 GAM110
 CAGCACCATAACACTAGACCCAGCCTAACTGTCCTGCAACAGGGGATGGGTAAAAGGGATGATGGCGCTG 1462
 TAACACTAGACCCAGCCTAACTGT 1463
 A AACA- AG- G AA CC
 CAGC CCAT CT ACCCA CCT CTGT T
 ||| ||| || ||||| |||
 GTCG GGTA GA TGGGT GGG GACA G
 C GTAGG AAA A -- AC
 GAM111 CAGCATCTGGTCCTTTTGTGTGACCCACCCCATCCCGGAGCTGGTCGGGTCTGGCTGGATGTGCTG
 1487 TCTGGTCCTTTTGTGTGACCCAC 1488
 CTG TTTT T - --- AT
 CAGCAT GTCC GCTG GACCC ACC CC C
 ||||| ||| ||| ||||| ||| ||
 GTCGTG TAGG CGGT CTGGG TGG GG /
 --- T--- - C TCGA CC
 GAM112 CAGCCACGCCTGGGGAGCCTGCCTGGGGCCATGTGACCATGGCCTCTCCCTGGGAACGGGCTG
 1494 TGGCCTCTCCCTGGGAACGGGCTG 1495
 ACG TG CCTGCCTG T
 CAGCCC CC GGGAG GGGCCATG G
 ||||| || ||||| |||||
 GTCGGG GG CCCTC TCCGGTAC A
 CAA GT ----- C
 GAM113
 CAGGCCCTAGGAGGGCGAGGGCTTAGTAGGTATCTTCAGGGTCAGAGCCTGAGTCCTCGCCTTGTTGGTTCTG
 1515 TAGGAGGGCGAGGGCTTAGTAGGT 1516
 GC T G AGT A TCA
 CAG CC AG AGGGCGAGGGCTT AGGT TCT G
 ||| ||| ||||| ||||| |||||
 GTC GG TT TTCCGCTCCTGAG TCCG AGA G
 TT - G --- - CTG
 GAM114 CAGTGTGCACGTGGGAACCTGTCCCCAGGCTGGAGCATAGGGGCATGATCCCAGCTCACTG 1525
 TAGGGGCATGATCCCAGCTCACTG 1526
 T ACG ACC CAG T
 CAGTG GC TGGGA TGTCCC GC G
 ||||| || ||||| ||||| ||
 GTCAC CG ACCCT ACGGGG CG G
 T --- AGT ATA A
 GAM115 CATCTCACTAAGTGCTGATCAGTTTTGATTCAGTTGGAGTAGAGCACATAGGTTCTTTGGAGATG 1575
 TCTCACTAAGTGCTGATCAGTTTT 1576
 ACT T GATCA A A
 CATCTC AAG GCT GTTTTG TTC G
 ||||| ||| ||| ||||| |||
 GTAGAG TTC TGG CGAGAT AGG T
 GT- T ATACA G T
 GAM116
 CATGAAAGAAGCCTGGTTACTGATTTGTATAAAATGTACTCTTAAAGTATAAAGTATAAGGTAAGGTAAATTTTCATG
 1589 TAAAGTATAAGGTAAGGTAAATTT 1590

GAA GGT GAT AAAA CT
 CATGAAA GCCT TACT TTGTAT TGTACT T
 ||||| ||| ||| ||||| |||||
 GTACTTT TGGA ATGG AATATG ATATGA /
 AAA --- --- AA-- AA
 GAM117 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1616
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- T
 CAT ACA AGAC CATTGAC GGTGGG T
 ||| ||| ||| ||||| |||||
 GTG TGT TCTG GTAGCTG CCGCCC T
 - CT - GCGAA A
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1643
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
 ||| ||| ||| ||||| |||||
 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1644
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
 ||| ||| ||| ||||| |||||
 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1645
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
 ||| ||| ||| ||||| |||||
 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1646
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
 ||| ||| ||| ||||| |||||
 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1647
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
 ||| ||| ||| ||||| |||||
 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1648
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT

CAT ACA AGAC CATTGAC GGTGG T
||| ||| ||| ||| ||| |||
GTG TGT TCTG GTAGCTG CCGCC /
- CT - GCGAA AT
GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1649
TGACAACAGACACATTGACATGGG 1617
G AC A ATG-- GT
CAT ACA AGAC CATTGAC GGTGG T
||| ||| ||| ||| ||| |||
GTG TGT TCTG GTAGCTG CCGCC /
- CT - GCGAA AT
GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1650
TGACAACAGACACATTGACATGGG 1617
G AC A ATG-- GT
CAT ACA AGAC CATTGAC GGTGG T
||| ||| ||| ||| ||| |||
GTG TGT TCTG GTAGCTG CCGCC /
- CT - GCGAA AT
GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1651
TGACAACAGACACATTGACATGGG 1617
G AC A ATG-- GT
CAT ACA AGAC CATTGAC GGTGG T
||| ||| ||| ||| ||| |||
GTG TGT TCTG GTAGCTG CCGCC /
- CT - GCGAA AT
GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1652
TGACAACAGACACATTGACATGGG 1617
G AC A ATG-- GT
CAT ACA AGAC CATTGAC GGTGG T
||| ||| ||| ||| ||| |||
GTG TGT TCTG GTAGCTG CCGCC /
- CT - GCGAA AT
GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1653
TGACAACAGACACATTGACATGGG 1617
G AC A ATG-- GT
CAT ACA AGAC CATTGAC GGTGG T
||| ||| ||| ||| ||| |||
GTG TGT TCTG GTAGCTG CCGCC /
- CT - GCGAA AT
GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1654
TGACAACAGACACATTGACATGGG 1617
G AC A ATG-- GT
CAT ACA AGAC CATTGAC GGTGG T
||| ||| ||| ||| ||| |||
GTG TGT TCTG GTAGCTG CCGCC /
- CT - GCGAA AT
GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1655
TGACAACAGACACATTGACATGGG 1617
G AC A ATG-- GT
CAT ACA AGAC CATTGAC GGTGG T

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 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1656
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
 ||| ||| ||| ||| ||| ||| |||
 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1657
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
 ||| ||| ||| ||| ||| ||| |||
 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1658
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
 ||| ||| ||| ||| ||| ||| |||
 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1659
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
 ||| ||| ||| ||| ||| ||| |||
 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1660
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
 ||| ||| ||| ||| ||| ||| |||
 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1661
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
 ||| ||| ||| ||| ||| ||| |||
 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTTCGATGGTCTTCTGTGTG 1662
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
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GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1663
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
 ||| ||| ||| ||| ||| |||
 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1664
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
 ||| ||| ||| ||| ||| |||
 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1665
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
 ||| ||| ||| ||| ||| |||
 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1666
 TGACAACAGACACATTGACATGGG 1617
 G AC A ATG-- GT
 CAT ACA AGAC CATTGAC GGTGG T
 ||| ||| ||| ||| ||| |||
 GTG TGT TCTG GTAGCTG CCGCC /
 - CT - GCGAA AT
 GAM119
 CATGCTTGAGCAAAACAACAGACATTGGTGAGGGCTGGGTCGCCTGGACCACAAGTTTGACTGATGTTTGCCAG
 GCGTG 1667 AACAAACAGACATTGGTGAGGGCTG 1668
 A ACAA--- AT- GA TG
 CATGCTTG GCAAA CAGAC TGGT GGGC G
 ||||| |||| |||| ||| |||
 GTGCGGAC CGTTT GTTTG ACCA TCCG G
 - GTAGTCA AAC GG CT
 GAM120 CATGTGATGATAATGGTCTTCTCGCCATCCCAAGATGGGTTGGCAGCCATGATCTTTGCATG 1684
 TGTGATGATAATGGTCTTCTCGCC 1685
 TG T A T TCTC T AA
 CATG A GAT ATGG CT GCCA CCC G
 |||| | ||| ||| || ||| |||
 GTAC T CTA TACC GA CGGT GGG /
 GT T G - ---- T TA
 GAM121 CATGTTATACCTGGAAAGGACCGTGGGCACTAATCTGCACTTTGTTCCAGGTAATCCATG 1699
 TGTATACCTGGAAAGGACCGTGG 1700
 TTA AG CC TG CA
 CATG TACCTGGAA GA G GG C
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GTAC ATGGACCTT TT C CT T
 CTA GT CA GT AA
 GAM122
 CATGTTATAGATTATTTGGAAAGACTGTATTTCCCATTGTCACAAAGCAAGTTTATTTCAAATGCTTTATCACATG
 1702 TGTTATAGATTATTTGGAAAGACT 1703
 T T - - ATTTCCCA
 CATGT ATAGA TATTTGGAA AGACT GT T
 |||| |||| |||| |||| ||
 GTACA TATTT GTAAACTTT TTTGA CG T
 C C A A AAACACTG
 GAM123 CATTCTGAGGGGTTGGCCTCATGACCCAAAGACACCCATTAGGCCCCAGCTCCAACATTGGGATG
 1722 TTAGGCCCCAGCTCCAACATTGGG 1723
 TGA--- -- C ACCCAA
 CATTCC GGGGTT GGCCT ATG A
 |||| |||| |||| ||
 GTAGGG CCTCGA CCGGA TAC /
 TTACAA CC T CCACAG
 GAM124
 CATTCTGGATTTGGTCGATTGCTTCTTTTAGTATCTTTAACTTATTAGATCTCAAACCTCAGCTGCACATCAGAATG
 1734 TTAGATCTCAAACCTCAGCTGCACA 1735
 ATTT- C -- CT- TTTT ATC
 CATTCTGG GGT GA TTG TCT AGT T
 ||||| ||| ||| ||| ||
 GTAAGACT TCG CT AAC AGA TCA /
 ACACG A CA TCT TTAT ATT
 GAM125
 CCAACAGGATGCCACGCTGGGCCGAGCGACTATTTCTGCCAATGTTGCTCACTCGGTGTACGTCCTGGAGG
 1741 ACTCGGTGTACGTCCTGGAGG 1742
 AA CC CC TATTTT
 CC CAGGATG ACGCTGGG GAGCGAC C
 || ||||| ||||| |||||
 GG GTCCTGC TGTGGCTC CTCGTTG T
 AG A- A- TAACCG
 GAM126
 CCAACCACATGGCACATCGGGCTATTTGAACACGGTGACTGTCTCTCCCAGATGGATCCCTCTGTGCTTCTTGGG
 CGG 1770 TGGCACATCGGGCTATTTGAACAC 1771
 AA CAT TC -- AACAC T CT
 CC CCA GGCACA GGG CTATTTG GG GA G
 || ||| |||| ||| ||||| ||||
 GG GGT TCGTGT CCC GGTAGAC CC CT /
 CA TCT CT TA ----- T CT
 GAM127
 CCAACCAGAGCAGTTCGACTGGGCCATCAATGACCGCATCAATGAGATGGTCCACTTCGACCTGCCAGGGCAGG
 1780 TGAGATGGTCCACTTCGACCTGCC 1781
 AA AGA T C- AA-- CC
 CC CC GCAG TCGA TGGGCCATC TGA G
 || || |||| ||| ||||| ||
 GG GG CGTC AGCT ACCTGGTAG ACT /
 AC GAC C TC AGTA AC
 GAM128
 CCAAGACCAACAGGATGCCACGCTGGGCCGAGCGACTATTTCTGCCAATGTTGCTCACTCGGTGTACGTCCTG

GAGGACTCTATTGTGG 1786 GCTCACTCGGTGTACGTCCTGGAG 1787

---- -- AA CC CC TATTC
CCA AGA CC CAGGATG ACGCTGGG GAGCGAC C
||| ||| || ||||| ||||| |||||
GGT TCT GG GTCCTGC TGTGGCTC CTCGTTG T
GTTA CA AG A- A- TAACCG

GAM129

CCAAGTTCATTGAGGTATCTAAAGAGGCCCGGAAGCGGTTCTGGGGCCCCCTGCACCCCTCCTTCAACCTGG
1803 TGAGGTATCTAAAGAGGCCCGGAA 1804
A CATT TATCTAA A- - G
CCA GTT GAGG AG GGCCC GGAA C
||| ||| ||| || ||||| |||||
GGT CAA CTCC TC CCGGG CCTT G
C CTTC CCACG-- CC T G

GAM130

CCAATGGCACATGGACTGGTGTAGCAAGGAAGGGACCCTTTGTTTAGAACGGGTCAGATGGGCCGTGGG 1812
TGGCACATGGACTGGTGTAGCAA 1813
A A G- G GTT- AAG
CC ATGGC CAT GACT GT AGCAAGG G
|| ||||| ||| ||||| || |||||
GG TGCCG GTA CTGG CA TTGTTTC G
G G GA G AGAT CCA

GAM131

CCAATGGGAGGTTTGTGTACAGTCAGTGAAATTGAAGAACATTTATGTCATTAATGGACTTACATAGCTATTGG
1825 TGTCATTAATGGACTTACATAGCT 1826
GAGGT C ---- AAT GA
CCAATGG TTGTGTA AGTC AGTGA TGAA A
||||| ||||| ||||| ||||| |||||
GGTTATC GATACAT TCAG TTA CT ATTT /
----- - GTAA GT- AC

GAM132

CCACCCCATGATTTTAGCATTTCATTGATGATTCTTGTGTGAACGTTTAATACATTTGTGATTATGGAATTTTAACGT
GG 1842 TTAGCATTTCATTGATGATTCTTGT 1843
CCCAT GCAT T - CT- G
CCAC GATTTTA TCAT GATG ATT TGT T
||||| ||||| ||||| ||||| |||||
GGTG TTAAGGT AGTG TTAC TAA GCA G
CAATT ATT- T A TTT A

GAM133

CCACCTGCCGGGAGCATGCCTCTGCGCCACTGGGGGATGGCCAGGGCAGTAAGCCCGTTGGGGATGG 1857
TGCCAGGGCAGTAAGCCCGTTGG 1858
-- GC AGCA- T C -TG
CCA CCT CGGG TGCC CTG GCCA C G
||| ||| ||||| ||||| ||||| |||||
GGT GGG GCCC ACGG GAC CGGT G /
AG TT GAATG - - A GG

GAM134 CCACGCCTGGCTAATTTTTGTATTTTTAATAAAGATGCAGTGTACCATATTGGCCAGGCTGG 1880
TGCAGTGTACCATATTGGCCAGG 1881
C TT----- A
CCA GCCTGGCTAAT TTGTATTTTT A

||| ||||| |||||
 GGT CGGACCGGTTA GACGTAGAAA /
 - TACCACTGT T
 GAM135
 CCACGGGCACCTACCACGGGGACAGCGACCTGCAGCTGGAACGCATCAACGTGTACTACAATGAGGCCACCGG
 CGGCAGTACGTGCCCCGCGCGCTGCTCGTGG 1887 TGAGGCCACCGGCGGCAGTACGTG 1888
 CTACCA A G AC A AAC A AC T
 CCACGGGCAC CGGGG CA CG CTGC GCTGG GC TCA GTG A
 ||||| ||| || ||| ||| ||| |||
 GGTGCTCGTG GCCCC GT GC GACG CGGCC CG AGT CAT /
 CCGC-- - - AT G AC- G AA C
 GAM136
 CCACTGCTTCATGAGCTCAAATCTGTTTTTCTAGCTAAGAGACCACAGGCCAAAGAACTAAAGGGCAAGCAGGG
 1898 TGAGCTCAAATCTGTTTTTCTAG 1899
 A CATGA AAATCT CTA AAGAG
 CC CTGCTT GCTC GTTTTTT GCT A
 || |||| ||| ||||| |||
 GG GACGAA CGGG CAAGAAA CGG /
 - ---- AAAT-- C-- ACACC
 GAM137
 CCAGCTTCTAGATGACATAGAATGACATGTAATGCTAAATTTTCATTTTGGCTTTGCAAGTCATGAAGCTTAGG 1907
 TGACATAGAATGACATGTAATGCT 1908
 -- TAGATGACATAGA A T TT
 CC AGCTTC ATGAC TGTA GCTAAA T
 || |||| |||| |||| ||||
 GG TCGAAG TACTG ACGTT CGGTTT C
 AT ----- A T TA
 GAM138
 CCAGGATCAGGAGGACCCCGAGGAGTTCTACGTGCTGAGCGAGACCACCTTGGCCCAGCCCCAGAGCCTGG
 1922 TCAGGAGGACCCCGAGGAGTTCTA 1923
 A A A ACC-- AGT A GC
 CCAGG TC GG GG CCGAGG TCT CGT T
 |||| || ||| |||| ||| |||
 GGTCC AG CC CC GGTTC AGA GCG /
 G A - GACCC ACC - AG
 GAM139
 CCAGGCCGGGCCACCGCCGGCCCCCTGGGCTGTCCGCGGGAGCCGACTGCCTGAACAGCTTTACCGCCGGGG
 TGCCTGGCTTCGTGCTGG 1947 AACAGCTTTACCGCCGGGGTGCCT 1948
 ----- C G CCCCT C C G C
 CCAG GCCGGGC ACC CCGGC GGGCTGT CG GG AG C
 ||| ||||| || |||| ||||| || |||
 GGTC CGGTCCG TGG GGCCG TTCGACA GT CC TC G
 GTGCTT - - CCAT- A - G A
 GAM140
 CCATCCCCCAGCTGGCATACTGTGTAGTGCAGTTTTTTAGGAAAGAGGACCGCACCCCTCAGGGAACCAAGTGGTGA
 TGG 1954 TGGCATACTGTGTAGTGCAGTTTT 1955
 C CA CATA TGTA A AG
 CCATC CC GCTGG CTG GTGC GTTTTT G
 |||| || |||| ||| |||| ||||
 GG TAG GG TGACC GAC CACG CAGGAG A

T -- AAGG TCC- C AA
 GAM141 CCATGACACAGTTCTGTCTTGGCCAGGGACCTGGCTGGTGGAGAGGTGGAAGTTGCATGG 1967
 TGACACAGTTCTGTCTTGGCCAGG 1968
 ACA---- G G -TG G
 CCATG CA TTCT TC T GCCAG G
 |||| || ||| ||||
 GGTAC GT GAGA GG G CGGTC A
 GTTGAAG G - T GT C
 GAM142 CCATGGAGTAGATTACAGCGTGTTGGACAAGGACATTCCCCCGCGTGAAGGCACACTCCATGG 1983
 TGGAGTAGATTACAGCGTGTTGGA 1984
 AGATTACA TT CAAG
 CCATGGAGT GCGTG GGA G
 ||||| |||| ||
 GGTACCTCA TGCGC CCT /
 CACGGAAG CC TACA
 GAM143
 CCCAATTAACATCGAGGTCTCAGCAAACAATTACCACATTTAACATATATGGAGTTAAAGTAGATTGGATTTGCTG
 AAAATCGGTGCTGGG 1992 TCTCAGCAAACAATTACCACATTT 1993
 ATTAA GGTC -- ACC A ATAT
 CCCA CATCGA TCAGCAAA CAATT AC TTAAAC A
 ||| |||| ||||| |||| || |||||
 GGGT GTGGCT AGTCGTTT GTTAG TG AAATTG /
 C---- AAA- AG A-- - AGGT
 GAM144
 CCCAGGATGAGTTCTACCGCAGCGGCTGGGCCCTGAACATGAAGGAGCTGAAGCTGCTGCAGACCATCGGG
 2008 TGAGTTCTACCGCAGCGGCTGGGC 2009
 AG A T ACC G- - GAA
 CCC GATG GT CT GCAGCGGCT GGC CCT C
 ||| |||| || || ||||| ||| |||
 GGG CTAC CA GA CGTCGTCGA TCG GGA A
 -- - - - AG A AGT
 GAM145 CCCCATCTAAACTGGAGAAGCCCCCAACACTTTTAAGCTATGTGGAGGGGTGGGAGTTTGGGAGGGG
 2020 TCTAAACTGGAGAAGCCCCCAACA 2021
 AT GGAGAA CAA TTTTA
 CCCC CTAAACT GCCCC CAC A
 |||| ||||| |||| |||
 GGGG GGTTTGA TGGGG GTG /
 AG GGG--- AG- TATCG
 GAM146 CCCCTTCCCATCCCCCACC CGCCTGCCATGGGCCAGTCCTAGGAGCAGCTGGGGATGAAGGGG
 2040 TAGGAGCAGCTGGGGATGAAGGGG 2041
 CC CCACCC C - AT C
 CCCCTTC ATCCCC GC TGC CC GGG C
 ||||| |||| || ||| || |||
 GGGGAAG TAGGGG CG ACG GG CCT A
 -- T----- - A AT G
 GAM147 CCCGGCAGCACCCCTAGCAAATAGGTCTGTATCAAAGATTCTGTACAGCTGGTTTTGGGGGTGAAGGG
 2112 CAGCTGGTTTTTGGGGGTGAAGGG 2113
 GGCAG GC A T T AAG
 CCC CACCCCTA AAAT GG CTGTA CA A
 ||| ||||| |||| || |||| ||

GGG GTGGGGGT TTTG TC GACAT GT /

AA--- -- G - - CTT

GAM148

CCCGGCCCGGAATGGAATGGGATTCACGCGACTGCACCAGGTGGGCAATTTGTTGATCTCAGGGCACGTGG

2125 TGGAATGGGATTCACGCGACTGCA 2126

- - GGAATGGAA C C C A A

CC CG GCCC TGGGATT ACG GA TGC CC G

|| || ||| ||||| ||| || ||| ||

GG GC CGGG ACTCTAG TGT TT ACG GG G

T A ----- T - A - T

GAM149

CCCGGCCTCGTTGCCCCCTGGCGACCCTCAGCTCATCGCTATCATCGTGGGGCAGCTCAAGAGCAGGG 2132

TATCATCGTGGGGCAGCTCAAGAG 2133

G - C-- CTG CCCTC TC

CCC GC CT GTTGCCCC GCGA AGC A

||| || ||||| ||| |||

GGG CG GA CGACGGGG TGCT TCG /

A A ACT --- ACTA- CT

GAM150

CCCGGGGACTGAGAGTTAAGGAGAGTTGGAGGCTTTACTGGGCCACAGGGTTCCTACTCGCCCCTGGG 2141

TGAGAGTTAAGGAGAGTTGGAGGC 2142

ACTGA TA AG GA T

CCCGGGG GAGT AGGAG TTG GGCTT A

||||| ||| ||||| ||| |||||

GGGTCCC CTCA TCCTT GAC CCGGG C

CG--- -- GG A- T

GAM151 CCCTCATACCAACTGTGGACTTGGAATATCAGCAGAGTAGTAGGCACAGTTGTAAAAAGGG 2157

TACCAACTGTGGACTTGGAATATC 2158

CATAC GA TGGAATA A

CCCT CAACTGTG CT TC G

||| ||||| || ||

GGGA GTTGACAC GA AG C

AAAAT G- TGATG-- A

GAM152 CCCTGGCAGACTTCACACCTCATTGCTTTACCCCTGGGCCTGGGGAAATGTCTGTACTTTGGG 2170

TGGCAGACTTCACACCTCATTGCT 2171

TG--- TTCACA TT TAC

CCC GCAGAC CCTCA GCTT C

||| ||||| ||||| |||||

GGG TGTCTG GGGGT CGGG C

TTTCA TAAA-- C- TCC

GAM153

CCGCCCCGTGCCCCGCGCGCCCCCTGCGGGGGCGAGGTGCGGCCTGGCGCTGCGGGCCTGTGCCCCTCGG

CGGGGGGTGCGGGTGCAGCGGGCGG 2182 TGTCGCCCTCGGCGGGGGGTGCGG 2183

C G C - - GGT GC

CCGCCC GT CC CGCC GCGCCCCCTGC GGGGGCGA CGGGCCTG G

||||| || ||| ||||| ||||| |||||

GGCGGG CA GG GTGG CGTGGGGGGCG CTCCCGCT GTCCGGGC C

- - C G G --- GT

GAM154 CCGCGAGAAGACGTGGAACATCTCGTTGCGGGCTGCGGCTTCCTCGGCGTCTACTACGTCCG 2194

TGCGGCTTCCTCGGCGTCTACTAC 2195

- - A --- ---- T T
 CCG CG AG AGACGT GGAA CA CTCG T
 ||| || ||||| ||| || ||||
 GGC GC TC TCTGCG CCTT GT GGGC C
 T A A GCT CGGC C G
 GAM155
 CCGCGGGTGGAGGTTCGATGGCAGCATCATGGAAGGGGGCGGCCAGATCCTGAGAGTCTCTACGGCCTTGAGCT
 GTCTCCTAGGCCTCCCCTTGCGG 2204 TGGCAGCATCATGGAAGGGGGCGG 2205
 T GAT-- A T AA-- GGC A
 CCGCGGG GGAGGTC GGCAGC TCA GG GGGGGC CAG T
 ||||| ||||| ||||| ||| ||||| |||
 GGCGTTC CCTCCGG CTGTCTG AGT CC TCTCTG GTC /
 C ATCCT - T GGCA AGA C
 GAM156
 CCGCTTCACTGGCACCATGGATGCCTTCGTGAAGATCGTGAGGCACGAGGGCACCAGGACCCTCTGGAGCGG
 2227 TGGCACCATGGATGCCTTCGTGAA 2228
 CT CA A A AAGA G
 CCGCTTCA GG CC TGG TGCCTTCGTG TC T
 ||||| || || || ||||| ||
 GGCGAGGT CC GG ACC ACGGGAGCAC GG G
 CT CA - - ---- A
 GAM157
 CCGGATGGAACGTACTCTGTGCTTATATCATCACAGAGCTTGGATGAAAGAGAGCGAGAAGAGTTCTATAGG
 2240 TGAAAGAGAGCGAGAAGAGTTCTA 2241
 GG GTAC G ATA- A A
 CC ATGGAAC TCT TGCTT TCATC CAG G
 || ||||| || ||||| ||||| |||
 GG TATCTTG AGA GCGAG AGTAG GTT /
 A- AGA- - AGAA - C
 GAM158 CCGGGGCGCAATGCGAGCGGCTGGCGTAGGCTTGGTGGACTGTCACTGCCACCTCTCCGCCCCGG
 2266 TGCCACCTCTCCGCCCCGG 2267
 CAATGC C C TA TTGG
 CCGGGGCG GAG GG TGGCG GGC T
 ||||| ||| || ||||| |||
 GGCCCCGC CTC CC ACCGT CTG G
 ----- T - CA TCAG
 GAM159 CCTAACGCCTCGGTCAGCAACGGAGCTACCTTCCTGGAGTCCCCACGTGCGCCGGGGCTGGG 2277
 TAACGCCTCGGTCAGCAACGGAGC 2278
 AC CA AC--- AG A TT
 CCTA GCCTCGGT GCA GG CT CC C
 ||| ||||| ||| || ||||
 GGGT CGGGGCCG CGT CC GA GG /
 -- -- GCACC CT - TC
 GAM160 CCTCCACTACTGGTTGTGGAGTCCCAGAAGGATCCCGAGAACAGCCCTGTGGTGCTTTGG 2290
 TCCCGAGAACAGCCCTGTGGTGCT 2291
 TC-- T- ---- AG CA
 CC CACTAC GGTTGT GG TCC G
 || ||||| ||||| || |||
 GG GTGGTG CCGACA CC AGG /
 TTTC TC AGAG CT AA

GAM161

CCTCCTGACACCCTTCTCCCACTCTCCTAGGCATTCTGGACCTCTGGGTTGGGATCAGGGGTAGGAATGG 2295
 TGACACCCTTCTCCCACTCTCCTA 2296
 -- AA TC CT CT CATT
 CC TCCTG C CCCT TCCCA CTC AGG C
 || ||||| |||| |||| ||||
 GG AGGAT G GGGA AGGGT GGG TCC /
 TA -- CT T- TC AGGT

GAM162

CCTGAAGCCGACCATCTGCTCCGACCAGGACAACACTACTGCGTGACTGTGTCTGCTAGTGCCGGGCATTGGG 2312
 GACTGTGTCTGCTAGTGCCGGGCAT 2313
 TG A AC CT TCC - GACA TA
 CC A GCCG CAT GC GAC CAG AC C
 || |||| |||| |||| ||||
 GG T CGGC GTG CG CTG GTC TG T
 GT A C- AT T-- T AG-- CG

GAM163

CCTGCGCACGCGTCGCGAGCCATCTCCGCGCACAGTGGTGGCCACCGCGACTGGTGCTGAAGTGTGGGCGTGTG
 CCGGG 2328 TCGCAGCCATCTCCGCGCACAGTG 2329
 C CAGC TC C A G C
 CCTG GCACGCGTCG CA TC GCGC CAGT GTGG C
 |||| |||| |||| |||| ||||
 GGGC CGTGTGCGGC GT AG CGTG GTCA CGCC /
 - T-- GA T - G A

GAM164 CCTGGCACCTGTGTTCCAGCCCACATCCCACATGCGGCTCGGGCTTCGGAACACGGAGTGGCCGGG
 2345 TGGCACCTGTGTTCCAGCCCACAT 2346
 - - -- ACATC AC

CCTGGC AC CTGTGTTCC AGCCC CC A
 |||| |||| |||| |||| ||||
 GGGCCG TG GGCACAAGG TCGGG GG T
 G A CT CTC-- CG

GAM165

CCTGGCAGACAGGCGGGCAAACAGTGAGCGCCCCACCCAGACCGGCTGCTGCGCCCCCTCCTGCCAGG 2363
 TGGCAGACAGGCGGGCAAACAGTG 2364
 AC C AAA G GCCAC
 CCTGGCAG AGG GGGC CAGT AGC C
 |||| |||| |||| |||| ||||
 GGACCGTC TCC CCCG GTCG TCG C
 C- - C-- - GCCAGA

GAM166 CCTTTATTAGTCCACCCCTTGGAGCTAGACATCCTGTACTTAGTCACGGGGATGGTGGGAAGAGG 2389
 TATTAGTCCACCCCTTGGAGCTAG 2390

ATTAG -- GA -- AT
 CCTTT TCCACC CTTG GCTA G AC C
 |||| |||| |||| |||| ||||
 GGAGA AGGTGG GGGG TGAT C TG /
 ---- TA AC TA TC

GAM167 CCTTTGCCCGCATGCTGATCGCGCAAGAGGGGCTGCTGTGCGGTGGCAGTGCTGGCAGCACGG 2400
 GTGCGGTGGCAGTGCTGGCAGCAC 2401
 T-- C - G AG G
 CC TTGCC GCA TGCT ATCGCGCA AG G

II IIII III IIII II
GG GACGG CGT ACGG TGGCGTGT TC /
CAC T G - CG G
GAM168 CCTTTATATGATGATCTGGAGAATTCTGCTCTTTGATAACAACACTCAGGATTTTTTTTGATCACGTTTGG
2422 TATGATGATCTGGAGAATTCTGCT 2423
TTTTAT A TG CTCT A
CC ATG TGATC GAGAATTCTG TTG T
II III IIII IIII III
GG TGC ACTAG TTTTAGGAC AAC A
TT---- - TT TC-- A
GAM169 CGACCCTCGACTGCGGGGCCCGGGCGGGCGGCTAGCAGATCCAGCGGATGAAGCGGTTCG 2434
TAGCAGATCCAGCGGATGAAGCGG 2435
- - A - GCCCG- G
CGACC CT CG CTGC GGG GGCG C
IIII II IIII III III
GCTGG GA GT GGCG CCT TCGC G
C A A A AGACGA G
GAM170
CGAGATTGAGCAATAACAGGTCTGTGATGCCCTTAGTTGTCCGGCCCCGGACAACGACAGGATTGACAGATTGATA
GCTCTTTCTCG 2448 TAACAGGTCTGTGATGCCCTTAGT 2449
TT AATAACA - G CTTA G
CGAGA GAGC GGTCTGT GAT CC GTTGTCCG C
IIII III IIII III II IIII
GCTCT CTCG TTAGACA TTA GG CAACAGGC /
TT ATAG--- G - ACAG C
GAM171 CGCAGCCCTGCTCGTGGGTCCAAGAGCTGCTTACTTCTGGGGGCACCCATGCTGAGGGGGGCTGCG
2458 GGGGGGCACCCATGCTGAGGGGGGCT 2459
G --- ---- AG CTG
CGCAGCCCT CTC GTGGGT CCA AG C
IIIIIII III IIII III II
GCGTCGGGG GAG TACCCA GGT TC /
- TCG CGGG CT ATT
GAM172
CGCGTGCCCCGCCCGCTGGAGCACCTGCCACCGAGGCGCGCGTGGGGCCACTGCCGTGGCGGCGGCTGCC
TCCTCACACTCGGCTCCGCGCCGCTCCGCGCACCGTGCGTCCC GCGTGGGGCGCCTCG 2477
TCACACTCGGCTCCGCGCCGCTC 2478
C- CC T -- CT-- ACC C ACTGCC C C C
CG GTGCCCCGC GC GGAGC AC GCC GAGGCG GCGTGGGGCC GTGG GG GG T
II IIIII II IIII II III IIII IIII III II
GC CGCGGGGTG CG CCTCG TG CGG CTCCGC CGCGCCTCGG CACT CC CC G
TC -- C CG CCAC C-- - CTCA-- - T C
GAM173 CGCTTTCGCTCCGCGTTCGCGCTTTCGACCAGAGGGGGGGGGGGCGCACCTCGCTTACCGAAAGTG
2516 TCGCTCCGCGTTCGCGCTTTCGAC 2517
CTCC TTC- TT GA A
CGCTTTCG GCG GCGCT C CC G
IIIIII III IIII I II
GTGAAAGC CGC CGCGG G GG A
CATT TCCA GG GG G
GAM174
CGGGGGAGTTGTGGTGCTTCTGGGTCTCTGGGCCCCGCTGCTGGCCTGGGATGCCCTCATGTTGGGAAGCAT
TCCGTGCCCCCCG 2524 GGGATGCCCTCATGTTGGGAAGCA 2525

A - TG G TCTCT -- -- T
CGGGGG GT TG GTGCTTCT GG GGGC CCC GCC G
||||| || ||||| || ||| ||| ||
GCCCCC CG GC TACGAAGG TT CCGG GGG CGG C
- T CT G GTACT TA TC T

GAM175

CGTGAGCCAATTCTCCCTAATAAACTCCCTTATATATGTAGTCATATATCCTACTAGTTCTGTTCCCTCTGGAGAATC
ATG 2532 TATCCTACTAGTTCTGTTCCCTCTG 2533

GCCAA CT--- - CCCTT- T
CGTGA TTCTCC AATA AACT ATATATG A
||||| ||||| ||| ||| |||||
GTACT AAGAGG TTGT TTGA TATATAC G
----- TCTCC C TCATCC T

GAM176 CTACCCTCACCCCATCACAGCACCCCTGAGAATCACGGGTCCAACCTGTGTGGGAGGGGGGCTGTGG
2540 TACCCTCACCCCATCACAGCACCC 2541

-- AC T C--- - AG
CTAC CCTC CCCA CACAG ACCC TG A
||||| ||||| ||||| ||||| |||||
GGTG GGGG GGGT GTGTC TGGG AC /
TC GA - AACC C TA

GAM177

CTATAAACACGGAAGCCAAATTTGGGAAAGGTGTGTTATTAAGAATATGTTGCGACAAGCGTGGTCCGTGCTTTG
AG 2564 TGTTGCGACAAGCGTGGTCCGTGC 2565

A - AA AA GGAAA TG AT
CT TAAA CACGG GCCA TTTG GG TGTT T
|| ||||| ||||| ||||| || |||||
GA GTTT GTGCC TGGT GAAC TT ATAA A
- C -- GC AGCG- GT GA

GAM178 CTATCATCATCTAGCACCTGTCCGGTTCACCGTGAGCCTTGGGCAGGACGCTGCAGTGTTGATGG
2583 TATCATCATCTAGCACCTGTCCGG 2584

T C- A- -- CCC
CTATCA CAT TAGC CCTGTCC GGTT C A
||||| ||| ||||| ||||| |||||
GGTAGT GTG GTCG GGACGGG CCGAG /
T AC CA TT TGC

GAM179 CTATTTTTTATTTGCAACTACATGATTTACACAATTCTCTTAAACAACGACATAAAATAG 2595
CTTAAACAACGACATAAAATAG 2596

TTAT CAACTACAT- TTTCA
CTATTTT TTG GA C
||||| ||| ||
GATAAAA AGC CT /
TAC- AACAAATTCT TAACA

GAM180 CTCCAGAGCTCCTATAGGGCAAGACACTGTTTCTCATATATTTCTGGATCCTTGAGCTTAGCTCGGAG
2600 ATTTCTGGATCCTTGAGCTTAGC 2601

- --- TAT CA- CAC TTC
CTCC AG AGCTCC AGGG AGA TGT T
||||| ||||| ||||| ||||| |||||
GAGG TC TCGAGG TCCT TCT ATA /
C GAT T-- AGG TT- TAC

GAM181 CTCCCACCCTGCCGGCCTCAGGAACAGCTGGCTCCAGATGGGGGGTGGCAGGCAGTGAAGTGGGAG
2619 TGGGGGGTGGCAGGCAGTGAAGTG 2620

----- G AGGAACAG G
 CTCCCAC CCTGCCG CCTC CTG C
 ||||| ||||| ||| |||
 GAGGGTG GGACGGT GGGG GAC T
 AAGTGAC G GTA----- C
 GAM182
 CTCTCTCTTCCAGCTGCAGATGCCACACTGTCCTCTGCTTCCCGGGGACGAGGGGGTGGGCGGGACTGGGTAC
 AGGTTGGGAGGGGAG 2643 TGCCACACTGTCCTCTGCTTCCCG 2644
 T GCAGA A CT --TG - G
 CTCTC CTTCCAGCT TGCC CA GTCCT C CTTCC CG G
 |||| ||||| ||| || |||| | |||| ||
 GAGGG GAGGGTTGG ATGG GT CAGGG G GGGGG GC G
 - AC--- - -- CG GT A A
 GAM183
 CTCTGACAACAGTGGCTGGACTGAAATCCGCCGGGAAGCCTGGGTCTCCTCTAGCTTATTGGTGTCTCCAGAG
 2666 ACAACAGTGGCTGGACTGAAATCC 2667
 --- A - CT A CC G
 CTCT GACA CAGTG GCTGGA GA ATCCG GG A
 |||| ||||| ||||| || |||| ||
 GAGA CTGT GTTAT CGATCT CT TGGGT CC A
 CCT G T C- C -- G
 GAM184
 CTCTGCACAGCAGCCAGCAGGGATGTCCTCTCTAGAGATGGTTTATCAAGGGTACCCCATGAGAGGGCAGCTC
 CTGATGCAGCTGCCGGAAGAG 2682 TGAGAGGGCAGCTCCTGATGCAGC 2683
 GCACA C- G A- TAGAG TT CA
 CTCT GCAGC CA CAGGG TGTCCTCTC ATGG TAT A
 |||| |||| || ||||| |||| |||
 GAGA CGTCG GT GTCCT ACGGGAGAG TACC ATG /
 AGGC- AC A CG ----- CC GG
 GAM185 CTGACACATGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAG 2692
 TGACACATGAGGCAAAAGGCTCCG 2693
 A C-- - AAAAGGC A ATGC
 CTG CA ATGA GGC TCCG CG T
 ||| || ||||| |||| ||
 GAC GT TACT CCG AGGC GC C
 - AAC A GCAC--- - AGAC
 GAM186 CTGACTTGTTGGACGGGAATCTGGTTATTTGGCACCGCCCTTCTGTTCATAACAGGTTGG 2706
 TGACTTGTTGGACGGGAATCTGGT 2707
 TG -- ATC TAT
 C ACTTGT TGGACGGGA TGGT T
 | ||||| ||||| ||||
 G TGGACA ACTTGTCTT GCCA T
 GT AT CCC CGG
 GAM187 CTGAGAATTTCTCTTGCATGCCTTAGCTTTACAGCTTTTGCATTCCTGTGGATTATTCTCAG 2715
 TGAGAATTTCTCTTGCATGCCTTA 2716
 T- CTTGC- CTT T
 CTGAGAAT TCT ATGC AGCT T
 ||||| || |||| ||||
 GACTCTTA AGG TACG TCGA A
 TT TGTCTT TTT C

GAM188 CTGCACATATCATCGCGGAATTCATTTCGGCTTCCAGCAAGCTGACACTCCATGATACAAGCGG 2734
TATCATCGCGGAATTCATTTCGGCT 2735

ACA CGC ATTCAT CC
CTGC TATCAT GGA TCGGCTT A
||||| ||| |||||
GGCG ATAGTA CCT AGTCGAA /
AAC --- CAC--- CG

GAM189

CTGCATCAAAGGTAGACTTTCGCACAGGTTGTGAGGTTGGAGTCACAGTGTTATTTGTTGTACCTGATGTAG 2737
TCAAAGGTAGACTTTCGCACAGGT 2738

AA - TTTC- AGGT GGT
CTGCATCA GGTA GAC GCAC TGTGA T
||||| ||| ||| ||| |||||
GATGTAGT CCAT TTG TGTG ACACT G
-- G TTTAT --- GAG

GAM190 CTGCCAATGTTCGATTGGCCTTAATTTGGCAAAAAAAAAAATGGGGGGCCGAAATAAATGGGCGG 2744
TGGGGGGCCGAAATAAATGGGCGG 2745

AATGTCGA A- GGCAA
CTGCC TTGGCCTT ATTT A
||||| ||||| |||
GGCGG AGCCGGGG TAAA /
GTAAATAA GG AAAAA

GAM191 CTGCCAGTATGCTGTTAGTCAAGAGTCCTCAGTAGGAGAACTTGAGTGAAACGTACACCCAG 2753
TGCCAGTATGCTGTTAGTCAAGAG 2754

CCA CTG G AG- C
CTG GTATG TTA TCAAG TCCT A
||| |||| ||| ||||| |||
GAC CATGC AGT AGTTC AGGA G
CCA AA- G AAG T

GAM192 CTGCGAGCCATTCACCCAGCTGGTCCCTCCAAGACAGAGCCGGGGCCAGCGGCAGACTCCCAG 2763
TGCGAGCCATTCACCCAGCTGGTC 2764

C CCAT AC A TCCAAG
CTG GAG TC CC GCTGGTCCC A
||| ||| || ||| |||||
GAC CTC AG GG CGACCGGGG C
C ---- AC - CCGAGA

GAM193 CTGCTGCGCCCTGTCTCCGTCGGCTCTGCGGGCTCCCGGGCCTACAGCGGCTGCGGCAG 2783
TCCCGGGCCTACAGCGGCTGCGGC 2784

- - CC- TC CT
CTGCTGC GCC CTGT TCCG GGCT G
||||| ||| ||| ||| |||
GACGGCG CGG GACA GGGC TCGG /
T C TCC CC GC

GAM194

CTGGGAATATAATGGCCTATTCACCAGGCACCAGTTAAGGGTGCCACTAATTGGCCGTGAACTTCCCAG 2794
TATAATGGCCTATTCACCAGGCAC 2795

TATA T CACCA AGT
CTGGGAA ATGGCC ATT GGCACC T
||||| ||||| ||| |||||
GACCCTT TGCCGG TAA CCGTGG /

CAAG T TCA-- GAA
GAM195
CTGGGATGGGGACCGCGGAAGTTCCCACCGATGCGGCCGGCGGGGGCCCAGCCTTGGTCCCCAGCTCCGG
2807 TGGGATGGGGACCGCGGAAGTTCC 2808
A- C AAGT- A ATG
CTGGG TGGGGACCG GG TCCC CCG C
||||| ||||| || ||||| |||
GGCCT ACCCCTGGT CC GGGG GGC /
CG T GACCC C CGG
GAM196
CTGGGCTTTGGGCCTGGTGGTTGGGAGTCACCTACTGACATCGGGACTGACATTCCTGAACCCCTGGTATGAGG
CCAG 2826 TGACATTCCTGAACCCCTGGTATG 2827
G TGG T T - -- CCTA A
CTGG CTT GCC GG GGTT GGA GTCA CTG C
||||| ||| ||||| ||||| ||| |||
GACC GAG TGG CC CCAA TCCT CAGT GGC A
G TA- T - G TA CAG- T
GAM197
CTGGGGTGTTTATGGCAAGTCACTTTGACAGACATTATTGTGGGCAAATGTTGTCTGACTTACTGTTTCAACAAAC
CAG 2846 TGGCAAGTCACTTTGACAGACATT 2847
GG T-- C CTTT A AT T
CTGG TGTT ATGG AAGTCA GACAG CATT TG G
||||| ||| ||||| ||||| ||||| ||
GACC ACAA TGTC TTCAGT CTGTT GTAA AC G
AA CTT A ---- - -- G
GAM198
CTGGTGTCATCAGTTGTTCCCGGCGCAGGCCCGCGTTGATCGTGGCGCTGGTGCTGCTGACGGAGCTGCTGGTT
CTGCTGCCAG 2858 TCAGTTGTTCCCGGCGCAGGCCCG 2859
- --- T ---- A - C TT
CTGGT GCA TCAGT GTTCC CGGCGC GGC CC CG G
||||| ||| ||||| ||||| ||||| ||| ||
GACCG CGT GGTCG CGAGG GTCGTG TCG GG GC /
T CTT T CAGTC G C T TA
GAM199 CTGGTTAACTTCTTGAGCTATTTCTGGAACCTTGAACACAGCCTGCCACCCAGTGAAGTGTCCAG
2874 CACCCAGTGAAGTGTCCAG 2875
TTA TTGA ATTTC AAC- GA
CTGG ACTTC GCT GTGG TTG A
||||| ||||| ||| ||||| |||
GACC TGAAG TGA CACC GAC /
TG- ---- CC--- GTCC AC
GAM200
CTGTCCCCAAGCGCATGCCATCTGCAGCCAGCAGTCTTGGAACCTTTGGTTGGTGGCACCAGGGGACAG 2880
TGGTTGGTGGCACCAGGGGACAG 2881
AAGCGCA CTG C CT
CTGTCCCC TGCCAT CAGCCAG AGT T
||||| ||||| ||||| |||
GACAGGGG ACGGTG GTTGGTT TCA G
ACC---- --- - AG
GAM201 CTGTCTGTTTCATATGTTGGTTATGACTTTTACATTAAAATATCATTTAAACGAATGAGCAATCAG 2898
CATTTAAACGAATGAGCAATCAG 2899

TC A GGTT CT AC
 CTG TGTTTCAT TGTT ATGA TTT A
 ||| ||||| ||| ||| |||
 GAC ACGAGTA GCAA TACT AAA T
 TA A ATT- AT AT
 GAM202 CTGTGAACAGAGAGGCCATGGGAAGATTTCGAAATTATTCACGAAAAATCCTAAGATTTTCAGTTCAGAG
 2921 TGAACAGAGAGAGGCCATGGGAAGAT 2922
 G A GGCCA AGA AAAT
 CT TGAAC GAGA TGGGA TTCG T
 || ||||| ||| ||||| |||
 GA ACTTG CTTT ATCCT AAGC A
 G A AGA-- AAA ACTT
 GAM203 CTGTGATGGCGCAATTAACGTTTCCTAGCCTCCCATGTAATCCTAGGACGTGTACGCTTCGTCAGAG
 2946 TGTGATGGCGCAATTAACGTTTCC 2947
 G C AATTA TT CCTCCC
 CT TGATGG GC ACG TCCTAG A
 || ||||| || ||| |||||
 GA ACTGCT CG TGC AGGATC T
 G T CATG- -- CTAATG
 GAM204
 CTGTGGACCACTGTTTCTCCATCAAAGGCCTAAGGGCACTGTGAGTGACAGGGGACCAGTCCTTTGCAG 2953
 TGTGAGTGACAGGGGACCAGTCCT 2954
 TG CC T --- - A - T
 CTG GA ACTG TTCTC CA TCA AG GCC A
 ||| || ||||| || ||| || |||
 GAC TT TGAC AGGGG GT AGT TC CGG A
 GT CC C ACA G G A G
 GAM205 CTGTGTTCTGGCGGCCCCATTTCGTAGCCACTGGGGGTCAGCTTGTAGGCCGTCAGTGTACAG 2967
 TGTTCCTGGCGGCCCCATTTCGTAGC 2968
 TT CC TC A- AC
 CTGTG CTGGCGGCC AT GT GCC T
 ||||| ||||| || || |||
 GACAT GACTGCCGG TG CG TGG G
 GT A- TT AC GG
 GAM206
 CTGTTGGTTCTTTCTCCTGACTCCTGTGGTTTTTGCTAATGGCACTTTACAGACTCCATGGAGATGTCAGGTGGACC
 ATCTTCTAGGGCCCAGCAGGAGTAGGGAATGTGCCAACAG 2973 TGTCAGGTGGACCATCTTCTAGGG 2974
 TCT T A -- CTA- -- T GA C
 CTGTTGGT TTC CCTG CTCCTGT GGTTTTG ATGG CACTT ACA CTC A
 ||||| || ||| ||||| ||||| ||| ||||| || |||
 GACAACCG AAG GGAT GAGGACG CCGGGAT TACC GTGGA TGT GAG T
 TGT - - AC CTTC AG C A- G
 GAM207 CTTAGGGAGGAAGGACTAGGAGGGAAAACGTACGGTGGGCTCTGTCTTGCGTCTTGAG
 3004 TTAGGGAGGAAGGACTAGGAGGGA 3005
 AGGA TAGG AAA GGAA
 CTTAGGG AGGAC AGGG ACTG A
 ||||| ||||| ||| |||||
 GAGTTCT TTCTG TCTC TGGC A
 GCG- ---- GGG ATGC
 GAM208
 CTTTCAGCAATGTCAGTAAAATGATCTTCCGATGCTGACGCCAGCATTTTCCCATCATGGCTGAAACTGAGG 3021

TGTCAGTAAAATGATCTTCCGATG 3022
 CAATG AAA CTTCC A
 CTTCAG TCAGT ATGAT GATGCTG C
 ||||| |||| |||| |||||
 GGAGTC AGTCG TACTA TTACGAC G
 AA--- G-- CCCTT C
 GAM209
 GAAAATATAAGAACATTCTAGAAGGTTGTGAGACATAAGGTACAAAAACCTTCTAGCATAATTTCAAAAAATTTTC
 3030 TAAGAACATTCTAGAAGGTTGTGA 3031
 ATAA- C-- T GTGAG AT
 GAAAAT GAA AT CTAGAAGGTT AC A
 ||||| ||| || ||||| |||
 CTTTTA CTT TA GATCTTCCAA TG /
 AAAAA TAA C AAACA GA
 GAM210
 GAAATGAGGTCGGGTTTATATGCACTTATTGGTATTGGAATTTCTGGTGCAACTTATAGGTTTGATTTTAATTT
 3043 TGAGGTCGGGTTTATATGCACTTA 3044
 A GG --- TATT AT
 GAA TGAGGTCG TTTATA TGC ACT GGT T
 ||| ||||| ||||| ||||| |||
 TTTATTTAGT GGATAT ACGTGG TTA G
 A TT TCA TCT- AG
 GAM211
 GAAGACAAATTGAAGGGAGAGATGATGGATCTCCAACATGGCAGCCTTTTCCTTAGAACACCAAAGATTGTCTC
 3049 TGGCAGCCTTTTCCTTAGAACACC 3050
 A A-- ----- A A
 GA GACAA TTG AAGGGAGAG ATG TGG T
 || ||||| ||| ||||| ||| |||
 CT CTGTT AAC TTCTTTTC TAC ACC C
 - AGA CACAAGA CGACGG A T
 GAM212 GAAGCTGTCCGCATTTATGTGGCATCGGTCCAAGCATCCCTGGGCCAGTCGTGCGACAGACTC 3069
 TGTCGCATTTATGTGGCATCGGT 3070
 AG C TTATGT ATC AGC
 GA CTGTC GCAT GGC GGTCCA A
 || ||||| ||| ||| |||||
 CT GACAG CGTG CTG CCGGGT T
 CA - ----- A-- CCC
 GAM213 GAATCCAGATGGCATGGTTGCTCTATTGGACTACCGTGAGGATGGTGTGACCCCATATATGATTT 3075
 TGGCATGGTTGCTCTATTGGACTA 3076
 CAG- CAT TG T TGGACTA G
 GAATC ATGG GGT C CTAT CC T
 ||||| |||| ||| ||||| |||
 TTTAG TACC CCA G GGTA GG G
 TATA --- GTT ----- A
 GAM214 GAATGAGCTGCTAAATCCTGAAGATGACCTCTTACCAGGGAAGATTGAGACAGCAATCGTTC 3081
 TGAGCTGCTAAATCCTGAAGATGA 3082
 GC AAA C GATGA CT
 GAATGA TGCT TC TGAA CCT T
 ||||| |||| ||| ||||| |||
 CTTGCT ACGA AG GCTT GGA A

A- C-- A AGAAG CC
 GAM215
 GAATTCTGATCATACCAAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGACAATCCC
 ACAGCAGTTC 3101 TACCAGTTTCCATCAGGATTTATC 3102
 - A----- T CCAT- TTA G
 GAATT CTG TCA ACCAGTTT CAGGAT TCA A
 ||||| ||| ||||| ||||| |||
 CTTGA GAC AGT TGGTCGAA GTCCTA AGT T
 C ACCCTAAC - TAGAC CAA C
 GAM216
 GACACCGGTGTCCTTCCTCGAGTAACCGACCTTCCAGTTCCAGCCCTCCAAGTCCCACGGCTCGGAAGAGCGAC
 TACCATCGTC 3118 TCCAAGTCCCACGGCTCGGAAGAG 3119
 ACC - - CC AACC- CTTCCA- T
 GAC GGT GTC CTT TCGAGT GAC GT C
 ||| ||| ||| ||| ||| ||| ||| |||
 CTG CCA CAG GAG GGCTCG CTG CG C
 CTA T C AA GCACC AACCTCC A
 GAM217 GACCCGGGGCTGGACGCCAGCCTCTGTGATGAGTTCTGGCTGTGTCCACGCTCCTGGCTC 3132
 TGGCTGTGTCCACGCTCCTGGCTC 3133
 C - - --- C- TG
 GA CCGGG GC TGGAC GCCAG CTC T
 || |||| || |||| |||| |||
 CT GGTCC CG ACCTG CGGTC GAG G
 C T C TGT TT TA
 GAM218 GACTATGGCAAGGACCTGATGGAGAAGGTCAAGAGCCCAGAGCTTCAGGCCGAGGCCAAGTC 3172
 TGGCAAGGACCTGATGGAGAAGGT 3173
 A AA- A T AGAA- CA
 GACT TGGC GG CCTGA GG GGT A
 |||| ||| || |||| || |||
 CTGA ACCG CC GGA CT TC CCG /
 - GAG - - GAGAC AG
 GAM219
 GACTGAAGGAGGAATATCAGTCCCTTATCCGGTATGTGGAGAACAACAAGAATGCTGACAACGATTGGTTCCGAC
 TGGAGTC 3204 TATCAGTCCCTTATCCGGTATGTG 3205
 GA GA AT CCTTATC G-- GAG
 GACT AG GGA ATCAGTC CGGTAT TG A
 |||| || ||| ||||| ||||| |||
 CTGA TC CCT TGGTTAG GTCGTA AC A
 GG AG -- CAACA-- AGA AAC
 GAM220
 GACTTCAGGCAAATCATTTATTTTTTGGGGCATCAGTGTCAAACTATAACATCAGAGAATAAACCAAATGACCT
 CATGTC 3210 TAACATCAGAGAATAAACCAAATG 3211
 TTC - AATCA GGCATC GTC
 GAC AGG CA TTTATTTTTTGG AGT A
 ||| ||| || ||||| ||||| |||
 CTG TCC GT AAATAAGAGACT TCA /
 TAC A AAACC ACAATA AAC
 GAM221 GACTTTGCTTCCGGTACAAACAGGCCACCTGAGCACTGGTGGTGGCCTGCTCCGGCTGCTTGTC 3247
 ACTTTGCTTCCGGTACAAACAGGC 3248
 TTT TT TACAAA TGAGC

GAC GC CCGG CAGGCCACC A
 ||| || ||| |||||
 CTG CG GGCC GTCCGGTGG /
 TT- TC TC---- TGGTC
 GAM222 GAGAGCATTAGACCCAAGACCATTGTGGAGAAGATTGACTTGACAGTGTGTCCAGCATAATGCTCTC
 3266 CAGTGTGTCCAGCATAATGCTCTC 3267
 GACCCAA - G AAG
 GAGAGCATT GAC CATTGT GAG A
 ||||| || ||||| ||
 CTCTCGTAAT CTG GTGACA TTC T
 ACGAC-- T G AGT
 GAM223 GAGAGCGCTATAGGATCCCTTTTACAAGGGGCACTAATCCCACTCATGATCTAATTAGCTCTC 3279
 CCCACTCATGATCTAATTAGCTCT 3280
 GCT A CCTTTTACAA CA
 GAGAGC AT GGATC GGG C
 |||| ||||| ||
 CTCTCG TA TCTAG CCT T
 AT- A TACTCAC--- AA
 GAM224
 GAGATGAAATGTTTTACTTCTGACTGTGGGACTAATGTGTTCTACAGGTTGCAACATAAAACGGATTTCTC 3287
 TGAAATGTTTTACTTCTGACTGTG 3288
 TGAAA CTTCTGA-- -TA
 GAGA TGTTTTA CTGTGGGA C A
 ||| ||||| ||||| |
 CTCT GCAAAT GACATCCT G T
 TTAG- ACAACGTTG T TG
 GAM225 GAGATGAGACATTTTGCCTAGCTGATGACCACTTAGTTCTCAAGAAGCAACTATCTCTTTC 3306
 TGAGACATTTTGCCTAGCTGATGA 3307
 T CATT CTAG - T CA
 GAGA GAGA TTGC CT GA GAC C
 ||| ||| ||| || |||
 CTTT CTCT AACG GA CT TTG T
 - ATC- AA-- A C AT
 GAM226 GAGATGGGATTTTACCATGTTGGCCAGGCCTGTCTTGAACCTCTTGACCTCAAGTGATCCACCCACCTC
 3315 TGGGATTTTACCATGTTGGCCAGG 3316
 A ATT- CA TT C CCT CT
 GAG TGGG TCAC TG GG CAGG GT T
 ||| ||| ||| || ||| ||
 CTC ACCC AGTG AC CC GTTC CA /
 C ACCT A- T- A T-- AG
 GAM227 GAGATGGGGTTTACCATGTTGGCCAGGCTCGTCTCGAACTCCTGACTTCAGGTGATCCACCCATCTC
 3343 TGGGGTTTACCATGTTGGCCAGG 3344
 GTT- A TT C C-- T
 GAGATGGG TCACC TG GG CAGG TCG C
 ||||| |||| || ||| ||
 CTCTACCC AGTGG AC TC GTCC AGC /
 ACCT - T- A TCA T
 GAM228
 GAGCGGCAGCGCCGCGATGCCAGGCGCGTCCCTACAGCGGGCCTGCCGCCTGCTCGTGGCCGTCTGCGCTC
 3350 TGCCGCCTGCTCGTGGCCGTCTGC 3351

G - - T C C --- TA
 GAGCG CAG CG CCGCGA GC AGGCG GT CCC C
 |||| || || |||| || |||| || ||
 CTCGC GTC GC GGTGCT CG TCCGC CG GGG A
 - T C - - - TCC CG
 GAM229
 GAGCGGGCGTGCATATGCGGTGGCGGGTGGGGTGGAAGGGGGAGATCCTGCTGCACTGGCCGCCAAGTATGA
 GGGGCGAGCTC 3375 TATGCGGTGGCGGGTGGGGTGGA 3376
 GG GTG- GC G G GGA GG
 GAGC GC CATAT GGTGGC GGTG GGT AGGG A
 |||| || |||| |||| |||| || ||
 CTCG CG GTATG CCGCCG TCAC TCG TCCT /
 AG GGA AA G G --- AG
 GAM230 GAGCGGTGCGTGACAGCCTCAAGGGCTTCAGCACCGCGCCCATGGCAGAGCCAGACCGACTC 3409
 TGGCAGAGCCAGACCGACTC 3410
 - - GACA TCAA TTCAG
 GAG CGGTC GGT GCC GGGC C
 |||| |||| || |||| ||||
 CTC GCCAG CCG CGG CCCG /
 A A AGA- TA-- CGCCA
 GAM231 GAGCTAACAGCACGAGAAGCCAGTTGGGGACTGCCCCCTCCTGGAGCAGCTCCTGGGCTGTGCTC
 3419 TAACAGCACGAGAAGCCAGTTGGG 3420
 TA AC-- AAG-- TT AC
 GAGC ACAGC GAG CCAG GGGG T
 |||| |||| || |||| ||||
 CTCG TGTCG CTC GGTC CCCC /
 -- GGTC GACGA CT CG
 GAM232
 GAGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTGCGGTGCCCTAGGAGGCCGAGCTCTGTTGCTT
 C 3431 TGGCGGTTCTCTGGAGGCTGAGTG 3432
 - - ATGG TC A TGAGT T
 GAGG AAC GAG CCGT TCTGG GGC GCCG T
 |||| |||| |||| |||| |||| ||||
 CTTC TTG CTC GCCG GGATC CCG TGGC T
 G T GA-- GA - ---- G
 GAM233 GAGGATGAAAGAGGACCTGGGAGCGGCAACTTTGTTCTGGTTTGTGTTTCTCTTCCCTACCTC 3449
 TGAAAGAGGACCTGGGAGCGGCAA 3450
 ATGAA A CCT GG - TTG
 GAGG AG GGA G AGCGGCAA CT T
 |||| |||| | |||| |||| ||
 CTCC TC CCT C TTGTTGTT GG /
 A---- - TCT TT T TCT
 GAM234
 GAGGATTTTATTTCAAGATAAAACATAACTTCTACCCATACTATTGATTCCAAAGGTTAGAAAAAGTGTTTTTCTC
 ATCTTATCCTT 3465 TTCAAGATAAAACATAACTTCTAC 3466
 TTTATTTCA AT AAC C ATACTATT
 GAGGAT AG AAAACAT TTCTA CC G
 |||| || |||| |||| |||| ||
 TTCCTA TC TTTGTG AAGAT GG /
 TTCTAC--- CT AAA T AAACCTTA

GAM235

GAGGCGGGCGGATCACCGGAGGTTCGGGAGTTTGAGACCAGCCTGACCAACATGGAGAAACCCCATCTC 3469
TGACCAACATGGAGAAACCCCATC 3470

GC CGGA A GA-- AGT A
GAG GGG TC CCG GGTCTGGG TTG G
||| ||| ||||| |||
CTC CCC AG GGT CCAGTCC GAC A
TA CAA- A ACAA --- C

GAM236

GAGGGATAGCATTCTGAAGGACTCGGGGATATCTAACAGCAATACCTGATCACTACTTCGCACTAGTTTCTC 3494
TCACTACTTCGCACTAGTTTCTC 3495

GG - CATT GAC--- GATATCTA
GAG AT AG CGAAG TCGGG A
||| ||| ||||| |||||
CTC TG TC GCTTC AGTCC /
TT A AC-- ATCACT ATAACGAC

GAM237

GAGGGTGTTATCTCCAATGTCAATAAGAATTGATGAATAAGAATGTATATCAATATGGAGGAGATAGGTGGAGAAA
GACGTGTTT 3506 ATCAATATGGAGGAGATAGGTGGA 3507

GG A- A- AATAAGA- A A
GAG TGTT TCTCCA TGTC ATTGATG ATA G
||| ||||| ||||| ||||| ||||| |||
TTT GCAG AGAGGT ATAG TAACTAT TGT A
GT AA GG AGGAGGTA A A

GAM238

GAGGTGCCGGTGGGCCTGTGTTGCTGCGATTTTAGTCTGTGCTGGGAGGCAGGGCTCCGCTGCGCCTC 3522
TGGGAGGCAGGGCTCCGCTGCGCC 3523

C - TGTGTTG GA C
GAGGTGC GGTGG GCC CTGC TTTTAGT T
||||| ||||| ||| ||||| |||||
CTCCGCG TCGCC CGG GACG AGGGTCG G
- T ----- G- T

GAM239 GAGGTGGGAGGTCACCCGAGGTCAGGTGTCTGTGACCAGGCCGGCCAACATGGTGAAACCCCGTCTC
3543 TGGGAGGTCACCCGAGGTCAGGTG 3544

GT AGG CGA-- A GT T
GAG GGG TCACC GGTC GGT CTG G
||| ||| ||||| ||||| ||| |||
CTC CCC AGTGG CCGG CCG GAC A
TG CAA TACAA - -- C

GAM240

GAGTCCACTGGTGCCAGTAACACCCTCCGTGGGACCACCTTGGGAAGCATGTGCCGCGGAGTCCACCACGGG
GGGTCCTGGGTCCCGGGAGGGCTC 3570 TAACACCCTCCGTGGGACCACCTT 3571

A- TG TAAC -- CA T GAAG
GAGTCC CTGG CCCAG ACCCTCCGTGG GAC CC TGG C
||||| ||| ||||| ||||| ||| |||
CTCGGG GGCC GGGTC TGGGGGGCACC CTG GG GCC A
AG CT C--- AC A- C GTGT

GAM241 GAGTCGATAACTGTTGTCCTACTCACCGGTGGTTTCAGTGGCTAATTAGAAGTGTGGTATTGATTG 3578
TAACTGTTGTCCTACTCACCGGTG 3579

A TG T C CTCA- G G

GAGTCGATA C T GT CTA CCG TG T
 ||||| | | || || ||
 CTTAGTTAT G G CA GAT GGT AC T
 - GT T A TAATC G T
 GAM242 GAGTGCCTCGCTCGGTAACCTGCTTGGTCCTGAACATTCTCTCGTTTCAGGAACTGATGAGGTTCTC
 3584 CAGGAACTGATGAGGTTCTC 3585
 T C AACTGCTTGG - ATT
 GAG GCCTCG TCGGT TCCTGAA C C
 || |||| |||| |||| |
 CTC TGGAGT AGTCA AGGACTT G T
 T - ----- T CTC
 GAM243
 GAGTTGCGAGGGAGGCTGCGGGGGCGGGCGGACGTATGTTGAGACCCTATGCAGCCTCCTGCTCTCCCGAGG
 GCTCCTGCGGCTC 3593 GCAGCCTCCTGCTCTCCCGAGGGC 3594
 GA G G -- C AC TTGA
 GAGTTGC GGGAG CT CGGG G GCGGG GG GTATG G
 |||| | ||| | ||| | |||
 CTCGGCG TCCTC GG GCCC C CGTCC CC CGTAT /
 -- G A TT T GA CCA
 GAM244 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAATCTCCTTTAACAACCAAGCAGTTCTCATT C 3622
 TAAGGACCTGTTTGGGGCAGCAGG 3623
 TA- C GGCAGC CA
 GA AGGA CTGTTTGG AGGGAG A
 || ||| ||||| ||||
 CT TCCT GACGAACC TTCCTC A
 TAC T AACAAT TA
 GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAATCTCCTTTAACAACCAAGCAGTTTCCTCATT C
 3643 TAAGGACCTGTTTGGGGCAGCAGG 3623
 TA- C- GGCAGC CA
 GA AGGA CTGTTTGG AGGGAG A
 || ||| ||||| ||||
 CT TCCT GACGAACC TTCCTC A
 TAC TT AACAAT TA
 GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAATCTCCTTTAACAACCAAGCAGTTTCCTCATT C
 3644 TAAGGACCTGTTTGGGGCAGCAGG 3623
 TA- C- GGCAGC CA
 GA AGGA CTGTTTGG AGGGAG A
 || ||| ||||| ||||
 CT TCCT GACGAACC TTCCTC A
 TAC TT AACAAT TA
 GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAATCTCCTTTAACAACCAAGCAGTTTCCTCATT C
 3645 TAAGGACCTGTTTGGGGCAGCAGG 3623
 TA- C- GGCAGC CA
 GA AGGA CTGTTTGG AGGGAG A
 || ||| ||||| ||||
 CT TCCT GACGAACC TTCCTC A
 TAC TT AACAAT TA
 GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAATCTCCTTTAACAACCAAGCAGTTTCCTCATT C
 3646 TAAGGACCTGTTTGGGGCAGCAGG 3623
 TA- C- GGCAGC CA

GA AGGA CTGTTTGG AGGGAG A
|| ||| ||||| |||||
CT TCCT GACGAACC TTCCTC A
TAC TT AACAAT TA
GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3647 TAAGGACCTGTTTGGGGCAGCAGG 3623
TA- C- GGCAGC CA
GA AGGA CTGTTTGG AGGGAG A
|| ||| ||||| |||||
CT TCCT GACGAACC TTCCTC A
TAC TT AACAAT TA
GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3648 TAAGGACCTGTTTGGGGCAGCAGG 3623
TA- C- GGCAGC CA
GA AGGA CTGTTTGG AGGGAG A
|| ||| ||||| |||||
CT TCCT GACGAACC TTCCTC A
TAC TT AACAAT TA
GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3649 TAAGGACCTGTTTGGGGCAGCAGG 3623
TA- C- GGCAGC CA
GA AGGA CTGTTTGG AGGGAG A
|| ||| ||||| |||||
CT TCCT GACGAACC TTCCTC A
TAC TT AACAAT TA
GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3650 TAAGGACCTGTTTGGGGCAGCAGG 3623
TA- C- GGCAGC CA
GA AGGA CTGTTTGG AGGGAG A
|| ||| ||||| |||||
CT TCCT GACGAACC TTCCTC A
TAC TT AACAAT TA
GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3651 TAAGGACCTGTTTGGGGCAGCAGG 3623
TA- C- GGCAGC CA
GA AGGA CTGTTTGG AGGGAG A
|| ||| ||||| |||||
CT TCCT GACGAACC TTCCTC A
TAC TT AACAAT TA
GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3652 TAAGGACCTGTTTGGGGCAGCAGG 3623
TA- C- GGCAGC CA
GA AGGA CTGTTTGG AGGGAG A
|| ||| ||||| |||||
CT TCCT GACGAACC TTCCTC A
TAC TT AACAAT TA
GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3653 TAAGGACCTGTTTGGGGCAGCAGG 3623
TA- C- GGCAGC CA
GA AGGA CTGTTTGG AGGGAG A

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 CT TCCT GACGAACC TTCCTC A
 TAC TT AACAAT TA
 GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
 3654 TAAGGACCTGTTTGGGGCAGCAGG 3623
 TA- C- GGCAGC CA
 GA AGGA CTGTTTGG AGGGAG A
 || ||| ||||| |||||
 CT TCCT GACGAACC TTCCTC A
 TAC TT AACAAT TA
 GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
 3655 TAAGGACCTGTTTGGGGCAGCAGG 3623
 TA- C- GGCAGC CA
 GA AGGA CTGTTTGG AGGGAG A
 || ||| ||||| |||||
 CT TCCT GACGAACC TTCCTC A
 TAC TT AACAAT TA
 GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
 3656 TAAGGACCTGTTTGGGGCAGCAGG 3623
 TA- C- GGCAGC CA
 GA AGGA CTGTTTGG AGGGAG A
 || ||| ||||| |||||
 CT TCCT GACGAACC TTCCTC A
 TAC TT AACAAT TA
 GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
 3657 TAAGGACCTGTTTGGGGCAGCAGG 3623
 TA- C- GGCAGC CA
 GA AGGA CTGTTTGG AGGGAG A
 || ||| ||||| |||||
 CT TCCT GACGAACC TTCCTC A
 TAC TT AACAAT TA
 GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
 3658 TAAGGACCTGTTTGGGGCAGCAGG 3623
 TA- C- GGCAGC CA
 GA AGGA CTGTTTGG AGGGAG A
 || ||| ||||| |||||
 CT TCCT GACGAACC TTCCTC A
 TAC TT AACAAT TA
 GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
 3659 TAAGGACCTGTTTGGGGCAGCAGG 3623
 TA- C- GGCAGC CA
 GA AGGA CTGTTTGG AGGGAG A
 || ||| ||||| |||||
 CT TCCT GACGAACC TTCCTC A
 TAC TT AACAAT TA
 GAM246 GATAAGGACCTGTTTGGTGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTCCTCATTC 3660
 TAAGGACCTGTTTGGTGCAGCAGG 3661
 TA- C GCAGC CA
 GA AGGA CTGTTTGGT AGGGAG A
 || ||| ||||| |||||

CT TCCT GACGAACCA TTCCTC A
 TAC T ACAAT TA
 GAM247 GATACAAGACAGGCAAGAACAAGTGGTTCTTCCAGAACTGCGGTTTTAGATGCTTTGTTTTGATC 3675
 TACAAGACAGGCAAGAACAAGTGG 3676
 A - --- AA TG - TT
 GAT CAAGACAG GCA AGAAC G GTT C C
 ||| ||||| ||| ||||| | ||| |
 CTA GTTTTGTT CGT TTTTG C CAA G /
 - T AGA G- GT A AC
 GAM248 GATACCAGCCTCCCCTGTGGTGCCTGGTGGAGAACTGGCCAAGGTACAAGGAAGGCTGTGTT 3696
 TACCAGCCTCCCCTGTGGTGCCT 3697
 C C ACTGTG - GGAG
 GATAC AGCCT CC GTGCCT GGT A
 ||||| ||||| || ||||| |||||
 TTGTG TCGGA GG CATGGA CCG /
 - A AA---- A GTCA
 GAM249 GATCACATAGAATCTAGGGAAGAAATGAGAAATTCTGGGATTTTTTTTTTTAACAGAAGTGTGTGATC
 3709 TAGAATCTAGGGAAGAAATGAGAA 3710
 TAGAA AGG AAT C
 GATCACA TCT GAAGA GAGAAATT T
 ||||| ||| ||||| |||||
 CTAGTGT AGA TTTTT TTTTTTAG G
 TGTGA CAA --- G
 GAM250
 GATCTCGGCGTTGTGCATGTCGGGCGACTGCTCCATGATCTTGCGCCGCTCGATCTGCGACCACACCATGAAGG
 CGTTCATGGGTCGCTTGATGTGCCCACTCGGGGTC 3717 TGAAGGCGTTCATGGGTCGCTTGA 3718
 C TT TGCT TCTT GC ATC CG
 GATCTCGG GT G GCATGTCGGGCGAC CCATGA GCGCC TCG TG A
 ||||| ||| ||||| ||||| ||||| ||| ||| ||| |||
 CTGGGGCT CA C CGTGTAGTTCGCTG GGTACT TGCGG AGT AC C
 - - C --- --- A- ACC AC
 GAM251
 GATGCTCCCAAACATCCTATATGCATCCATGGAAATTTAAAGATCCTGGAATAGCGTCTTCCATGTGGGACATC
 3735 GAATAGCGTCTTCCATGTGGGACA 3736
 C AA CCTAT A-- T AATT
 GATG TCCC ACAT ATGC TCCA GGA T
 ||||| ||||| ||||| ||||| ||||| |||||
 CTAC AGGG TGTA TGCG AGGT CCT A
 - -- CCTTC ATA - AGAA
 GAM252
 GATGGAACACATGAAATCTTTGGTTCACAGACTATTTACAATCTTGCAATTTAGAAGAGTCTCAGAAAAAGAGAGAG
 CACCATT 3745 TGAAATCTTTGGTTCACAGACTAT 3746
 AACACA AAA GG AC A ACAATCT
 GATGG TG TCTTT TTC AGACT TTT T
 ||||| || ||||| ||| ||||| |||||
 TTACC AC AGAGA AAG TCTGA AAG /
 ----- GAG AA AC G ATTTACG
 GAM253
 GATGGAATAGTTCAGAAGGAATGGTACCAGTTCCTCCTTGACCTCTGGTAGAATTCGGCTGTGAATCCATC 3761
 TGGAATAGTTCAGAAGGAATGGTA 3762

ATAGTT AAG GG TTCCTCC
 GATGGA CAG GAAT TACCAG T
 ||||| || ||| |||||
 CTACCT GTC CTTA ATGGTC /
 AAGT-- GG- AG TCCATGT
 GAM254 GATGGACTCTTTCTTTTAAATGTGTCCAGCTCTTGTCTTTTTCATTTCTTAGCCTGCAGAGTTCATC
 3779 TGGACTCTTTCTTTTAAATGTGTC 3780
 TT--- TTTT TGTCC- T
 GATGGACTCT CT AATG AGC C
 ||||| || ||| |||
 CTACTTGAGA GA TTAC TTG T
 CGTCC TTCT TTTTTC T
 GAM255
 GATGGTTTTAGATGATAACCACAGGTCTACAAGAGCGTTTTTAGTAAAGTGCCTGTGTTCAATTGTGGACAAAGTTA
 TTATTTTGCAACATC 3815 TAACCACAGGTCTACAAGAGCGTT 3816
 GTTTT CACAG - TTTT TAA
 GATG AGATGATAAC GTCTACAA GAGCG TAG A
 ||| ||||| ||||| ||| |||
 CTAC TTTATTATTG CAGGTGTT CTTGT GTC G
 AACGT AAA-- A ---- CGT
 GAM256 GATGTAAACACAAAAGAAAGTGTCTCAGCAGGGCTGAGCCCTCCTTCTCGTGTCTGCATT 3848
 TGTAACACACAAAAGAAAGTGTCTC 3849
 A AAA -- TT A
 GATGTA ACAC AGAA AG G CTCAGC G
 ||||| ||| ||| ||| |||||
 TTACGT TGTG TCTT TC C GAGTCG /
 C C-- CC C - G
 GAM257
 GATGTCAATGCTGCCATTGCCACCATCAAAACAAGCGCAGCATCCAGTTTGTGGATTGGTGCCCCACTGGCTTCA
 AGGTGGCATC 3858 CATTGCCACCATCAAAACAAGCGC 3859
 A-- CT T C-- TCAAA GCAG
 GATGTCA TG GCCA TG CACCA ACAAGC C
 ||||| || ||||| ||||| |||||
 CTACGGT AC CGGT AC GTGGT TGT TTG A
 GGA TT C CCC TAGG- ACCT
 GAM258 GATTAGCTCATTTGAAGAATACCACAACAGTGGTTTTAAACATTTTGAATTGACTAGTC 3884
 TAGCTCATTTGAAGAATACCACAA 3885
 C T G ----- A
 GATTAG TCA TT AAGAAT ACCAC A
 ||||| ||| ||| ||||| |||||
 CTGATC AGT AA TTTTAA TGGTG C
 - T G CAAATTT A
 GAM259 GATTGACCTCCCTGAAGCCCAAGCCAATCTGTCCCAGCTCCGGGATCACTTGGGACAGGAGGTCATC
 3899 TCACTTGGGACAGGAGGTCATC 3900
 T C AAG CCAATCT AG
 GAT GACCTCC TG CCAAG GTCCC C
 ||| ||||| || ||||| |||||
 CTA CTGGAGG AC GGGTTC TAGGG T
 - - A-- AC----- CC
 GAM260
 GATTTGACACTGCAGGCAGATGAGGTCTTGGGATGCCTCTTGCGTTCCCCCTTCTGTGGGAGCAGGTGCCTTCC

TAC C - AGA CT T- CT GT CCT
GATTG ACTG AG GC TGAGGT TGGGA GC CTTGC TCCC T
|||| |||| || |||| |||| || |||| ||||
CTAA C TGAC TC CG ACTCCA ACCCT CG GGACG AGGG C
- CC - A --- -- TC T- -- TGT

GCAAGACACTAGGCTGTCCCGAACCCCTGGTAATAGAATTGTTTACCTTTATACCAAGAAGAGTTGGGAAAGCAC
CAAAATCTGC 3917 TACCAAGAAGAGTTGGGAAAGCAC 3918

GAM262 GCAAGTCTTCTTAGAGCTGGGGCCAAGTGACTTCTCCTTGACTCCTCTGAGCAAAGCCCAGC 3922
CAAGTCTTCTTAGAGCTGGGGCCA 3923

GAM263 GCAAGTGCCTCCGGACATGTGGATCACAGGCTACTAGAAACCACGAGTTCCCTCCATTTGT 3947
AGAAACCACGAGTTCCCTCCATTT 3948

GAM264 GCAATGCCAGGTT CAGTAGCCGTCCCCCGGAAAGGGGTGACCTTTATGCTCGTGCTTGATGTTGC
3961 TGCCAGGTT CAGTAGCCGTCCCCC 3962

GAM265 GCAATGTAATTTGAAATCAGTTGAATTTCTGTTTTCTCTCATAGGTTCAACTACTCAATTTCATGC
3977 TGTAATTTGAAATCAGTTGAATTT 3978

GAM266

GCACCTTTTAACTTTTCGCCATGGAACAACGACCCTAAAGAAAGGATAAAAGGGGGCAGTTGCCATGCTGGAACGT
GAAAAGGC 3988 TTTAACTTTTCGCCATGGAACAAC 3989

A A T C AA GA AAAGAAA
 GC CTTT AC TTTCG CATGG CAAC CCCT G
 || ||||| || ||||| ||||| ||||| |||||
 CG GAAAA TG AAGGT GTACC GTTG GGGG G
 - G C C -- AC GAAAATA

GAM267

GCAGAATTGAAGATGGGAAGTTCATTGGGACTGTGTCTTGGAAAAGCACCAAGTTCGTCTCAGTTGTTCTGTTTT
TTGC 4007 TGGGAAGTTCATTGGGACTGTGTC 4008

TTGAA GTTC T TGT AAA
GCAGAA GATGGGAA ATTGGGAC G CTTGG A
||||| ||||| ||||| | ||||
CGTTTT TTGTCCTT TGACTCTG C GAACC /
----- GT-- - TT- ACG

GAM268

GCAGAGCTTGTGTAGGAAGAATGAAATCTGCAATTTGACTTTTAGGAGTGTCTGTTTTCCGGGTCAGGCAGATTGG
TATTCAGCGCTGGCTCTGC 4018 TGAAATCTGCAATTTGACTTTTAG 4019

T AGGAA A- AAT TTA TGT
GCAGAGCT GTGT GAATG AATCTGC TTGACTT GGAG C
||||| ||| ||| ||||| ||||| |||
CGTCTCGG CGCG CTTAT TTAGACG GACTGGG CCTT /
T A---- GG --- --- TTG

GAM269 GCAGCCGCTTTGGATGCTCTTCGGCCTGCACGGGACCATCACGCAGATCCGCATCCTCGGTGAGTGC
4038 TCACGCAGATCCGCATCCTCGGTG 4039

GC TT TCTTC GC ACG A
GCA CGCT GGATGC G CTGC GG C
||| ||| ||||| | ||| ||
CGT GTGG CCTACG C GACG CT C
GA CT C--- TA CA- A

GAM270

GCAGGAGCGGGGGGAATCATTGACCTTGAGGCTGAGCGAAACCGATACTTCATCAGCCTTCAGCAGCCTCCTG
CCCCTGC 4052 TCAGCCTTCAGCAGCCTCCTGCCC 4053

A GAATCA AC T GC ACC
GCAGG GCGGGGGG TTG CT GAGGCTGA GAA G
||||| ||||| ||| || ||||| |||
CGTCC CGTCCTCC GAC GA TTCCGACT CTT A
C ----- -- C A- CAT

GAM271 GCAGGATGATTGAGGATGCAATTCGAAGTCACAGCGAATCAGCCTCACCTTCAGCCCTGT 4068
TCAGCCTCACCTTCAGCCCTGT 4069

A- T-- A CA AAGT
GCAGG TGA TGAGG TG ATTCG C
||||| ||| ||||| || |||||
TGTCC ACT ACTCC AC TAAGC /
CG TCC G -- GACA

GAM272

GCAGTGGAGGGGGCAGGACCTCCTGCTGGTGCAGCACCAGCTGCTGTGAGCAGGTCCACCGGCCCTACACTG
C 4104 TGTGAGCAGGTCCACCGGCCCTA 4105

GA A ACCT GGT- A
GCAGTG GGGGGC GG CCTGCT GCAGC C
||||| ||||| || ||||| |||||
CGTCAC TCCCCG CC GGACGA CGTCG C
A- G ACCT GTGT A

GAM273 GCATATGAGGACGGCCATTATTGTTGGGGGCAAATGGAAATGCTCTAGGCGGGGCCGCGTAGC 4125
TATGAGGACGGCCATTATTGTTGG 4126

A AGGA ATTA TG AAT
GC TATG CGGCC TTGT GGGGCA G

||||| |||| ||| |||||
 CG ATGC GCCGG GGCG TCTCGT G
 - ---- GA AAA
 GAM274 GCATCAGAGTAATCTTCAGTGTGGAATGTTAAATAACGCTTTTATACTGTATTTTGTACTATGATGT 4137
 TCAGAGTAATCTTCAGTGTGGAAT 4138
 G ATCTT-- - A
 GCATCA AGTA CAGTGTGGAA TGTT A
 ||||| |||| ||||| ||||
 TG TAGT TCAT GTCATATTTT GCAA A
 A GTTTTAT C T
 GAM275 GCATCTAATGTGATAAGGCTGCACGTTTTATATCGATGGTCATTCTTTATTGTATTGGTGC 4142
 TCTAATGTGATAAGGCTGCACGTT 4143
 T TG C- CA TTA
 GCA CTAATG ATAAGG TG CGTT T
 ||| ||||| ||||| || |||||
 CGT GGTTAT TATTTC AC GTAG /
 - GT TT TG CTA
 GAM276 GCATGAGGAAGATAATCCTTTGAAACATCATTAATTGAAGTGATTTTAAATAGGATTTCCCTTTTGT 4157
 TGAGGAAGATAATCCTTTGAAACA 4158
 T GATA TTG- C AA
 GCA GAGGAA ATCCT AAA ATCATT T
 ||| ||||| |||| ||| |||||
 TGT TTCCTT TAGGA TTT TAGTGA T
 T ---- TAAA - AG
 GAM277
 GCATGGCCAGGGAGGGCAAATGGAAAGGCAACCACTCTCTGCCGGTCCTGGGCTTATCCCTGCAATGTGC 4177
 TGGCCAGGGAGGGCAAATGGAAAG 4178
 GC- - AAAT AA ACCA
 GCATG CAGGGA GGGC GGA GGCA C
 ||||| ||||| |||| ||| |||||
 CGTGT GTCCCT TTCG CCT CCGT /
 AAC A GGT- GG CTCT
 GAM278
 GCCAATTAGAGGTAAATAAAATTGCTTAAAAGTGTTCTCAAACTTGCAGTTTCTTCAATCTTATGAAATTGGC
 4202 TTAGAGGTTAAATAAAATTGCTTAA 4203
 A--- A T TTAA GTTC
 GCCAATT GAGGTT AA AAATTGC AAGT T
 ||||| ||||| ||| ||||| |||||
 CGGTAA TTCTAA TT TTTGACG TTCA /
 AGTA C C ---- AAAC
 GAM279 GCCACCACTCGGGTACGGAGGCTCAGAGACTACTATAGCAGCCGGAGTCAGAGTGGTGGC 4234
 TAGCAGCCGGAGTCAGAGTGGTGG 4235
 G TA- AG CAG A
 GCCACCACTC GG CGG GCT AG C
 ||||| ||||| || ||| ||| ||
 CGGTGGTGAG CT GCC CGA TC T
 A GAG GA TA- A
 GAM280 GCCACCCTACGCCGTAGCCGTCCAGAGACTGGCAGGCCTCGGCTAAAGGTCTGGAGGGTGAGC 4245
 TGGCAGGCCTCGGCTAAAGGTCTG 4246
 - AC----- TA GT A

GC CACCCT GCCG GCC CCAG G
 || ||||| |||| ||| ||||
 CG GTGGGA CGGC CGG GGTC /
 A GGTCTGGAAT TC AC A
 GAM281
 GCCAGCAAAGACTGCCTCTTCGCCATCGTGGGGAACAAAGTGGACCTCACTGAGGAGGGGGCCTTGGCGGGC
 4261 TCACTGAGGAGGGGGCCTTGGCGG 4262
 A A A G CCATC AA AA
 GCC GC AAG CT CCTCTTCG GTGGGG C A
 ||| || ||| || ||||| ||||| |
 CGG CG TTC GG GGAGGAGT CACTCC G /
 G G C G ---- AG TG
 GAM282 GCCATCACTGCCACCCAGAAGACTGTTGGATGGCCCCTCCGGGAAAAGTGTGGCGTGATGGC 4276
 TCACTGCCACCCAGAAGACTGTTG 4277
 T CCAGAAGA TT AT
 GCCATCAC GCCAC CTG GG G
 ||||| |||| ||| ||
 CGGTAGTG CGGTG GGC CC G
 - TCAAAAG- CT CC
 GAM283
 GCCATGGCGGCCATGAGTTGTTGCGGCGGGTTTCGGTACTGCGGTGGCAGCTCTGTCTGGCCGGCCCCCTTGG
 C 4290 TGGCGGCCATGAGTTGTTGCGGCG 4291
 T-- - T--- TG G GTTT
 GCCA GGC GGCCA GAGTTGT C GCGG C
 |||| || |||| ||||| | ||||
 CGGT CCG CCGGT CTCGACG G CGTC G
 TCC G CTGT GT G ATTG
 GAM284
 GCCCAGCCCATGGCTGCCATGGGAGGCCTGAAGGTGCTTCTGCACTGGGCTGGTCCAGGCGGCGGGGAGCCC
 TGGGT 4301 TGGCTGCCATGGGAGGCCTGAAGG 4302
 ---- ATG A A- GAA T
 GCCCAG CCC GCTGCC TGGG GGCCT GGTGC T
 ||||| ||| ||||| |||| ||||| ||||
 TGGGTC GGG CGGCGG ACCT TCGGG TCACG C
 CCGA G-- - GG --- T
 GAM285 GCCCCAACCTCCTGGCTTGGTCTCCGCTTGTTGTTGGCTACCTAGTTCCAGGTTGAGGGC 4318
 TACCTAGTTCCAGGTTGAGGGC 4319
 - CCT T CT - TT
 GCCC CAACCT GGCT GGT CCG C G
 |||| ||||| |||| ||| ||||
 CGGG GTTGGA TTGA CCA GGT G /
 A CC- T TC TTT
 GAM286
 GCCCGCGCCCTGCCGCGGGAATCCTGAAGCCCAAGGTCTGCCCGGGGGCGGTCCGGCGGGCGCCGGCGATGG
 GGC 4328 TGCCGCGGGAATCCTGAAGCCCAA 4329
 --- CC AT TGAA AA TC
 GCCOC GCC TGCCGCGGGA CC GCCC GG T
 |||| ||| ||||| |||| || |||| ||
 CGGGG CGG GCGGCGGCCT GG CGGG CC /
 TAG CC -- ---- GG CG

GAM287

GCCCCCAAGTCGGGTATGAAGGAGCTGGCCGTGTTCCGGGAGAAGGTCACTGAGCAGCACCGGCAGATGGGC
4344 TCGGGTATGAAGGAGCTGGCCGTG 4345
C AA GTA AAGG C GTG C
GCCC TC GTCGG TG AG TGGCC TTC G
||||| || ||| ||||| ||
CGGG AG CGGCC AC TC ACTGG GAG /
T A- ACG GAG- - AA- G

GAM288

GCCCTCCCTTTGGTCTCCCTGTTCTTCTATGTGGTGACAGATGGCAAGGAAGTCCTACTACCAGAGGTTGGGGC
4353 TGGCAAGGAAGTCCTACTACCAGA 4354
C- CTCCCTG-- - G G
GCCCT CCTTTGGT TTCTT CTAT TG T
||||| ||||| ||||| ||||| ||
CGGGG GGAGACCA AGGAA GGTA AC G
TT TCATCCTGA C G A

GAM289

GCCCTCGCCCGGCCTGTCAGCGCTGCTCTCCGCCGCAGCTTCAGCACCTCGGCCCAGAACAAATGCTAAAGTAG
CTGTGCTAGGGGC 4369 TGTCAGCGCTGCTCTCCGCCGCAG 4370
C- C -- GTC C C CC CA-- T
GCCCT GC CGGC CT AGCG TG TCT GCCG GC T
||||| ||||| || ||||| ||||| ||
CGGGG CG GTCG GA TCGT AC AGA CGGC CG C
AT T AT AA- A A CC TCCA A

GAM290 GCCGCATCTTCTTTTGCCTCGCCAGCCGAGCCACATCGCTCAGACACCATGGGGAAGGTGAAGGT
4378 CGCTCAGACACCATGGGGAAGGTG 4379

G- - C- GCC C GC
GCC CATCTTCTTT TG GTC AGC GA C
||| ||||| || ||| ||||| ||
TGG GTGGAAGGGG AC CAG TCG CT A
AA T CA AC- - AC

GAM291 GCGCCGCCTCCTTGAAACTTAGCGCTCTGACCCAGAGTCTGACCAGGGTACGGCAGGCGC 4400
GTCTGACCAGGGTACGGCAGGCGC 4401

- T-- AAAC C A
GCGCC GCC CTTG TTAG GCTCTG C
||||| ||||| ||||| ||||| ||||| ||
CGCGG CGG GGGAC AGTC TGAGAC /

A CAT C--- - C
GAM292 GCGCTCACTTGTCTTCAGGAAGCTCGGAGCCTTTGGTGGAGCCGGGGAGAGGAAGGGTGGGTGC
4429 TCACTTGTCTTCAGGAAGCTCGGA 4430

TG AGGAAG AG TT
GCGCTCACT TCTTC CTCGG CC T
||||| ||||| ||||| ||||| ||
CGTGGGTGG AGGAG GGGCC GG G
GA AG---- GA TG

GAM293

GCGGGAGCTGGGGGTGTGCCTCCAGGAGCTGCTGATGGCTGACGGGCGGCCCGGGACTGGTGGATCTCCCGG
CTGACCGT 4449 TGGGGGTGTGCCTCCAGGAGCTGC 4450
G- - G -- A A GA GC
GCGG AGCTGGG GGT TGCC TCC GG GCTGCT TG T

|||| ||||| || |||| || || ||||| ||
 TGCC TCGGCCC CTA GTGG AGG CC CGGCGG GC /
 AG T G TC G - -- AG
 GAM294
 GCGGGCAGCCACAGTTACCAAGAAGACTTATGAGATCTGGCATCGACGGCATGACTACTGGCTGCTAGC 4458
 TGGCATCGACGGCATGACTACTGG 4459
 G C- -- AA- ---- - T
 GC GGCAGCCA AGTTA CC GA AGA CT A
 || ||||| |||| || || ||||
 CG TCGTCGGT TCAGT GG CT TCT GA T
 A CA AC CAG ACGG A G
 GAM295
 GCGGGGCCCCGGGCGGCGGCGCTAGCAGATCCAGCGGATAAAAGCGGTCTGAAGAAGCCGGGTTGCGC 4462
 TAAAAGCGGTCTGAAGAAGCCGGGT 4463
 G G GG--- - AGCAG A
 GCG GGCCCCG C CGGC GCT ATCC G
 || ||||| | |||| ||||
 CGC TTGGGCC G GCTG CGA TAGG /
 G - AAGAA G AAA-- C
 GAM296
 GCGGTAATGATCAGAGACCGAGGCTGCACCGGCAGAGGCTGCGGGGCGGACGCGCGGGCCGGCGCAGCCAT
 GGTGAAGATTAGCTTCCAGC 4473 TCAGAGACCGAGGCTGCACCGGCA 4474
 - TAA- AGAG A A AGAG T GGG
 GC GG TGATC ACCG GGCTGC CCGGC GC GCG C
 || || |||| |||| ||||| |||| ||||
 CG CC ATTAG TGGT CCGACG GGCCG CG CGC /
 A TTCG AAG- A C GG-- - AGG
 GAM297
 GCGTTTTTTTGAAGTTATTGAGATTCTACATTGCATTGACTGGGATTCCAGTAGCAATTTTCATAACTCTGGTGAATG
 T 4488 AGCAATTTTCATAACTCTGGTGAA 4489
 T GA T TTCTAC ATTG G
 GCGTTT TT AGTTAT GAGA ATTGC ACTGG A
 ||||| || ||||| |||| |||| ||||
 TGTAAG GG TCAATA CTTT TAACG TGACC T
 T TC - ----- A--- T
 GAM298
 GCTATGGCGGATATGATTATACTGGGTATAACTATGGGAACTATGGATATGGACAGGGATATGCAGACTACAGTG
 GC 4508 TATGATTATACTGGGTATAACTAT 4509
 GGC ATA AT A- GG A G
 GCTAT GG TG TAT CTG TATA CTATGG A
 |||| || || |||| |||| ||||
 CGGTG TC AC ATA GAC GTAT GGTATC /
 ACA AG- GT GG AG A A
 GAM299 GCTATTCCAAGAACATGAATGGAGGAATGTTGGGCCGAATTACAGCGTGGTTGTGCATGGGAGTGGT
 4521 TTCCAAGAACATGAATGGAGGAAT 4522
 AAGAA A TG AGGA GGCC
 GCTATTCC CATG A G ATGTTG G
 ||||| |||| | ||||
 TGGTGAGG GTAC T T TGCGAC A
 ----- G GT GG-- ATTA

GAM300

GCTCCGCCTTTTCTGGGTACTTACGGTCCTGAGTCTCAAGTTCGTCTTCGAGATGCTGTTGTGCCAGAAGCTGGC
GGAGC 4544 TCTGGGTACTTACGGTCCTGAGTC 4545

T- G TT CCTGA - TT
GCTCCGCC TTTCTGG TAC ACGGT GTCTC AAG C
||||| ||||| || |||| |||||
CGAGGCGG GAAGACC GTG TGTCG TAGAG TTC /
TC - T- ---- C TG

GAM301 GCTGACATTAACATAATTATGGGAAATGCAAAAGCTGTTTGGATATGGTAGTGTGTGGT 4556
TGACATTAACATAATTATGGGAA 4557

G TA AAT GG AT A
GCT ACAT ACTAC TAT GAA GC A
||| ||| |||| ||| ||| ||
TGG TGTG TGATG ATA TTT CG A
- -- GT- GG GT A

GAM302 GCTGACCATGCAGCAACTGAACTGGCTCTGTACCATCAGAGCCTTTCCCGGCGATCTGGCTCAGC
4578 TGACCATGCAGCAACTGAACTGGC 4579

- TGCA AACT CT TA
GCTGA CCA GC GAA GGCTCTG C
||||| ||| || ||| |||||
CGACT GGT CG CTT CCGAGAC C
C CTAG GCC- T- TA

GAM303

GCTGACGCCGGCTAGGGAGGAGCAGCCCCACAAACATCGATCCAAGAGGGGGAGCTCAGTGGGCGGCGTGTG
C 4591 TGACGCCGGCTAGGGAGGAGCAGC 4592

TG G GGGAG AG ACAACATC
GC ACGCCG CTA GAGC CCCCC G
|| ||||| ||| ||| |||||
CG TGCGGC GGT CTCG GGGGG /
TG G GA--- A- AGAACCTA

GAM304 GCTGACGTGGGTGTGATCGCTAGCAGCTTCGAGATCGGGAACCTGGCGCTCATCCTCTTCGTGAGC
4618 TGACGTGGGTGTGATCGCTAGCAG 4619

G T- TG T CAG T A
GCT ACG GGG TGA CGCTAG CT CG G
||| ||| ||| ||| ||||| |||
CGA TGC CTC ACT GCGGTC GG GC A
G TT CT C CAA - T

GAM305

GCTGAGAAGCAGTGACCCGCAGATGCCGGCTGAATGGACTGCTCCGGTCTTGGAGTCACTGCTACTCAGC 4627
TGAGAAGCAGTGACCCGCAGATGC 4628

A - C AT CTGAAT
GCTGAG AGCAGTGAC CCG AG GCCGG G
||||| ||||| ||| ||| |||||
CGACTC TCGTCACTG GGT TC TGGCC G
A A - -- TCGTCA

GAM306

GCTGCATCAAAGGTAGACTTTTCGCACAGGTTGTGAGGTTGGAGTCACAGTGTTATTTGTTGTACCTGATGTAGT
4647 TCAAAGGTAGACTTTTCGCACAGGT 2738

AA - TTTC- AGGT GGT
GCTGCATCA GGTA GAC GCAC TGTGA T

||||||| ||||| ||| |||||
TGATGTAGT CCAT TTG TGTG ACACT G
-- G TTTAT ---- GAG

GAM306

GCTGCATCAAAGGTAGACTTTTCGCACAGGTTGTGAGGTTGGAGTCACAGTGTTATTTGTTGTACCTGATGTAGT
4648 TCAAAGGTAGACTTTTCGCACAGGT 2738

AA - TTTC- AGGT GGT
GCTGCATCA GGTA GAC GCAC TGTGA T
||||||| ||||| ||| |||||
TGATGTAGT CCAT TTG TGTG ACACT G
-- G TTTAT ---- GAG

GAM306

GCTGCATCAAAGGTAGACTTTTCGCACAGGTTGTGAGGTTGGAGTCACAGTGTTATTTGTTGTACCTGATGTAGT
4649 TCAAAGGTAGACTTTTCGCACAGGT 2738

AA - TTTC- AGGT GGT
GCTGCATCA GGTA GAC GCAC TGTGA T
||||||| ||||| ||| |||||
TGATGTAGT CCAT TTG TGTG ACACT G
-- G TTTAT ---- GAG

GAM306

GCTGCATCAAAGGTAGACTTTTCGCACAGGTTGTGAGGTTGGAGTCACAGTGTTATTTGTTGTACCTGATGTAGT
4650 TCAAAGGTAGACTTTTCGCACAGGT 2738

AA - TTTC- AGGT GGT
GCTGCATCA GGTA GAC GCAC TGTGA T
||||||| ||||| ||| |||||
TGATGTAGT CCAT TTG TGTG ACACT G
-- G TTTAT ---- GAG

GAM306

GCTGCATCAAAGGTAGACTTTTCGCACAGGTTGTGAGGTTGGAGTCACAGTGTTATTTGTTGTACCTGATGTAGT
4651 TCAAAGGTAGACTTTTCGCACAGGT 2738

AA - TTTC- AGGT GGT
GCTGCATCA GGTA GAC GCAC TGTGA T
||||||| ||||| ||| |||||
TGATGTAGT CCAT TTG TGTG ACACT G
-- G TTTAT ---- GAG

GAM307

GCTGGACGAGCTGACCTTGGAAGGGGTGGCCCGGTACATGCAGAGCGAACGCTGTCGCAGAGTCATCTGTTTG
GT 4652 TGACCTTGGAAGGGGTGGCCCGGT 4653

TG G C C - A G G- CCG A
GC GAC AG TGAC TTG GA GG GT GC GT C
|| ||| ||||| ||| ||| || || ||
TG TTG TC ACTG GAC CT TC CA CG CG A

GT - T A G G G AG AGA T
GAM308 GCTGGATAGCTCTGGAGCAGCTTAGTGTGTCTGGGGCAGACCGACCACCTTCTATCTTGAGTGCCAGC
4667 TAGCTCTGGAGCAGCTTAGTGTGT 4668

ATA T GC CTTA T T GG
GCTGG GCTC GGA AG GTG GTC GG C
||||| ||||| ||| || ||| ||| ||
CGACC TGAG TCT TC CAC CAG CC A
G-- T A- TTC- - - AG

GAM309

GCTGTGACTGCCTGCAGGGTTTCCAGCTGACCCACATCCCTGGGTGGGGGGACTGGGTCTGGGATGGGTACCC
TCATCATCAGC 4680 TGCAGGGTTTCCAGCTGACCCACA 4681

- CTGCC C T G- - CA- G

GCTG TGA TG AGGGT TCCA CT GACCCA TCCCT G

||||| || ||||| ||||| || ||||| |||||

CGAC ACT AC TCCCA GGGT GG CTGGGT GGGGG G

T ---- - T AG T CAG T

GAM310 GCTTCCTTCGTCTACCACTCTGTGCCAGCTCCAACAGACCTGGCAACTAATAGGACTAGAAGGAGGC
4701 GGCAACTAATAGGACTAGAAGGAG 4702

-- ACCACTCTG C CA

GCTTCCTTC GTCT TGCCAG TC A

||||||| ||||| ||||| ||

CGGAGGAAG CAGG ACGGTC AG /

AT ATAATCA-- C AC

GAM311

GCTTCTTGCTGATCAGAGCTTGGTTGGCACAGCCGGGGTCCTCGCCCTCGGCCCTGCTGTTCTCCCGGATCGCT
CTGATCCAGCCCAGC 4719 TCAGAGCTTGGTTGGCACAGCCGG 4720

TCTT - --- TT C C T TCG

GCT GCTG ATCAGAGC TTGG GG ACAGC GGGG CC C

||| ||||| ||||| ||||| || ||||| |||||

CGA CGAC TAGTCTCG GGCC CT TGTCTG TCCC GG C

CC-- C CTA CT - - - CTC

GAM312

GCTTGACGCAGAGGCGGGCGGCAGACGGTGCCCGGCGGAATCTCCTGAGCTCCGCCGCCAGCTCTGGTGC
CAGC 4738 GAGCTCCGCCGCCAGCTCTGGTG 4739

T G GC AGAC T C C A

GCT GCAC CAGAG GGGCGGC GG GC CGG GG A

||| ||||| ||||| ||||| || ||||| ||

CGA CGTG GTCTC CCCGCCG CC CG GTC CT T

C - GA ---- T A - C

GAM313

GCTTGGCCTATGACAGGTCACCGTGTGTAAATCTTTCCCAATAAAGTGTTGCACAAAGGCATCCTGTCCGTGCAG
GT 4771 TGACAGGTCACCGTGTGTAAATCT 4772

- CTAT TCA G- AT CC

GCTTG GC GACAGG CC TGTGTAA CTTT C

||||| || ||||| || ||||| |||||

TGGAC TG CTGTCC GG ACACGTT GAAA A

G C--- TAC AA GT TA

GAM314

GCTTTTAACTTGGAAGTAGTGTAACTCCTTCATGCAATAAACTGAAAAGAGCCATGCTGTCTAGTCTTGAAGT 4781
AAAAGAGCCATGCTGTCTAGTCTT 4782

TAAC T AA C- TGCA

GCTTT TTGGAC AGTGT CTC TTCA A

||||| ||||| ||||| ||| |||||

TGAAG GATCTG TCGTA GAG AAGT T

TTCT - CC AA CAAA

GAM315

GCTTTTCTAGTTTGCAACTTCTAATCTGCTGTGAGTCAGGAAAACATATGGCAGAGTTAAATTGTGCTTTTGGTTA
GGT 4798 TGGCAGAGTTAAATTGTGCTTTTG 4799

TT TTT ACTTCTAA- A CAG
 GCTT CTAG GCA TCTGCTGTG GT G
 |||| ||| || ||||| ||
 TGGA GGTT CGT AGACGGTAT CA /
 TT TT- GTTAAATTG A AAA
 GAM316
 GGAAATGGTTATTGAATCAGATAGACCAGTTCTGTTGAGGGTCTTAAAGAGTCTCAATTTTCTCATCTATAAAACCA
 ATACCTTTCC 4812 TCAGATAGACCAGTTCTGTTGAGG 4813
 T T AATCAG CC TTCT G TT
 GGAAA GGT ATTG ATAGA AG GTTGAGG TC A
 |||| |||| |||| || ||||| ||
 CCTTT CCA TAAC TATCT TC TAACTCT AG /
 - - CAAAA- AC TTT- G AA
 GAM317 GGAACATGACAGCAGGCACACTCATGGAATACAATGGGTTTTCCATGCACCCTGTCATCCTCAGTCC
 4819 TGACAGCAGGCACACTCATGGAAT 4820
 ACAT- CA CACACT T AA
 GGA GA GCAGG CATGGAA AC T
 ||| || |||| ||||| ||
 CCT CT TGTCC GTACCTT TG /
 GACTC AC CAC--- T GG
 GAM318 GGAAGACCGTAATTGTGGCTGCACTGGATGGGACCTTCCAGAGGAAGCCATTTGGGGCCATCC 4843
 AGACCGTAATTGTGGCTGCACTGG 4844
 AGA G TT GCA- TGG
 GGA CC TAA GTGGCT CTGGA G
 ||| || |||| ||||| |||||
 CCT GG GTT TACCGA GACCT A
 ACC G -- AGGA TCC
 GAM319
 GGAAGCCGTCAGCCAAGTCGCCACATTTCTCTGCAAAATGTCATAGCTTATATTAATGTACAGTATTCCATGGTAT
 GCTGCCTTCCGTTGTAAGTAGCAGATCTCTCCGTGACTTGACACGGGCTACT 4858
 TGTCATAGCTTATATTAATGTACA 4859
 A CAGC CACATTTT AAAATGTCATA TTAATGTA TCC
 GG AGCCGT CAAGTCGC TCTGC GCTTATA CAGTAT A
 || ||||| ||||| |||| ||||| |||||
 TC TCGGCA GTTCAGTG AGACG TGAATGT GTCGTA T
 A CA-- CCTCTCT- A----- TGCCTTCC TGG
 GAM320
 GGAAGCTCTTTGCCCCACAGCAGATTCTGCAATGCAGGCCTGACAACTGAGGGAACTGCGAGGGCCGCC 4873
 TGACAACTGAGGGAACTGCGAGGG 4874
 AA T --- A --- AT A
 GG GC CTTTGC CCC CAG CAG TCTGC A
 || || ||||| ||||| ||| |||||
 CC CG GGAGCG GGG GTC GTC GGACG /
 GC - TCAA A AACA C- T
 GAM321 GGAAGGCAGCCAAGAGGAAGTGGGCGGCACAGACCATCCGGCGGCTCATCCGAGGCTTCATCC 4918
 AGGCAGCCAAGAGGAAGTGGGCGG 4919
 A C AAGA AG G ACA AC
 GGA GG AGCC GGA TGGGC GC G C
 ||| || |||| ||||| |||
 CCT CT TCGG CCT ACTCG CG C /

A - AG-- -- G GC- TA
 GAM322 GGAATAAAAATAACAACCTCTTTGTGGGCGCGGCGTTTTGGGCCCGAGAAGAGGTTTTTTTAAACC 4923
 TAAAAATAACAACCTCTTTGTGGGC 4924
 AA T AA G G C
 GG TAAAA AAC CTCTTT TGGGC CGG G
 || ||||| || ||||| ||||| |||||
 CC ATTTTT TTG GAGAAG GCCCG GTT T
 AA - -- A G T
 GAM323
 GGAATCTCGAAGCTGCTAAATGAGTTCCACGAAGAACTTGCCCTCCAATTAAGGCGCGTATTTATATACCTTTCA
 TAGGGCGGGGGGAGATTTT 4942 AATGAGTTCCACGAAGAACTTGCC 4943
 GAAG AA TTCCACG- A T CCAA
 GGAATCTC CTGCT ATGAG AAG AC TGCCT T
 ||||| ||||| ||||| ||||| |||||
 TTTTAGAG GGCGG TACTT TTT TG GCGGA /
 GGG- GA TCCATATA A C AAAT
 GAM324 GGAATGAGAATACCTGAAACCAAACCGTTAACAAGGAATGGTAGTGAAGTTAAGGAGTTAGCTCATTCT
 4958 TGAGAATACCTGAAACCAAACCGT 4959
 AAT - GA -- A- AAC
 GGAATGAG AC CT AAC CA ACCGTT A
 ||||| ||||| ||||| ||||| |||||
 TCTTACTC TG GG TTG GT TGGTAA /
 GAT A AA AA GA GGA
 GAM325
 GGACACCATCTTTATAAAAGTAAACTTCTAGATCCTGAAATGTACTACAGTAGAGTCTATAGTTTACACTTTTAAT
 CACAGATTGGAATTC 4970 TAAAGTAAACTTCTAGATCCTG 4971
 CA - TTA-- A- TC TC AAA TA
 GGA CCA TCT TAAAGT AACT TAGA CTG TG C
 ||||| ||||| ||||| ||||| |||||
 CTT GGT AGA ATTTTCA TTTGA ATCT GAT AC /
 AA T CACTA CA T- GA G-- AT
 GAM326 GGACCAACTGATACCTCGCTATGTAGCTTTACTCCTTTATCCTCTAGGTGGCGTATTAGAATGGTGCC
 4974 GTGGCGTATTAGAATGGTGCC 4975
 - A- CTC G CTTTACTC
 GG ACCA CTGATAC GCTAT TAG C
 ||||| ||||| ||||| ||||| |||||
 CC TGGT GATTATG CGGTG ATC /
 G AA --- G TCCTATTT
 GAM327 GGACCTGTCACCCCACCATGGAGAAAAGAGTCTTTTGGTTCTTTTAAACATAAGTGATTAGTTT 4979
 TGTCACCCCCACCATGGAGAAAAGA 4980
 CT CCCACC GA GT T
 GGAC GTCAC ATG GAAAAGA C T
 ||||| ||||| ||||| ||||| |||||
 TTTG TAGTG TAC TTTTCT G T
 AT AA---- AA TG T
 GAM328 GGAGAAGCGCGAGGGCTACGAGCGTCTCCTGAAGATGCAAAACCAGCGTGGCGGCCGCGCTCTCT
 4987 TGCAAAACCAGCGTGGCGGCCGCG 4988
 A AGG A----- CC
 GGAGA GCGCG GCTACG GCGTCT T
 ||||| ||||| ||||| ||||| |||||

TCTCT CGCGC CGGTGC CGTAGA /
- CGG GACCAAAA AG

GAM329

GGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACTTAGGTGG
CACC 5001 GTCCTGCAAATGAAGGAGGAGGAT 5002

A - - --- AAA - --- A
GG GCC CTTGA TG TCCTGC TG AAGGAG GAGG T
|| ||| |||| || ||||| ||||
CC CGG GGATT AC AGGACG AC TTCCTT TTCC G
A T C CCA --- G GAA T

GAM330

GGAGCGGATGGGCGGCGCGGGCGGCGAGGGCAGCGACGACGACACCTCGCTCACCTGAGCGCCGCACCGCT
TC 5006 TGGGCGGCGCGGGCGGCGAGGGCA 5007

ATGG -- C- GCAG A
GGAGCGG GCGGCGC GGG G GCGAGG CG C
||||| ||||| ||| ||||| ||
CTTCGCC CGCCGCG TCC C CGCTCC GC G
A--- AG A T ACA- A

GAM331

GGAGCTGGAGAGGTGCAGGCCCAGGGCGTCGTCCGAGTGAGCAGCGGTGCTGGCCGTGTGGGACCCGGGCC
CGCTTAGCACC 5078 TGGCCGTGTGGGACCCGGGCCCGC 5079

A AGAGGT A A CG TC A G G
GG GCTGG GC GGCCC GGG TCG CG GT AGCA C
|| |||| || ||||| || || || ||||
CC CGATT CG CCGGG CCC GGT GC CG TCGT G
A ----- C - AG GT - G G

GAM332

GGAGCTGGCCCTGGGCAGCAACAAGCTGGGTGATGTGGGCATGGCGGAGCTGTGCCAGGGCTGCTCC 5105
TGGCGGAGCTGTGCCAGGGCTGC 5106

T G ACAA GG G T
GGAGC GGCCCTGGGCA CA GCT GT ATG G
||||| ||||| || || ||||
CCTCG TCGGGACCCGT GT CGA CG TAC G
- - ---- GG G G

GAM333

GGAGGGCCAGGGTTTCCCCGGGCGCGGGGCTTATCTTCCTTTGCCTGCTATGAAAAACATTCTCACCTTCC 5123
GCCTGCTATGAAAAACATTCTCAC 5124

CC ---- CC-- C CTT
GGAGGG AGGGT TTC CGGGCG GGGG A
||||| |||| || ||||| ||||
CCTTCC TCTTA AAG GTCCGT TCCT /
AC CAAA TATC T TCT

GAM334

GGAGGGCGGGGGAGAGACGAGCGGCTCTGGCCCCTTAATTGTACTTCGGGCTCGTATTGTCTCTCCTTTGCGCA
CCTCC 5135 TATTGTCTCTCCTTTGCCCACCTC 5136

-- - - GCTCT CTTAAT
GGAGG GCGGG GGAGAGACGA GCG GGCCC T
||||| |||| ||||| || ||||
CCTCC CGCTT CCTCTCTGTT TGC TCGGG G
AC T A ----- CTTCAT

GAM335 GGAGGTGGGAGGGGAGGGCCACACGATGCGTTGCTGCGCCCCCGCCTTCCTCTCACTCCTCT 5145
TGGGAGGGGAGGGCCACACGATGC 5146
TGG CACACGAT T
GGAGG GAGGGGAGGGC GCGT G
|||| ||||| |||
TCTCC CTCTCCTTCCG CGCG C
TCA CCCC--- T
GAM336
GGAGTCTCCTCTCTACCGCCACTGTCACACCGTAGCCACATGGATAGCACAGTTGTCAGACAAGATTCC 5161
TAGCACAGTTGTCAGACAAGATTCC 5162
CC CTACC C CACA- AGC
GGAGTCT TCT GC ACTGT CCGT C
||||| || || ||| |||
CCTTAGA AGA TG TGACA GGTA /
AC C--- T CGATA CAC
GAM337 GGATAACAGCAATGTTTCAGGGAACAAAGGAGATAA CTTTAAACTCTGACGTGCCGTGAGCC 5176
TAACAGCAATGTTTCAGGGAACAAA 5177
ATA A A T AAC GAG
GG AC GCA TGT CAGGG AAAG A
|| || || || || || |||
CC TG CGT GCA GTCTC TTTC /
GAG C - - AAA AAT
GAM338 GGATACAAGTGGGGCCATGCCTCCCTGGCCCTGACTCCAGGCTGGGGTATCCTGAACTGTATCC 5197
TACAAGTGGGGCCATGCCTCCCTG 5198
A G- CC -- CCC
GGATACA GT GGG ATGCCTC CCTGG T
||||| || || ||||| |||
CCTATGT CA TCC TATGGGG GGACC G
- AG -- TC TCA
GAM339 GGATATCATCACTCAGATTAAAGCAGCTTCTGGACTTTGTTTTGAAATGTAAAAGTGATGAAAATCC
5213 TATCATCACTCAGATTAAAGCAGC 5214
A- --- GA CTTC
GGAT TCATCACT CA TTAAAGCAG T
|||| ||||| || |||||
CCTA AGTAGTGA GT AGTTTTGTT G
AA AAAT AA TCAG
GAM340 GGATATGGGGTGCAAGTCGAGTTCGGGACCACGCTTGGGGAAGTGCGCCAGAACTATCC 5220
TATGGGGTGCAAGTCGAGTTCGGG 5221
TGG--- AG GAG AC
GGATA GGTGCA TC TTCGGG C
|||| ||||| || |||||
CCTAT CCGCGT AG GGGTTC A
CAAAGA GA --- GC
GAM341 GGATGAAAACATGGACCTCTTGGAAGGTATAA CTTGACTTTGAAGACTCTGTCCGAAAGTTTATCT 5228
TGAAAACATGGACCTCTTGGAAGG 5229
AACA C--- G G T
GGATGAA TGGAC TCTT GAAG TA A
||||| |||| ||| ||| ||
TCTATTT GCCTG AGAA TTTC GT A
GAAA TCTC G G C

GAM342

GGATGGGGCAGAGCTGAGAAGCCAAGGGGGGAAGAGTTGGGGCTGACCTCTTCTTCACCTCGGGCCTTAATCA
CTGACCAAGTCC 5248 TGAGAAGCCAAGGGGGGAAGAGTT 5249

GG - AGC- AA AA G TT GG
GGAT GG CAG TGAG GCC GGGG GAAGAG GG C
|||| ||| ||| ||| ||| ||| ||| ||
CCTG CC GTC ATTC CGG CTCC CTTCTT CC T
AA A ACTA -- G- A CT AG

GAM343

GGATGTAGTTCGTTCAACTAACGGTGACTTTTACAAATGAGACGGAAAATCATGTAAACTGTATCCTTTAGTTTTATC
GCTGTATCT 5284 TGTAAGTGTATCCTTTAGTTTTA 5285

C TC C TG T- AA GACG
GGATGTAGT GT AACTAA GG AC TTTACA TGA G
||||||| || ||||| || || ||||| ||
TCTATGTCG TA TTGATT CC TG AAATGT ACT /
C TT T TA TC -- AAAA

GAM344

GGCAAAGACGGCCATAGGGTGCTCTGAGTTTTGGGATGGTCACATGACACAATCCAGCACTTGAACCTGGGGCC
TCGTGCC 5296 TAGGGTGCTCTGAGTTTTGGGATG 5297

AA C ATA GC T T A - A
GGCA GA GGCC GGGT TC GAGT TTGGG TG GTC C
|||| ||| ||| ||| ||| |||| ||| ||
CCGT CT CCGG TCCA AG TTCA GACCT AC CAG A
G- - GG- -- - C A A T

GAM345

GGCAACTTCAGGATGACAAAAACCAAAGTCTCTTCTGCTGGGAAATCCCAGTACAGATCGTTTCTCATCTCTAAGT
GCC 5306 TGACAAAAACCAAAGTCTCTTCTG 5307

A CA CAA CAAA CTTC A
GGCA CTT GGATGA AAAC GTCT TGCTGGG A
|||| ||| |||| ||| ||| |||||
CCGT GAA TCTACT TTTG TAGA ATGACCC A
- TC C-- C--- C--- T

GAM346 GGCAGTAGGGACTCTTTGCAGGGTTCCTTCCTCGGATCATCCAAGGCTGTCCCTACTGTGCC 5337
TCCAAGGCTGTCCCTACTGTGCC 5338

-- T- CAG T TT
GGCAC TAGGGAC CTTTG GGT CC C
|||| ||||| |||| ||| ||
CCGTG ATCCCTG GGAAC CTA GG C
TC TC CTA - CT

GAM347

GGCAGAGCTGGGCTGACACAGACGGACTGGGATTGGCTAAGGAAGATCACCTGGCCCCTCCAGCCCTAGCCCT
GGCTCTTTTGTG 5348 TGACACAGACGGACTGGGATTGGC 5349

--- - ACACAGAC A ATT A AAG
GGCA GAGCT GGGCTG GG CTGGG GGCTA GG A
|||| |||| |||| || |||| |||| ||
CTGT CTCGG CCCGAT CC GACCT CCGGT CC /
TTT T ----- C CC- - ACT

GAM348 GGCATCAGAGTAGGTATATGACTTTTTTTTTTTTTTTTTTTAGGAGAGATGGGTCCCCGCTCTGGTGCC
5360 TCAGAGTAGGTATATGACTTTTTT 5361

TA TATAT TT TT

GGCATCAGAG GG GACT TTTTTTTT T
||||||| || ||| |||||
CCGTGGTCTC CC CTGG AGAGAGGA T
GC ---- GT TT

GAM349

GGCATCGGGAAGAGCCTAAGTCCACATTATAAAATAGGAAGTGATGCGGGTACAGTTACTCCCGGGACC 5370
TGCGGGTACAGTTACTCCCGGGAC 5371
CA AGA---- AA ATTATAA
GG TCGGGA GCCT GTCCAC A
|| ||||| ||| |||||
CC GGCCCT TGGG TAGGTG /
AG CATTGACA CG AAGGATA

GAM350

GGCCATTGTTCCGCGCCGATGGCGAGATCCTTGTTCTCAGATAGCGTTCATCGCCCGTCGTGGTCAACGGGGCC
5379 TAGCGTTCATCGCCCGTCGTGGTC 5380
A- TT C AT - TCC CC
GGCC TTG CCGCG CG GGCGA GA TTGTT T
||| ||| ||||| || ||||| |||
CCGG AAC GGTGC GC CCGCT CT GATAG /
GC T- T -- A TGC AC

GAM351

GGCCCAGCGGCCTCTTTCCTACGTACCTCGGACTGACGGGGCGGTCTGACAAGTGCCGTGGGTTGGGCTTCGC
CGGGCT 5384 TGACAAGTGCCGTGGGTTGGGCTT 5385
A -- CTTT - C-- AC
GGCCC GCG GCCT CCTACG TAC TCGGACTG G
||||| ||| ||||| ||| |||||
TCGGG CGC CGGG GGGTGC GTG AGTCTGGC G
C TT TT-- C AAC GG

GAM352

GGCCGGTGATCCCTCCAAAGAACCAGAAGCGGGTGGGTTCACTATGAGATCTGAGGAGGCTTCGTGGGCT 5401
TGAGATCTGAGGAGGCTTCGTGGG 5402
G TC AA AC- GA C T
GGCC GTGA CCTCC AGA CA AG GGG G
||||| ||| ||||| ||| || |||
TCGG TGCT GGAGG TCT GT TC CTT G
G TC AG AGA A- A G

GAM353 GGCCTGGGAGGGCATGGGTCAAGGGCGTCCGGGAAGCTGGAGCTCTTCCTGCTGACCTTCCGGCC
5418 TGGGAGGGCATGGGTCAAGGGCGT 5419

T G - TC G G
GGCC GGGAGG CA TGGG AAGGGC TCCGG A
||||| ||||| || ||||| |||||
CCGG CCTTCC GT GTCC TTCTCG AGGTC A
- A C -- - G

GAM354 GGCGAGCGACAGCCCCTGCTGGGTCCCCCTGAGTCCATGCGGGAACATGTGGTCTGCTGCC 5459
TGCGGGAACATGTGGTCGCTGCC 5460

G A C---- - TCCC
GGC AGCGAC GC CCTGC TGGG C
||| ||||| || ||||| |||||
CCG TCGCTG TG GGGCG ACCT C
- G TACAA T GAGT

GAM355 GGC GGGG CCGGGGGCCCGGGGAGCGGCCTGGCTACGCTGCCCGGGCTCCCGCCCTCAGCC 5469
TGCCCGGGCTCCCGCCCTCAGCC 5470

- C G GCCT
GGC GGGG CCGGGGGCCCGGG AGCG G
||| ||| ||||| |||
CCG CTCC GCCCTCGGGCCC TCGC /
A C G ATCG

GAM356

GGCTCAATGAAATGAAAGTGAAAAGAACCTGACTTTACTTCATCTTTCTTTTGATTAAGTTGTGATCTTGAGCC
5507 TGAAATGAAAGTGAAAAGAACCTG 5508
T A-TG A-- G CC- CTT
GGCTCAA GA A A AGT AAAAGAA TGA T
||||| || | ||| ||||| |||
CCGAGTT CT T T TTA TTTTCTT ACT /
- AG GT CAA G TCT TCA

GAM357

GGCTCTGCTCCTCACATTGCCAGTTAATCTTCGTGTGACTACAGTACCTGGAAAAACGGGGACAGCAGCC 5514
TACAGTACCTGGAAAAACGGGGAC 5515
- C ACATTG T ATCT-- G
GGCT CTG TCCTC CCAG TA TC T
||||| ||||| ||||| ||
CCGA GAC AGGGG GGTC AT AG G
C - CAAAAA C GACATC T

GAM358 GGCTGACAGGGACCGCCGGCCGCCCGGCTCCGCTTTGCCGGCAGTGAGTCCGCTGTCTTCC 5522
TGACAGGGACCGCCGGCCGCCCG 5523

CT - --- CGCCC G
GG GACAG GGAC C GCCGGC CG C
|| ||||| ||||| ||
CC CTGTC CCTG G CGGCCG GC T
TT G A TGA TTTC- C
GAM359 GGGAAGTATAGGAAGTGAGAAGTCAGATTACCCTAGTCCTCTAGGGTGCTTAAAGCTAACTAGTCCC
5541 TAGGAAGTGAGAAGTCAGATTACC 5542

AC GA GAG CAGATT T
GGGA TTAG AGT AAGT ACCCTAG C
||||| ||| ||||| |||||
CCCT GATC TCG TTCG TGGGATC C
-- AA AAA ----- T

GAM360

GGGAATGATAGCATTGAAGGACTCGGGGATATCTAACAGCAATACCTGATCACTACTTCGCACTAGTTTCTC 5556
CACTACTTCGCACTAGTTTCTC 5557
TGA CAT GAC--- GATATCTA
GGGAA TAG TGAAG TCGGG A
||||| ||| ||||| |||||
CTCTT ATC GCTTC AGTCC /
TG- AC- ATCACT ATAACGAC

GAM360

GGGAATGATAGCATTGAAGGACTCGGGGATATCTAACAGCAATACCTGATCACTACTTCGCACTAGTTTCTC 5556
TCACTACTTCGCACTAGTTTCTC 5557
TGA CAT GAC--- GATATCTA
GGGAA TAG TGAAG TCGGG A

||||| ||| ||||| |||||
CTCTT ATC GCTTC AGTCC /
TG- AC- ATCACT ATAACGAC
GAM361
GGGAGAATCCCCTAAGCTCCAGGGCCCAGGGTCTAACCTGAGAGGTCTGGGGCTGCAGGAAGCTGGGGGAGGC
TCCC 5566 TCCCCTAAGCTCCAGGGCCCAGGG 5567
AA A - AG- AG GT AAC
GGGAG TCCCCTA GCT CC GGCCC G CT C
||||| ||||| ||| || ||||| | ||
CCCTC AGGGGGT CGA GG TCGGG C GA T
GG - A ACG G- TG GAG
GAM362 GGGAGGGTCACTTGAGCCCAGGAATTGTGAGATCAACTGGGCATATAGGGAGATCCTGTC 5577
TCAACTGGGCATATAGGGAGATCC 5578
G A- A-- GA- G
GGAGGGTC CTTG GCCCAG ATT T
|| ||||| ||| ||||| |||
CT TCCTAG GGAT CGGGTC TAG G
G AG ATA AAC A
GAM363 GGGAGTGAAATTTTCCTCTCTTCCCCTGCACATTAGGAAGGGTATCAGAGGGGTTGGTGTACATTCCC
5609 ATCAGAGGGGTTGGTGTACATTCC 5610
AA- TT TC-- GCACA
GGGAGTG ATT CCTCTCT CCCT T
||||| ||| ||||| |||
CCCTTAC TGG GGGGAGA GGGG /
ATG TT CTAT AGGAT
GAM364
GGGAGTGGACGCGCTGGCAGGATGGTGCTGGAGAGCGTGGCCCCGTATCGTGAAGGTGCAGCTCCCTGCATAT
CTGAAGCGGCTCCCACTCCC 5617 TGGCAGGATGGTGCTGGAGAGCGT 5618
G AC GGCA G T A GTG - GTAT
GGGA TGG GCGCT GGATG TGC GG GAGC GC CC C
||||| ||| ||||| ||||| ||| ||| ||| |||
CCCTACC CGGCGA TCTATACG CC CTCG CG GG G
G CT AG-- - T - A-- T AAGT
GAM365
GGGATGTCCTGCTCCAATACCCGCACTGCTCTGGAGTATTGCCCTCTTTCCCAAGGAGATGCTGCTGGTGGAGC
TGGTATGGGTGCGGTCTTCCC 5631 TACCCGCACTGCTCTGGAGTATTG 5632
TGTC T A C ATG CT - GC CTT
GGGA CTGC CC ATACC GC C CT GG AGTATT CCT T
||||| ||| ||||| ||| || || ||||| |||
CCCT GGCG GG TATGG CG G GG TC TCGTAG GGA C
TCT- T G T A GT -- G A- ACC
GAM366 GGGATTACAGGCGTTGAGTCACCGTGCCCGGCCAGTACCCACTTCTCTTAATGCTCTATGAGTTCC
5639 TTACAGGCGTTGAGTCACCGTGCC 5640
AC- - TCACC CCC CC
GGGATT AG GCGTTGAG GTG GG A
||||| || ||||| ||| ||
CCTTGA TC CGTAATTC CAC CC G
GTA T TCTT- --- AT
GAM367
GGGCAGGTGCCTGGTCAATCAGTCCTCGGGATGGCAGCCATCAACCCGTGGGCCTCCTGGGGTGACCTTACGG
ACCAATCTTGGGGGATGAAAGCTGTTGACCCATGGGCCTCCTGGGCTCTGTGTCC 5660

TGGCAGCCATCAACCCGTGGGCCT 5661

- T TG TCAATCA TC A --- AA ---- G TCCT G
GGGCA GG GCC G GTCC GGG TGGCAGC CATC CCCG TGG CC GGG T
|||| || || | ||| || ||||| ||| ||| ||| ||
CCTGT TC CGG C CGGG CCC GTTGTCTG GTAG GGGT ACC GG TCC G

G T GT CTC---- TA A AAA G- TCTA A CAT- A
GAM368 GGGCCAAAGAGCAGCACCAGAACGCTGTGGGGAAGAGCAGCTGGGTGCTCGCCAGGGCCC 5676
GCTGGGTGCTCGCCAGGGCCC 5677

AAAGA - AGAAC GGG
GGGCC GC AGCACC GCTGT G
|||| || ||||| ||||
CCCGG CG TCGTGG CGACG A
GAC-- C GT--- AGA
GAM369 GGGCCCTGAGATGGGGTCTGACCTCAGTTCCTGCGGGGAACCTTCACCAGTGACCCCAGTCAGTGCCC
5703 TGAGATGGGGTCTGACCTCAGTTC 5704

C GA TGACCTC- TG
GGGC CTGA TGGGGTC AGTTCC C
|||| ||| ||||| |||||
CCCG GACT ACCCCAG TCAAGG /
T G- TGACCACT GG
GAM370

GGGCGAGCTCGGTGGTGACGCGCGGCCCTCACGTGACCCAGAGCTGCAGAGCGACGCAGCCTTCGGTGCAGT
CGTCACTCGCGTCTGGCTACCAGCTCCCC 5719 CGGTGCAGTCGTCACTCGCGTCTG 5720
C C -- C-- C- - G CCC A AGA
GGG GAGCT GGTGGT GACGCG GGC CT CAC TGA AG GCTGC G
||| ||||| ||||| ||| || ||| || ||| |||||
CCC CTCGA CCATCG CTGCGC CTG GA GTG GCT TC CGACG C
- - GT TCA CT C - --- - CAG

GAM371
GGGCGCTAACACACACAACGGCGCTCTGGGGGGGCGCCACAACACCCCTTG TAGACGCAATTGGTCGTTTA
GCGCACC 5729 TAACACACACAACGGCGCTCTGGG 5730

- C - A CG C -- CGCC
GG GCGCTAA AC AC CAA GCG TCTG GGGGGG A
|| ||||| || || ||| ||| ||| |||||
CC CGCGATT TG TG GTT CGC AGAT TCCCC C
A - C - AA C GT ACAA
GAM372 GGGCGTATGCCTTTCCTGGAGGCGGGGACGATCCGGGTAGGAGACAAAGGGCGAGCTCCC 5747
TCCGGGTAGGAGACAAAGGGCGAG 5748

C A ----- GG G
GGG GT TGCCTTT CCTGGA CG G
||| || ||||| ||||| ||
CCC CG GCGGGAA GGGCCT GC G
T A ACAGAGGAT A- A
GAM373 GGGCTGGCGTCTGGGTGGGGTGGGCGCGGTTGGGCGGCGTCCGCCATAGTTCCGCGCGTGCCC
5765 TGGCGTCTGGGTGGGGTGGGCGCG 5766

TG C TG--- G TT
GGGC GCGT TGGG GGGTGGGCGC G G
|||| ||| ||| ||||| ||
CCCG TGCG GCCT CCCGCCTGCG C /
-- C TGATA G GG

GGGGAACGCGGTGGCTTCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTTCGCGGCCGTGGACGGG
GCCGGGGCCGAGGCCGCGGAGCTCGCGGAGGCAAGGCCGAGGATAAGGAGTGGATGCCC 5800
TGGCATCCGGGGCCGGGGTTCGCGG 5801

GAM375

GGGGAACCGCGGTGGCTTCGCGGAGGTTTCGGCAGTGGCATTCTGGGGCCGGGGTTCGCGGCCGTGGACGGG
GCCGGGGCCGAGGCCGCGGAGCTCGCGGAGGCAAGGCCGAGGATAAGGAGTGGATGCCC 5813
TGGCATTCTGGGGCCGGGGTTCGCGG 5814

GAM376 GGGGAGAATAGAAAAGAAAACAATTGACAAAATCCTCAAATGTAAACTCAATTTGCCTCCCT 5837
TGTAAGTCAATTTGCCTCCCT 5838

GAM377

GGGGATGGAAGGCGATGGCCCCCTGCGAGGACGATGGCCCGGCCCGCCTCGCCCCGGCGGCATCCCTGCCGTC
GCC 5849 AAGGCGATGGCCCCCTGCGAGGACG 5850

GAM378

GGGGGACTGAATGGCGCATTCGGGGCGGGAGGGCAAAACAACCCCACTGTTTTCCCGCCCCCCCTGGAATC
TGCCCCCGTGTCCCCC 5853 TGGCGCATTCGGGGCGGGAGGGCA 5854

GAM379

GGGGGAGTTGTGGTGCTTCTGGGTCTCTGGGCCCGCCTGCTGGCCTGGGATGCCCTCATGTTGGGAAGCATT
CCGTGCCCCC 5875 GGGATGCCCTCATGTTGGGAAGCA 2525

GAM379

GGGGGAGTTGTGGTGCTTCTGGGTCTCTGGGCCCCGCCTGCTGGCCTGGGATGCCCTCATGTTGGGAAGCATT

CCGTGCCCCC 5876 GGGATGCCCTCATGTTGGGAAGCA 2525

AGT TG G TCTCT -- -- T
GGGGG TG GTGCTTCT GG GGGC CCC GCC G
|||| || ||||| || ||| |||
CCCCC GC TACGAAGG TT CCGG GGG CGG C
GT- CT G GTACT TA TC T

GAM379

GGGGGAGTTGTGGTGCTTCTGGGTCTCTGGGCCCCGCCTGCTGGCCTGGGATGCCCTCATGTTGGGAAGCATT
CCGTGCCCCC 5877 GGGATGCCCTCATGTTGGGAAGCA 2525

AGT TG G TCTCT -- -- T
GGGGG TG GTGCTTCT GG GGGC CCC GCC G
|||| || ||||| || ||| |||
CCCCC GC TACGAAGG TT CCGG GGG CGG C
GT- CT G GTACT TA TC T

GAM379

GGGGGAGTTGTGGTGCTTCTGGGTCTCTGGGCCCCGCCTGCTGGCCTGGGATGCCCTCATGTTGGGAAGCATT
CCGTGCCCCC 5878 GGGATGCCCTCATGTTGGGAAGCA 2525

AGT TG G TCTCT -- -- T
GGGGG TG GTGCTTCT GG GGGC CCC GCC G
|||| || ||||| || ||| |||
CCCCC GC TACGAAGG TT CCGG GGG CGG C
GT- CT G GTACT TA TC T

GAM380

GGGGGGAGGAACCCACCAACAGGGGGGTCTCCACAACCTCCTCAGTGTCCGCCCACTTGTGTGCGGAAGCCC
CCCCC 5879 TCCGCCCACTTGTGTGCGGAAGC 5880

A AA- AC A G CTC AACT
GGGGGG GG CCC CA CAGG GGGGT CAC C
|||| || || ||||| |||
CCCCC CC GGG GT GTTC CCGG GTG /
- GAA CT - A CCT ACTC

GAM381 GGGGGGCACCAATGACAAGGGAATTGGGATGGGGATGACAGTCCCTATTTCTTTGCTGTGTTCCCC
5892 TGACAAGGGAATTGGGATGGGGAT 5893

CAATGA ATTGG G
GGGGGGCAC CAAGGGA GATGGGGAT A
|||||| ||||| |||||
CCCCTTGTG GTTTCCT TTATCCCTG C
TC---- ---- A

GAM382 GGGGGTCGTCCTTGGCACGCGCTGGGGAGTGCTAGTCCTGAGGCGAGCCGGTAGATCTCC 5913
AGGCGAGCCGGTAGATCTCC 5914

GT TT A G G GTG
GGGGGTC CC GGC CGC CT GGGA C
|||||| || ||| || |||
CCTCTAG GG CCG GCG GA TCCT /
AT -- A - G GAT

GAM383

GGGGTAGTGATGGCAACTGATGGAACAGGAGAATGCTCAGCAGCATTTGCTCTTCCAGCCTGTCACGCCTC
5924 TGGCAACTGATGGAACAGGAGAAT 5925

A AT AACTGA C GA C
GGGGT GTGG GGC TGGAA AG GAATGCT A
|||| ||| || |||| || |||||

CTCCG CACT CCG ACCTT TC TTTACGA G
- GT ----- C G- C
GAM384 GGGTAATCAGGGAAGTGGTATTTTCAGCAGGGACCTAAAGGATGAGAAGACACAAACCTGCAAAGACCC
5945 TGAGAAGACACAAACCTGCAAAGA 5946
AAT-- GAA GTA GC---- G
GGGT CAGG GTG TTTCA AG G
|||| ||| ||| ||| ||
CCCA GTCC CAC AGAGT TC A
GAAAC AAA AGA AGGAAA C
GAM385
GGGTCCACTATCATTTAATTTCCCTTGAACCTGCTCTGCTAGTTTAATCTGCTAATATGAAAGTTAATTAAGACCT
5969 TATCATTTAATTTCCCTTGAACCT 5970
C----- A TTAATTTCCC CT T
GGGTC ACT TCAT TTGAAC GC C
|||| ||| ||| ||| ||
TCCAG TGA AGTA AATTTG CG /
AATTAAT A TAATCGTCT- AT T
GAM386
GGGTGAAGATGGCGGCAGCCGAGGCCGCGAACTGCATCATGGAGGTGTCCTGTGGCCAGGCGGAAAGCAGTG
AGAAGCCC 5975 TGGCGGCAGCCGAGGCCGCGAACT 5976
GAAGATG- GGCA- GA AACT AT
GGGT GC GCC GGCCGCG GCATC G
|||| || ||| ||| ||| |||
CCCG CG CGG CCGGTGT TGTGG /
AAGAGTGA AAAGG A- CC-- AG
GAM387 GGGTGAGAGGCTGGTGGTTGCCTCCCGTCCTGGGCAGGCTGCAGCCTCATGCCATGTCTCTCTCCC
5985 TGAGAGGCTGGTGGTTGCCTCCCG 5986
T - ---- CT C CC
GGG GAGAGGC TGGT GGTTCG CC GT T
||| ||| ||| ||| ||| ||| |||
CCC CTCTCTG ACCG CCGACG GG CG /
T T TACT TC A GG
GAM388 GGGTGCGGGACTTAAACACAACCTGGACCTCGTGGGGCGGGTGCCCACTAAAGTGCTGGACCC 6007
TGCGGGACTTAAACACAACCTGGA 6008
G G AAACACA- GA T
GGGT CGG ACTT ACCTG CC C
|||| ||| ||| ||| ||| |||
CCCA GTC TGAA TGGGC GG G
G G ATCACCCG GG T
GAM389
GGGTGGCAGCACCAGGGGACACACCTGCCAAACCCACCAGATGGAGGGGCCCTCCCTGGTCTCTGGCCACCC
6019 TGGCAGCACCAGGGGACACACCTG 6020
- C- ACACA G AACCC
GGGTGGC AG ACCAGGGG CCT CCA A
||||| || ||| ||| ||| |||
CCCACCG TC TGGTCCCT GGA GGT /
G TC CCCGG - AGACC
GAM390
GGGTTATCTGCAACTGAGAGGGGGCTGGTTAAGGCGTCCCCAAGTTGGAAGGGCGCTTTGCTTCTGTTTTCTGGA
TGCAGAGTCCT 6033 TGAGAGGGGCTGGTTAAGGCGTCC 6034

TTA A - G CT T -- AA
GGG TCTGCA CT GAGAG GG GGT AAGGCGTCC CC G
||| ||||| || ||||| || ||| ||||| ||
TCC AGACGT GG CTTTT TC TCG TTTCGCGGG GG /
TG- A T G T- - AA TT

GAM391

GGGTTCCAATGGGTGCACAGTTCCAAAAATGTGGAGGGACCCTTCTCAGTTTTGAGGCCATGAATCCAAAGCCC
6044 TGGGTGCACAGTTCCAAAAATGTG 6045
CCAA G CA TC A T G
GGGTT TGGGT CA GT CAAAA TG GGAGG A
||||| ||||| || || ||||| || |||||
CCCGA ACCTA GT CG GTTTT AC CTTCC /
A--- A AC GA G T C

GAM392

GGTAGGGAGTGAAAGGCCCGGCCACCTAAAGGCACAGCTGGTGCCTGGGTCAAGCTGAGGCGGCATCTCTCTG
CC 6066 TGAAAGGCCCGGCCACCTAAAGGC 6067
- AAAG - C-- AA AG
GGTAGGGAG TG GCC CGGC ACCT AGGCAC C
||||||| || ||| ||||| ||||| |||||
CCGTCTCTC AC CGG GTCG TGGG TCCGTG /
T GG-- A AAC -- GT

GAM393 GGTGAAGGTGCTGAGGAAAGCTCCCAGGATGAGCCTGGGAGTGCTTCAGGTATCAGCTTCCAGCC
6072 TGGGAGTGCTTCAGGTATCAGCTT 6073

-- G ---- AAA AT
GGT GAAG TG CTGAGG GCTCCCAGG G
||| ||||| || ||||| ||||| |||||
CCG CTTC AC GACTTC TGAGGGTCC /
AC G TATG G-- GA

GAM394 GGTGACAACATGCTGGAGCCAAGTGCTAACATGGCCTTGTTCAAGGGATGGAAAGTCACC 6089
TGACAACATGCTGGAGCCAAGTGC 6090

AA-- G G- T AA
GGTGAC CAT CT GAGCCAAG GCT C
||||| ||||| || ||||| ||||| |||||
CCACTG GTA GG CTTGGTTC CGG /
AAAG G AA - TA

GAM395

GGTGCCTGGTCAATCAGTCCTCGGGATGGCAGCCATCAACCCGTGGGCCTCCTGGGGTGACCTTACGGACC
6103 TCAGTCCTCGGGATGGCAGCCATC 6104
G T--- ATCAGT T AG CA
GGT CC GGTCA CCTCGGGA GGC CCAT A
||| || ||||| ||||| ||||| |||||
CCA GG CCAGT GGGGTCCT CCG GGTG C
- CATT ----- - -- CC

GAM396 GGTGGGGAAGACTGAAGAAGTGTTAACTGAAAACAGGTGACACAGAGTCACCAGTTTTCCGAGAACC
6117 TGACACAGAGTCACCAGTTTTCCG 6118

GG-- AA A--- A A
GGT GGAAGACTG GA GTGTTA CTG A
||| ||||| || ||||| ||||| |||||
CCA CCTTTTGAC CT CACAGT GAC A
AGAG CA GAGA G A

GAM397

GGTGTGCCCCGGAACCGGCCCTTGGTGGGGAAATAATGCCTTTGCTAAGGGGGCCCCGGATTCCGGGTGCGC
6135 TAAGGGGGCCCCGGATTCCGGGTC 6136

T - --- TG AAAT
GGTG GCCCGGAA CCGG CCCTTG GGG A
||||| ||||| ||| ||||| |||
CCGC TGGGCCTT GGCC GGGAATC TTC /
- A CCGG GT CGTA

GAM398

GGTTTTCAAGGTGTCATGAAAAGATGGGGATTTAAAGGCCAGCCTGCTACGCATGGTCAAACGAAAACCCACAG
GAGACCTGGAGCT 6161 TGAAAAGATGGGGATTTAAAGGCC 6162

CA G A AAAAGA GA AAA- - CTG
GGTTTT AGGT TC TG TGGG TTT GGCCA GC C
||||| ||||| || ||||| ||| ||||| ||
TCGAGG TCCA AG AC ACCC AAG CTGGT CG /
-- G G ----- AA CAAA A CAT

GAM399 GGTTTTTCTATGAGATGAGAATTATGAACACTTCATATAGGTAAATTCCATAGGTTGAGCT 6189
TATAGGTAAATTCCATAGGTTGAG 6190

T- AG GAGAAT- C
GGTTT TCTATG AT TATGAA A
||||| ||||| || ||||| |||
TCGAG GGATAC TA ATACTT /
TT CT AATGGAT C

GAM400 GTACAGATTTTTATAAAATCATCTATACAGATGAAGTACAAATTTTTATAAAATAATCTATAC 6197
TGAAGTACAAATTTTTATAAAATA 6198

C -- ----- A
GTA AGATT TTTATAAAA TCATCT T
||| ||||| ||||| ||||| |||||
CAT TCTAA AAATATTTT AGTAGA A
A TA TAAACATGA C

GAM401

GTACCAGGCCAGTTATAACCAGAGCTTTTCTAGTCAGCCTCACCAAGTAGAACAACAGAGCTTCAGCAAGAACA
GCTTCAAACAGTGTTGGCACTTAC 6201 TAACCAGAGCTTTTCTAGTCAGCC 6202

CC - TT AACCA- T A C-- C ACCAAGTA
GTA AG GCCAG AT GAGCT TTCT GT AGC TC G
||| || ||||| || ||||| ||||| ||| ||
CAT TC CGGTT TG TTCGA AAGA CG TCG AG /
-- A GG ACAAC C A ACT - ACAACAA

GAM402

GTACGGCGTGTCTCCTCCCTGCAGCGCGGCGTGCCGACTACATGCGCGCGCACCTGGCGGGAGGCGCGGGCCC
GGC 6210 TGC GCGCGCACCTGGCGGGAGGCG 6211

AC G - T A---- - GCC
GT GGC TGT CCTCCC GC GCGCG GCGTG G
|| ||| ||||| || ||||| |||||
CG CCG GCG GGAGGG CG CGCGC CGTAC A
GC G C - GTCCA G ATC

GAM403 GTAGAGCTTTATGCTGAAAAGGTGGCCACTAGAGGTCTGTGTGCCATTGCCAGGCAGAGTCTCTGC
6262 GTGTGCCATTGCCAGGCAGAGTC 6263

- TA GAAAA - T A
GTAGAG CTT TGCT GGTGGC CAC AG G

||||| ||| |||| ||||| ||| ||
CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T
GAM404
GTAGAGGAAGATGAGCTTGGCGTACAACCTCCTCCTCCAGCTCCAGCTCCCGAGTCTCCCGCACCCAGGAAGATGT
CCTGGCAGAGCTTGAGGATGCGGTCCACGCACGGCAGCTCCTCGAAC 6289
TGTCTGGCAGAGCTTGAGGATGC 6290
A- AATGA TG ACA CC- C CA CCCGA C GC
GT GAGGA G GCT GCGT ACT TCCTCAGCTC GCT GTCT CC A
|| ||||| || |||| || ||||| || |||||
CA CTCCT C CGG CGCA TGG AGGAG TCGAG CGG TAGA GG C
AG -GA-- CA CC- CGT T A- TCCTG A AC
GAM405
GTATACTGTTATCTCCCAGGGCACCCAGTGCAAGGCTCTTTATCTCATCCCGCTTGGGTGTACCTGGTTACCCTC
AGTGAC 6304 TCCCAGGGCACCCAGTGCAAGGCT 6305
A TTATCTC - T AA CTCTTT
GT TACTG CCAGG GCACCCAG GC GG A
|| |||| ||||| ||||| || ||
CA GTGAC GGTCC TGTGGGTT CG CC /
- TCCCATT A - C- TACTCT
GAM406
GTATCGACGGAGCATGTACAGGGAGGCATGCACCGCAGTGGTGAATACACGTCGAGCTGCAAGCATTCACTGCA
TGCTCTGGTAC 6311 TGTACAGGGAGGCATGCACCGCAG 6312
GAC CAG G A C-- CA GTG
GTATC GGAGCATGTA GGA GC TGCA CG GTG A
||||| ||||| ||||| || ||||| || |||||
CATGG TCTCGTACGT CTT CG ACGT GC CAC /
--- CA- A A CGA TG ATA
GAM407 GTATGAAAGGGGGAAACAAAGAACAGCCTTTTAGGTAAGGCTTTTCAGTACCTGCCTCGTG 6329
TGAAAGGGGGAAACAAAGAACAGC 6330
AA G AA AAA C TT
GTATGA GG GG AC GAA AGCCTT A
||||| || || || |||||
CGTGCT CC TC TG CTT TCGGAA G
-- G CA A-- T TG
GAM408
GTCAAGAGAATCAAATTTGCTCTTTACAGGTGCTGGGTCAAAGTCTTCCCGGTTGGAGTCAAGATCAGAATAGCT
CCTCTTGC 6357 TCAAATTTGCTCTTTACAGGTGCT 6358
T AATCAAA C T AGGT TCAA
G CAAGAG TTTG TCTT AC GCTGGG A
| ||||| ||||| || |||||
C GTTCTC AGAC AGAA TG TGGCCC G
- CTCGATA T C AGGT TTCT
GAM409
GTCATGTGATGCTCAATCAGCAAACCAGGGATTGGCTTCATCCTGGGAAAAAGCTATCTGGGTGCAACAAGAC
6372 TGTGATGCTCAATCAGCAAACCAG 6373
A GA ATC AAA--- ATTG
GTC TGT TGCTCA AGC CCAGGG G
||||| ||||| || |||||
CAG ACA GTGGGT TCG GGTCCCT C

A AC CTA AAAAAG ACTT
 GAM410
 GTCCCTCCCTCCCCTGCTGTGACCTTGTGGGGGTTGAGAAACCTAGGCACTCATGGCCCCCTGGAGGGGCAGG
 GCAGGCAGGGCTGGGGC 6380 TGGCCCCCTGGAGGGGCAGGGCAG 6381
 T- CC G A- GT -- AAACC
 GTCCC CCCT CCTGCTTG CCTT GGGGGT TGAG T
 ||||| ||||| || ||||| |||||
 CGGGG GGGA GGACGG AC GGAG CCCCCG ACTC /
 TC C- G GG GT GT ACGGA
 GAM411 GTCCTTTCTTTTCGCCAGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGAAGGC 6419
 TATCATCCTGGTCGCAGGGAAGGC 6420
 T T - C GG C C
 G CCTTTCTT CG CCAGG TG GAC CG T
 | ||||| || ||||| || |||||
 C GGAAGGGA GC GGTCC AC TTG GC /
 - C T T TA C T
 GAM412
 GTCTCACACATGACATGTGAAAATCTGACTCAAAGTTCTTTATCTTGAAGCTGTGTTTATATGTTCCGTGTGCAC
 6436 TGACATGTGAAAATCTGACTCAAA 6437
 CT AT AATCTGAC AG TC
 GT CACAC GACATGTGAA TCAA T T
 || ||||| ||||| ||||| |||||
 CA GTGTG TTGTATATTT AGTT A /
 C- CC GTGTGCA- CT TT
 GAM413 GTGACATTAACAAGGGGATATTACCCAAAAGGGGTGGGTGAAGTGATGGTTTGAATGTCAC 6452
 TGACATTAACAAGGGGATATTA 6453
 AA AAGGGG A AAA
 GTGACATT AAC AT TTACCCA G
 ||||| || ||||| ||||| |||||
 CACTGTAA TTG TG AGTGGGT /
 GC GTAG-- A GGG
 GAM414
 GTGAGGATGGCAGTGCAGGATGCAGTAGATGCCCTGATGCAGAAGTGCTTTCAACTCCTCGTCCTTCAACTCCAA
 CACCTTCCTCAC 6474 TGGCAGTGCAGGATGCAGTAGATG 6475
 ----- C GC- C-- A T- C GAT
 GTGAGGA TGG AGT AGGATG AGT GA GC CT G
 ||||| ||||| ||||| ||||| |||||
 CACTCCT ACC TCA TCCTGC TCA CT CG GA C
 TCCACA - ACT TCC A TT T AGA
 GAM415
 GTGATGAGCACGACGGGACGGGCAGATCCATTCATGCAACCGGTATGAGATCTCCTTACCCTCTGTTGCATCAT
 6489 GAGATCTCCTTACCCTCTGTTGCA 6490
 - C C AC C CAT AA
 GTGATG AGCA GA GGG GGG AGATC TCATGC C
 ||||| ||||| ||||| ||||| |||||
 TACTAC TTGT CT CCC TCC TCTAG AGTATG /
 G - - AT - --- GC
 GAM416
 GTGATGTCCGGAGATTCCGAGCGGCGATATCTGGATCTAAGTCTCCGCTCCGATGTGAAGTCTATCTCTGTGACA
 CCAAT 6500 TGTCCGGAGATTCCGAGCGGCGAT 6501

A - ----- C ATCTG
 GTG TGTC CGGAGAT TCGGAGCGG GAT G
 ||| ||| ||||| ||||| |||
 TAC ACAG GTCTCTA AGCCTCGCC CTG A
 C T TCTGAAGTGT T AATCT
 GAM417
 GTGCCAGCGATGATGAGATAGCCAGGCTGAAGAAGCCAGACCAAGGCATCAAGGGGCGATCAGCCTGGTCTCT
 ATGAAGACTGGCGC 6514 TGAGATAGCCAGGCTGAAGAAGCC 6515
 CGATGAT- ATA AGAA AGA AAGG
 GTGCCAG GAG GCCAGGCTGA GCC CC C
 ||||| || ||||| || ||
 CGCGGTC CTC TGGTCCGACT CGG GG A
 AGAAGTAT --- AG-- --- AACT
 GAM418
 GTGCTCCTTTTTGATATAGATAAAATATTTAATGCTTCTATTTACATCTGCTCATGTAGGTTTTACAATATTCCATGT
 ATATCCAATGTGGATGGTAC 6529 TAAAATATTTAATGCTTCTATTTA 6530
 -- TT- T G AA - T TCTATT CT
 GTGC TCC TT GATATA AT AATATT TAA GCT TACAT G
 ||| || || ||||| || ||||| || |||
 CATG AGG AA CTATAT TA TTATAA ATT TGG ATGTA C
 GT TGT C G CC C T ----- CT
 GAM419
 GTGGAGCAGATAAACCATTGTTTCTCGGCCGCTATCTGGTCAGAGGGGAGCTGGGCCGGGAAATTCTGCCTAC
 6547 TAACCATTGTTTCTCGGCCGCTAT 6548
 A TAACCATT -- A- GG
 GTGG GCAGA GTTTCTCGGCC GCT TCT T
 ||| ||||| ||||| ||| |||
 CATC CGTCT TAAAGGGCCGG CGA GGA C
 - ----- GT GG GA
 GAM420
 GTGGCACAGCTGGAGAGTGGGGAGCTGGGACTTGAGCCCAGGTAAGTGTGTCCCCAGCACCTTCAACTAAACTC
 CATTCTGTGCTGC 6550 CCCCAGCACCTTCAACTAAACTCC 6551
 TG C- --- -- A - TTGA- C
 G GCACAG TGGAG AGT GGGG GCTGGG AC GC C
 | ||||| |||| || ||||| || ||
 C CGTGTC ACCTC TCA TTCC CGACCC TG TG A
 GT TT AAA AC A C TGTGA G
 GAM421
 GTGGCAGAAGATCCCAGCTGACCACGGCCCCCTTTCTCTGGGGTCAGAGGGAGAAGACAGGCGCAGTCAGCAGG
 GGCAGCTGTTGC 6561 TCCCAGCTGACCACGGCCCCCTTTC 6562
 TG AAGA A CA G C---- TT G
 G GCAG TCCC GCTGAC CG CC CT CTCTG G
 | ||| ||| ||||| || || || |||||
 C TGTC GGGG CGACTG GC GG GA GAGAC G
 GT GAC- A AC - ACAGAA GG T
 GAM422 GTGGCCCACGTGGGCAGGACGGCCGCAGGATGGGGTGGCTGTGCTGGTCCGACACCTGGGCTAC
 6593 GTGCTGGTCCGACACCTGGGCTAC 6594
 C -- -- G AGG
 GTGGCCCA GTG GG CAG ACGGCCGC A
 ||||| || || || |||||

CATCGGGT CAC CC GTC TGTCGGTG T

C AG TG G GGG

GAM423

GTGGGGGGCGCTCAATAACTTTGGATACCGGTTCGGCATGGTCACAACACCCGACAGTGCTCTTCGCCAGAAGTTGG
CGGCCCTAC 6611 TAACTTGGATACCGGTTCGGCATGG 6612

G T AAC ATAC TC G ACAA

GTGGGG CGC CAAT TTGG CGG GGCAT GTC C

||||| ||| |||| |||| ||| ||||| |||

CATCCC GCG GTTG GACC GCT TCGTG CAG /

G - AA- ---- TC A CCCA

GAM424

GTGTGAGTGGCTTTGCAGGCCTGGTGGTGGGAGAGCCTCAGGCTCCCTCCTTCTTCGTTCCCTGACCATGCCCTT
GGGC 6623 TTGCAGGCCTGGTGGTGGGAGAGC 6624

G T TTTG- CCT-- T TG A T

GT TGAG GGC CAGG GG GG GG GAGCC C

|| |||| ||| |||| |||| || |||||

CG GTTC CCG GTCC TC TC CC CTCGG /

G - TACCA TTGCT T CT - A

GAM425

GTGTGCGCTGCCTCTGGCATCCTAGAGACCCGGATTTACTCAGCTAGGAGAGAGGATGGATCACAGGGTCTAAG
GGTGGCCATTC 6673 TGGCATCCTAGAGACCCGGATTTA 6674

T C TG TC C AGA C GA A AG

G GTG GC CC TGG ATCCT GA CCG TTT CTC C

| ||| || ||| ||||| || |||| |||||

C TAC CG GG ATC TGGGA CT GGT GAG GAG T

T - GT GA - CA- A AG A GA

GAM426

GTTGTGGGGCTGGTTGCTGTCTTTACGTTTCACAACCATGGAAGGACTGCCAACCTCTACTCCCTTCACAGC
6679 GAAGGACTGCCAACCTCTACTCCC 6680

-- CT---- -T A TTCA

GTTGTG GGG GGTTC C GTCTTT CGT C

||||| ||| ||||| ||||| |||

CGACAC CCC CCAAC G CAGGAA GTA /

TT TCATCT C T G CCAA

GAM427

GTTGTTCTCAGATATCAGTTCTTCCCAGGTGAACAGCAGTGAATCTGTGACTTCACCAAATGGATTAAAGTCAATG
AGCCAC 6693 TATCAGTTCTTCCCAGGTGAACAG 6694

T TCA ATC TTCCCA CA- TG

GT GTTC GAT AGTTC GGTGAA GCAG A

|| |||| ||| ||||| ||||| |||

CA CGAG CTG TTAGG CCACTT TGTC /

C TAA AAA TAAA-- CAG TA

GAM428

GTTTCATTCCAATGAGAGTTGCACACTGTCAGCTTGGTTTTGTGGCTGCTGATAGTCGTACTTTCTTGAAATGGAA
T 6716 TGAGAGTTGCACACTGTCAGCTTG 6717

C T T AC TT T

GTTTCATT CAA GAGAGT GC ACTGTCAGC GGTT T

||||||| ||| ||||| || ||||| |||

TAAGGTAA GTT CTTTCA TG TGATAGTCG TCGG G

A - - C- -- T

GAM429 TAAGATTTTAGCAATACTTCCAATATTGATTTCTTACCAAATGGAATCTAGAAGCTAAATTTTTA 6729
TGGAATCTAGAAGCTAAATTTTTA 6730

T AA- C- ATA ATTT
TAAGA TTTAGC TA TTCCA TTG C
||||| ||||| || ||||| |||
ATTTT AAATCG AT AAGGT AAC C
T AAG CT A-- CATT

GAM430

TAGAGATGGGGTTTCAACTTGTTGGCCAGGCTGGTCTTGAACCTCCTGGCCCCAGGTGATCCACCCACTTTA 6752
TGGGGTTTCAACTTGTTGGCCAGG 6753

A GTT- A TT CT CT
TAGAG TGGG TCA CTTG GGCCAGG GGT T
||||| ||||| ||| ||||| ||||| |||
ATTTC ACCC AGT GGAC CCGGTCC TCA /
- ACCT - C- -- AG

GAM431

TAGCCGTGATGTCCGGGGGGCCGTGTACATCATGTTACCGTGGGGTGGGGTCTGCATTGGCTGCTGGGCATATG
GCTG 6759 TGTCCGGGGGGCCGTGTACATCATG 6760

A G - C ATG G
TAGCCGTG TGTCCGG GGCCG TGTA ATC TTACC T
||||||| ||||| ||||| ||||| ||||| |||||
GTCGGTAT ACGGGTC TCGGT ACGT TGG GGTGG G
- G T C --- G

GAM432

TAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCGGTCCGTGTGCT
GTGCCAGGGCCTGAAGGACTCCCCCTG 6766 CTGCAGGTACCGGTCCGGAATTCC 6767

AA - GG C -- - - T ATTCCC T
TAGGG AG CT TA GCCT GCA GGTAC CGG CCGGA GGG C
||||| ||||| ||||| ||||| ||||| ||||| |||||
GTCCC TC GG GT CGGG CGT TCGTG GCC GGCCT CCC G
CC A AA C AC G T T GCGCA- A

GAM433

TAGGGCGCCTGGCAGTGGTCAAGCCTGAAACCAAGCAATACCCGTCTGTTTTACCCCAAGCCCCAGAGCCCTA
6788 TGGCAGTGGTCAAGCCTGAAACCA 6789

GC CAGT CAAGCC C AG AAT
TAGGGC CTGG GGT TGAAA CA C A
||||| ||||| ||||| ||||| ||||| ||||| |||||
ATCCCG GACC CCG ACTTT GT G /
A- ---- AACCC- T CT CCC

GAM434

TAGGGGTCTGTACCGGGCTGGCCTGTGCCTATCACCTCTTATGCAAACCTTCCCACCCCTGTATTCCCACCCCTG
6806 TGCAAACCTTCCCACCCCTGTATT 6807

CT-- C C CCTG--- C TCA
TAGGGGT GTAC GGG TGG TGC TA C
||||| ||||| ||||| ||||| ||||| ||||| |||||
GTCCCCA TATG CCC ACC ACG AT C
CCCT T C CTTCCAA T TCT

GAM435 TAGTATATGAATATGCGGGATATAAGTCTTATGAATAGACACCACGTATAACTCTTACTG 6817
TATGAATATGCGGGATATAAGTCT 6818

TATGAA - ATATAA TAT

TAGTA TATGCG GG GTCT G
 |||| ||||| || ||||
 GTCAT ATATGC CC CAGA /
 TCTCA- A A---- TAA
 GAM436 TATAAGAATATGCTGCCAATTTCTGTCAATTGTCTTTGACCTATCTGTTTGTGTATCCTAATA 6826
 TAAGAATATGCTGCCAATTTCTGT 6827
 A A T- CA TTCT TTG
 TAT AG ATATGC GC AT GTCA T
 ||| || ||||| || || ||||
 ATA TC TATGTG TG TA CAGT /
 A C TT TC TC-- TTC
 GAM437 TATAAGATGTATAAGAAGTCTTAACGGTTGCAGGGTAACCGATGAAATTTTACATCTAGTA 6856
 TAAGATGTATAAGAAGTCTTAACG 6857
 A TAAG C A A
 TAT AGATGTA AAGT TTA CGGTTGC G
 ||| ||||| ||| ||| |||||
 ATG TCTACAT TTTA AGT GCCAATG /
 A ---- A A G
 GAM438
 TATACAGGTAGAGATGTATGCAGATGTGTCCATATATGTTCCATATTTACATTTTGATAGCATGGATGTATGCATCT
 CTTGGTGTA 6869 ATAGCATGGATGTATGCATCTCTT 6870
 AGGT GA C-- TAT TCCA
 TATAC AGAGATGTATGCA TGTGT CA ATGT T
 |||| ||||| |||| || ||||
 ATGTG TCTCTACGTATGT GTACG GT TACA /
 GT-- AG ATA TT- TTTA
 GAM439 TATAGAATTATCTAAATGTTTCTTGAGGGAGAAAAAGCCAGCCGATCAAGACATTCGGATAATTTTTTA
 6887 TAGAATTATCTAAATGTTTCTTGA 6888
 T TA TT G- AGAAA
 TA AGAATTATC AATG TCTTGA GG A
 || ||||| ||| |||| ||
 AT TTTTAATAG TTAC AGAACT CC A
 T GC -- AG GACCG
 GAM440
 TATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAACTTTTCATA
 6903 TGAAAGGTGTGAACTTGCAATGTC 6904
 G- ACTT A CTC GTCTT
 TATGAAAGGT TGA GCA TGTC CT A
 ||||| ||| ||| ||| ||
 ATACTTTTCA ACT CGT ACAG GA A
 AA CTCC G TT- ACCCA
 GAM441 TATGAGAATGATCCAGAATTAGGATCCGAAGAGAGAGGAACTACTCCTGGATGGACATCATA 6916
 TGAGAATGATCCAGAATTAGGATC 6917
 GAATG AAT GA GAAG
 TATGA ATCCAG TAG TCC A
 |||| ||||| ||| |||
 ATACT TAGGTC ATC AGG /
 ACAGG CTC A- AGAG
 GAM442 TATGGCCGTGGGCCTCAACAAGGGCCACAAAGTGACCAAGAACGTGAGCAAGCCCAGGCACATG
 6920 TGGCCGTGGGCCTCAACAAGGGCC 6921

- G --- ACAAG-- C A
TATG GCC TGGGC CTCA GG CAC A
||||| ||| |||
GTAC CGG ACCCG GAGT CC GTG /
A - AAC GCAAGAA A A

GAM443

TATGGGGTTCAATAAGGTTGCACCTAAAAGTGCTCTTCCTTAGGAAGGATTATCGGGGGCATCTACTCATGAAAA
CCATG 6933 TAAGGTTGCACCTAAAAGTGCTCT 6934
GG ATAA- T A AAAAGTG T T
TATGG TTCA GG TGC CCT C CTTCC T
||||| ||| ||| |||
GTACC AAGT TC ACG GGG G GAAGG /
AA ACTCA T - GCTATTA - A

GAM444

TATTCCCGCTGGCAGCAGGCACCGCTGGCCCCCTTCGTTCCCGGCACGCTGGCTGATGGCGTGGTGTA 6946
TTCCCGCTGGCAGCAGGCACCGCT 6947
T - GG A ACC CCCCC
TAT CC CGCT CAGC GGC GCTGG T
||||| ||| ||| |||
ATG GG GCGG GTCG TCG CGGCC T
T T TA G CA- CTTGC

GAM445

TCAATGGAAGCGGTACTTTCTGGCTGGCTTGAGGTTGATGTATGTGGCCTTCATCTCCTCGGCCTCAGGGTTCCG
CACATCTTTGA 6957 TCTCCTCGGCCTCAGGGTTCCGCA 6958
T A-- T TT CT T TT TATGT
TCAA GGA GCGG ACT CTGG GGCT GAGG GATG G
||||| ||| ||| ||| ||| |||
AGTT TCT CGCC TGG GACT CCGG CTCC CTAC /
- ACA T -- -- - T- TTCCG

GAM446 TCACAGAGATATCAAACCTTCCAATATTCTTCTGGACAGAAGTGGAATATTAAGCTCTGTGA 6982
TATCAAACCTTCCAATATTCTTCT 6983

ATATCAAACC ATATT G
TCACAGAG TTCCA CTTCT G
||||| ||| |||
AGTGTCTC AAGGT GAAGA A
GAATTATA-- ----- C

GAM447

TCACCATCTGCAGCCTTGAAGGAGCTTGGTTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCTC
AGTACTTCCAGACCGTGA 7008 GTGTGGAGAGCCTGGTTTCTCAGT 7009
CA C- CC A T GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTGGTTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7028 GTGTGGAGAGCCTGGTTTCTCAGT 7009
CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G

CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7029 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA

TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A

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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G

CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7030 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA

TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A

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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G

CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7031 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA

TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A

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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G

CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7032 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA

TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A

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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G

CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7033 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA

TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A

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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G

CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7034 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA

TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A

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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G

CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7035 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7036 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7037 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7038 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7039 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7040 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7041 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7042 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7043 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7044 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7045 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7046 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7047 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A

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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7048 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA

TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A

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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7049 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA

TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A

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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7050 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA

TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A

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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7051 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA

TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A

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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7052 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA

TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A

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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG

GAM448

TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCCGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7053 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA

TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A

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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G

CC CT AT - T- AGGTG A AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCTGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7054 GTGTGGAGAGCCTGGTTTCTCAGT 7009
CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCTGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7055 GTGTGGAGAGCCTGGTTTCTCAGT 7009
CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCTGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7056 GTGTGGAGAGCCTGGTTTCTCAGT 7009
CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCTGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7057 GTGTGGAGAGCCTGGTTTCTCAGT 7009
CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCTGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7058 GTGTGGAGAGCCTGGTTTCTCAGT 7009
CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCTGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7059 GTGTGGAGAGCCTGGTTTCTCAGT 7009
CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTT ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
CC CT AT - T- AGGTG A AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCTGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT

CAGTACTTCCAGACCGTGA 7060 GTGTGGAGAGCCTGGTTTCTCAGT 7009

CA C- CC A TT GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTC ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G

CC CT AT - T- AGGTG A AG
GAM449 TCACCCTGTCGCACTTCACCGTGGGGATAACGGGGTCTACCATGGTCTAGAAGTGCACTGGTGA 7061
ACCATGGTCTAGAAGTGCACTGGT 7062

CT C --- - AA
TCACC GT GCACTTC ACCGTGG GGAT C
|||| || |||| |||| |||| |||
AGTGG CA CGTGAAG TGGTACC TCTG G
T- - ATC A GG

GAM450

TCAGGAACATGGTTACCCACGATCAACTTGGGTATTGTAGGAGACAACCCAGATGACTTACTCAATGCCTTGAA
TTGAGGGGTATTTCAGTCGTGCTTGA 7075 TGACTTACTCAATGCCTTGAATTG 7076

AACA-- GT A - ACTT TAG A ACC
TCAGG TG TACCCC CGAT CA GGGTATTG GAG CA C
|||| || |||| |||| || |||| ||| ||
AGTTC AC ATGGGG GTTA GT TCCGTAAC TTC GT /
GTGCTG TT A A ---- TCA A AGA

GAM451

TCAGTGCCCCAGCTGCAATGGCCCCATCTTCCCCCAACCAACTGGCTGGCCCGTGGCCTCCGCACTGA 7091
TGGCCCGTGGCCTCCGCACTGA 7092

CCCA TG AAT -- TCTTCCCC
TCAGTGC GC C GGCC CCA C
|||| || | ||| |||
AGTCACG CG G CCGG GGT /
CCTC GT C-- TC CAACCAAC

GAM452

TCAGTTATTCAGGAGTTTCTGTATGGGGCACAAATTAGCTCTTCTTAGCAGCAGACTAATCTGAAGAAATGA 7099
CTTAGCAGCAGACTAATCTGAAGA 7100

GTTA -- - AT--- ACA
TCA TTCAGG AGTTT CTGT GGGGC A
|| |||| |||| ||| ||||
AGT AAGTCT TCAGA GACG TCTCG A
AAAG AA C ATTCT ATT

GAM453 TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7115
TACCAGTTTCCATCAGGATTTATC 3102

T CCAT- TTA G
TCA ACCAGTTT CAGGAT TCA A
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AGT TGGTCGAA GTCCTA AGT T
- TAGAC CAA C

GAM453 TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7116
TACCAGTTTCCATCAGGATTTATC 3102

T CCAT- TTA G
TCA ACCAGTTT CAGGAT TCA A
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AGT TGGTCGAA GTCCTA AGT T

- TAGAC CAA C
GAM453 TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7117
TACCAGTTTCCATCAGGATTTATC 3102
T CCAT- TTA G
TCA ACCAGTTT CAGGAT TCA A
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AGT TGGTCGAA GTCCTA AGT T
- TAGAC CAA C
GAM453 TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7118
TACCAGTTTCCATCAGGATTTATC 3102
T CCAT- TTA G
TCA ACCAGTTT CAGGAT TCA A
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AGT TGGTCGAA GTCCTA AGT T
- TAGAC CAA C
GAM453 TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7119
TACCAGTTTCCATCAGGATTTATC 3102
T CCAT- TTA G
TCA ACCAGTTT CAGGAT TCA A
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AGT TGGTCGAA GTCCTA AGT T
- TAGAC CAA C
GAM453 TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7120
TACCAGTTTCCATCAGGATTTATC 3102
T CCAT- TTA G
TCA ACCAGTTT CAGGAT TCA A
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AGT TGGTCGAA GTCCTA AGT T
- TAGAC CAA C
GAM453 TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7121
TACCAGTTTCCATCAGGATTTATC 3102
T CCAT- TTA G
TCA ACCAGTTT CAGGAT TCA A
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AGT TGGTCGAA GTCCTA AGT T
- TAGAC CAA C
GAM453 TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7122
TACCAGTTTCCATCAGGATTTATC 3102
T CCAT- TTA G
TCA ACCAGTTT CAGGAT TCA A
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AGT TGGTCGAA GTCCTA AGT T
- TAGAC CAA C
GAM453 TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7123
TACCAGTTTCCATCAGGATTTATC 3102
T CCAT- TTA G
TCA ACCAGTTT CAGGAT TCA A
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AGT TGGTCGAA GTCCTA AGT T
- TAGAC CAA C

GAM453 TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7124
TACCAGTTTCCATCAGGATTTATC 3102

T CCAT- TTA G
TCA ACCAGTTT CAGGAT TCA A
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AGT TGGTCGAA GTCCTA AGT T
- TAGAC CAA C

GAM453 TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7125
TACCAGTTTCCATCAGGATTTATC 3102

T CCAT- TTA G
TCA ACCAGTTT CAGGAT TCA A
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AGT TGGTCGAA GTCCTA AGT T
- TAGAC CAA C

GAM453 TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7126
TACCAGTTTCCATCAGGATTTATC 3102

T CCAT- TTA G
TCA ACCAGTTT CAGGAT TCA A
||| ||||| ||||| |||
AGT TGGTCGAA GTCCTA AGT T
- TAGAC CAA C

GAM454

TCATCGATGGCAAGGGTGTCTTCGCCAGATCACTGTTAATGATTTGCCTGTGGGACGCTCCGTGGATGA 7127
TGGCAAGGGTGTCTTCGCCAGAT 7128

G CAAG TCGC- CTG
TCATC ATGG GGTGTCTT CAGATCA T
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AGTAG TGCC TCGCAGGG GTTTAGT /
G ---- TGTCC AAT

GAM455 TCATTTTGTTTTCTTTCTCTTAATTCTGTTAATTTATTTAATCTCATGGGAGAGAAAACATGA 7145
TCTCATGGGAGAGAAAACATGA 7146

TTT TTAATTCT TT
TCA TGTTTTCTTTCTC GTTAA T
||| ||||| ||||| |||||
AGT ACAAAGAGAGGG TAATT /
--- TACTC--- TA

GAM456 TCCAGGGTAGTTTTGTAGCCTCGGTGGCCCGTCGGCTCATGGACGCTCGAACTTCCGGCCCTTGGA
7191 TGGACGCTCGAACTTCCGGCCCTT 7192

- AGTT- T C G - C
TCCA GGGTT TTTG AGC TC GTG GCC G
||| ||||| ||| ||| ||| |||
AGGT CCCGG AAGC TCG AG TAC CGG T
T CCTTC - C G T C

GAM457

TCCCCCTACCCCACTTTTGCCTTCTAACTTTGGTGCCCAGCTCAGGGTGAGGCAGTTAAGGGTCCAGGGA 7205
TCAGGGTGAGGCAGTTAAGGGTCC 7206

CCT CACTT CTA T C
TCCC ACCC TTGCCTT ACTTTGG GC C
||| ||| ||||| ||||| ||
AGGG TGGG GACGGAG TGGGACT CG /

ACC AATT- --- - A
GAM458 TCCCGGGCCAAGGGGGTGGCCTGCACAGGCCCGATGTCTACTTGCTTGCACCAGCCCGGGA 7226
TGTCTACTTGCTTGCACCAGCCCG 7227
---- G ----- G
TCCCGGGC CAAG GGGT GGCCT C
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AGGGCCCG GTTC TTCA CCGGA A
ACCAC G TCTGTAGC C
GAM459 TCCCTTTCTGACCTTTAGTCTTTCACTTCCAATTTGTGGAATGATATTTTAGGAATAACGGA 7262
GAATGATATTTTAGGAATAACGGA 7263
CT-- CCTTTA - TTCC
TCC TTCCTGA GTC TTTTAC A
||| ||||| ||| |||||
AGG AAGGATT TAG AAGGTG /
CAAT TTA--- T TTTA
GAM460
TCCGAGGGCGAGCTCCAGAAAAGTTTTGCAATCTGGAGATAAGGAGCTTGATGGGCAGCTAGACTTGGA 7273
TAAGGAGCTTGATGGGCAGCTAGA 7274
--- GA T GAA GCA T
TCCGAG GGC GC CCA AAGTTTT ATC G
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AGGTTC TCG CG GGT TTCGAGG TAG G
AGA A- - AG- AA- A
GAM461
TCCGCGGAGGTTTTCGGCAGTGGCATCCGGGGCCGGGGTTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7290 TGGCATCCGGGGCCGGGGTTCGCGG 5801
G AG-- G AGT A G GG G GTG
TCC CGG GTTTC GC GGC TCCG GGCC GGTC CGGCC G
||| ||| ||||| || ||| ||||| ||| |||||
AGG GCC CGGAG CG TCG AGGC CCGG CCGG GCCGG A
A GGAA G C-- - G AG G GGC
GAM461
TCCGCGGAGGTTTTCGGCAGTGGCATCCGGGGCCGGGGTTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7291 TGGCATCCGGGGCCGGGGTTCGCGG 5801
G AG-- G AGT A G GG G GTG
TCC CGG GTTTC GC GGC TCCG GGCC GGTC CGGCC G
||| ||| ||||| || ||| ||||| ||| |||||
AGG GCC CGGAG CG TCG AGGC CCGG CCGG GCCGG A
A GGAA G C-- - G AG G GGC
GAM461
TCCGCGGAGGTTTTCGGCAGTGGCATCCGGGGCCGGGGTTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7292 TGGCATCCGGGGCCGGGGTTCGCGG 5801
G AG-- G AGT A G GG G GTG
TCC CGG GTTTC GC GGC TCCG GGCC GGTC CGGCC G
||| ||| ||||| || ||| ||||| ||| |||||
AGG GCC CGGAG CG TCG AGGC CCGG CCGG GCCGG A
A GGAA G C-- - G AG G GGC
GAM461
TCCGCGGAGGTTTTCGGCAGTGGCATCCGGGGCCGGGGTTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7293 TGGCATCCGGGGCCGGGGTTCGCGG 5801

G AG-- G AGT A G GG G GTG
TCC CGG GTTTC GC GGC TCCG GGCC GGTC CGGCC G
||| ||| |||| || ||| |||| ||| ||||
AGG GCC CGGAG CG TCG AGGC CCGG CCGG GCCGG A
A GGAA G C-- - G AG G GGC

GAM461

TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7294 TGGCATCCGGGGCCGGGGTCGCGG 5801

G AG-- G AGT A G GG G GTG
TCC CGG GTTTC GC GGC TCCG GGCC GGTC CGGCC G
||| ||| |||| || ||| |||| ||| ||||
AGG GCC CGGAG CG TCG AGGC CCGG CCGG GCCGG A
A GGAA G C-- - G AG G GGC

GAM461

TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7295 TGGCATCCGGGGCCGGGGTCGCGG 5801

G AG-- G AGT A G GG G GTG
TCC CGG GTTTC GC GGC TCCG GGCC GGTC CGGCC G
||| ||| |||| || ||| |||| ||| ||||
AGG GCC CGGAG CG TCG AGGC CCGG CCGG GCCGG A
A GGAA G C-- - G AG G GGC

GAM461

TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7296 TGGCATCCGGGGCCGGGGTCGCGG 5801

G AG-- G AGT A G GG G GTG
TCC CGG GTTTC GC GGC TCCG GGCC GGTC CGGCC G
||| ||| |||| || ||| |||| ||| ||||
AGG GCC CGGAG CG TCG AGGC CCGG CCGG GCCGG A
A GGAA G C-- - G AG G GGC

GAM461

TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7297 TGGCATCCGGGGCCGGGGTCGCGG 5801

G AG-- G AGT A G GG G GTG
TCC CGG GTTTC GC GGC TCCG GGCC GGTC CGGCC G
||| ||| |||| || ||| |||| ||| ||||
AGG GCC CGGAG CG TCG AGGC CCGG CCGG GCCGG A
A GGAA G C-- - G AG G GGC

GAM461

TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7298 TGGCATCCGGGGCCGGGGTCGCGG 5801

G AG-- G AGT A G GG G GTG
TCC CGG GTTTC GC GGC TCCG GGCC GGTC CGGCC G
||| ||| |||| || ||| |||| ||| ||||
AGG GCC CGGAG CG TCG AGGC CCGG CCGG GCCGG A
A GGAA G C-- - G AG G GGC

GAM461

TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7299 TGGCATCCGGGGCCGGGGTCGCGG 5801

G AG-- G AGT A G GG G GTG
TCC CGG GTTTC GC GGC TCCG GGCC GGTC CGGCC G

||| ||| |||| || ||| |||| ||| ||||
 AGG GCC CGGAG CG TCG AGGC CCGG CCGG GCCGG A
 A GGAA G C-- - G AG G GGC
 GAM461
 TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCCG
 GGAGCTCGCGGAGGCAAGGCCGAGGA 7300 TGGCATCCGGGGCCGGGGTCGCGG 5801
 G AG-- G AGT A G GG G GTG
 TCC CGG GTTTC GC GGC TCCG GGCC GGTC CGGCC G
 ||| ||| |||| || ||| |||| ||| ||||
 AGG GCC CGGAG CG TCG AGGC CCGG CCGG GCCGG A
 A GGAA G C-- - G AG G GGC
 GAM462
 TCCGGAGTAAACGGCTCTTCATTAGCTTGGAGTGGCCGCAGGTCCCGTGACCAGCACCCGCGAGACCCTGTGC
 GACAGCTGGGCTGATGCTCCGTTTCTCTGGG 7301 TAGCTTGGAGTGGCCGCAGGTCCC 7302
 T CTCTT TGA- G C - C ACCA
 TCCGGAG AAACGG CATTAGCT G GT GC GCAGG TC CGTG G
 ||||| ||||| ||||| | || ||||| |||||
 GGGTCTC TTTGCC GTAGTCGG C CA CG TGTCC AG GCGC /
 - TC--- GT GA G - C A CCAC
 GAM463
 TCCGTTACTGAGATTGGAGTGA CTTAGAAGAGGGTGACCTCCATGAAAGCAGGTAGGATCACAGATGCGGA 7309
 TGAAAGCAGGTAGGATCACAGATG 7310
 TA A GGAG- A AGAA- G
 TCCGT CTG GATT TG CTT GAGG T
 |||| ||| |||| || ||| ||||
 AGGCG GAC CTAG AC GAA CTCC G
 TA A GATGG - AGTAC A
 GAM464
 TCCTCCATCCCAGCATAGAGAATGGGGACTCCCTGAGTAATGGGAGTTCTTTCATGTCCTCTGCTTGGGGTGGG
 GGA 7323 TCCAGCATAGAGAATGGGGACTC 7324
 - T A AT--- TGA
 TCCTCCATCCCA GCA AG GA GGGGACTCCC G
 ||||| |||| ||| || || ||||| |||||
 AGGGGGTGGGGT CGT TC CT TTCTTGAGGG T
 T C - GTACT TAA
 GAM465
 TCGTCAATGGAAGAACCGCCTTTCGGGGCGTTGGACCTTCCAATTCCCGGTCAGATGGAGAACCAGCGCAGTAC
 CCGAGAAAAGGGTCGCCCGTTGACGA 7338 TGGAGAACCAGCGCAGTACCCGAG 7339
 AA A GCC ---- ACC AT CCG
 TCGTCAATGG GA CC TTTCGGG GCGTTGG TTCCA TC G
 ||||| || || ||||| ||||| |||| ||
 AGCAGTTGCC CT GG AGAGCCC CGCGACC GAGGT AG /
 CG G AAA ATGA AA- -- ACT
 GAM466 TCTATCATAAGAAAGTGGACAGCACGAAACTTGTGAAACCAATGTGCCTTTAAACTTCTAATATGCTTAGA
 7348 TAAGAAGTGGACAGCACGAAACTT 7349
 T- -- GGACA- AAAC TG
 TCTA CATA AGAAGT GCACG TTG A
 |||| |||| |||| |||| ||||
 AGAT GTAT TCTTCA CGTGT AAC A
 TC AA AATTTC ---- CA

GAM467

TCTCCCTCAGGACCAGCTGTCAGTCCCCAGGCCCTGAGGTGGTGCCTGCATCCTAGGTCTGTGGGGCATTACTG
GTGTCACTCTGAGGGAGA 7361 TGTCAGTCCCCAGGCCCTGAGGTG 7362

----- C TCA - CTGA T C

TCTCCCTCAGG ACCAG TG GTCCC CAGGCC GG GGTG C

||||||| ||||| ||||| ||||| |||||

AGAGGGAGTCT TGGTC AT CGGGG GTCTGG TC CTAC T

CACTG - TA- T A--- - G

GAM468 TCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATGCCTGTGAGA 7380
TGACAGCAGCCATTATCCTGCTCC 7381

G - GC TTATCCT-- ATA T

TCT ACAG CA CA GCTCC CC T

||| |||| || || |||| ||

AGA TGTC GT GT TGAGG GG T

G C A- TTCTTGTGT --- T

GAM469 TCTGACAGGGCCCATGTCCCACAAGGCTGCTTGGCCTCAGTGGGTGCTTGGCTGTGCTGGA 7395
TGACAGGGCCCATGTCCCACAAGG 7396

GA G CAT - A- G

TCT CA GGCC GT CCCAC AGGCT C

||| || |||| || |||| ||||

AGG GT TCGG CG GGGTG TCCGG T

TC G TT- T AC T

GAM470

TCTGGCTGCAGATCTGGAGGTGGAGGCAGTACCCTGGACTCTATTCTGCTGCCCCCTCAGGGTTTGGAGGAGCC
GGA 7429 CTGCAGATCTGGAGGTGGAGGCAG 7430

G--- - T A TACCCTG

TCTGGCT CAGATC TGGAGG GG GGCAG G

||||| ||||| ||||| || |||||

AGGCCGA GTTTGG ACTTCC CC TCGTC A

GGAG G - G TTATCTC

GAM471

TCTGTTATAACATCTCAACTTACCTGTTGCCACTTGGAATATATATCGATACATTATGGTGCCGAGTGGTAACATG
GGAGTGTTTGATCCAACAGA 7457 TCTCAACTTACCTGTTGCCACTTG 7458

ATAAC TCA- A - AA- TATCG

TCTGTT ATC ACTT CC TGTTGCCACTTG TATA A

||||| ||| ||||| ||||| ||||| |||||

AGACAA TAG TGAG GG ACAATGGTGAGCC GTAT /

CC--- TTTG - T GTG TACAT

GAM472

TCTTGCGCGCGGCACTGGGAGCCGCGGGCCGAGCCTGTCAAGCCCCGCAGCAGCAGCGCGTCAGGA 7463
TGTCAGCCCCGCAGCAGCAGCGC 7464

G A- - A C-- C

TCTTGCGCGCGC GC CTG GG GC GCGGGC G

||||||| || ||| || || |||||

AGGACTGCGCG CG GAC CC CG TGTCCG /

A AC G C AAC A

GAM473

TCTTGGAAGTGGAGTAAAGGTCACTCTTGCTACGCTTTAGCAGAGACTGGTGGCATTTTGCCCCTGCCCTGAGA
7481 AGCAGAGACTGGTGGCATTTTGCC 7482

TG AACT A - --- - CG

TCT GG GG GTAAAG GTCAC TCT TGCTA C
||| || || ||||| |||| ||| |||||
AGA CC CC CGTTTT CGGTG AGA ACGAT /
GT CGT- C A GTC G TT
GAM474 TCTTGGTGACAAAATATGTTGTGTAGAGTTCAGGGGAGAGTGCGTCATATGTTGTTCTAGGA 7493
TGACAAAATATGTTGTGTAGAGTT 7494
TG A T TG AGAG A
TCTTGG ACAA ATATG TG T TTC G
||||| ||| ||||| || | |||
AGGATC TGTT TATAC GC G GAG G
CT G T GT A--- G
GAM475
TCTTGTGTTGAGACTTCGTGGTGGTGCTAAGAAAAGGAAGAAGAAGTCTTACACCACTCCCAAGAAGAATAAGCA
CAAGA 7511 TACACCACTCCCAAGAAGAATAAG 7512
GAGA GT--- C AAAGGA
TCTTGTGTT CTTC GGTGGTG TAAGA A
||||||| ||| ||||| |||||
AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA
GAM476
TCTTGTTCAACATAGGGTAGGTGGCAGCCACGGGTCCAACTCGCTTGAGGCTGGGCCCTGGGCGCTCCATTTTG
TGTTCCAGGA 7541 TAGGGTAGGTGGCAGCCACGGGTC 7542
TTC A T A AC A- G
TCTTG AACATAGGGT GG GGC GCC GGGTCCA CTC C
||||| ||||| || ||| ||| ||||| |||
AGGAC TTGTGTTTTA CC TCG CGG CCCGGGT GAG T
C-- - - - GT CG T
GAM477
TCTTTATAGCAGTATGAGAATGAACTAACACAGTAAATTGGTACTGCGGAGAGTAGAGTATTGCTATAAAGA 7561
TAGCAGTATGAGAATGAACTAACA 7562
GAGAA AA AACA AA
TCTTTATAGCAGTAT TG CT CAGTA T
||||||| || || |||
AGAAATATCGTTATG AT GA GTCAT T
AG--- GA GGC- GG
GAM478
TGAAGTGAATGAGAGAGAAAAAGAGGTCCAGAGTAGTTTGTGGAGCGATGTTTCCATCTCTAATGCCACTCAGCT
CA 7578 TGAGAGAGAAAAAGAGGTCCAGAG 7579
A A ----- -- AAGAGG G T
TGA CTGA TG AGAGA GAAA TCCA AG A
||| ||| || ||||| ||| |||
ACT GACT AC TCTCT CTTT AGGT TT G
C C CGTAA AC GTAGCG G T
GAM479
TGAATGGCCGCTCGCCGAGTGCTGTTTGCAAACCTTAGGAACCCCCCTCGCGCGGGGCCTAGCGGGGGGTACGTGG
CGCATGCGGTAACACTCA 7602 TAGCGGGGGGTACGTGGCGCATGCG 7603
A -- T-- A G AAAC T AAC TC
TGA TG GCCGC CGCCG GTGCT TTTGC TAGG CCCC G
||| ||| ||||| ||||| ||||| ||| |||
ACT AC TGGCG GCGGT CATGG GGGCG ATCC GGGG C

C AA TAC G - ---- --- CG
 GAM480 TGAGCTGACTGTGTCCTGCCAAGGCAGTGGCTGCCCAAGGAAGCCTGCATAGGAGATCTCA 7622
 GGCTGCCCAAGGAAGCCTGCATAG 7623
 CTGA- C----- C
 TGAG CTGTGT CTGC A
 ||| ||||| |||
 ACTC GATACG GACG A
 TAGAG TCCGAAGGAACCCGTCGGT G
 GAM481 TGAGTATAGCAAAGGACTAAGATATTTTCTTCTTGAAGAGACTTTTCGATTAGTCCTCATATATTTA 7628
 TAGCAAAGGACTAAGATATTTTCT 7629
 GCAA -- TAT- C
 TGAGTATA AGGACTAA GA TTTCTT T
 ||||| ||||| || |||||
 ATTTATAT TCCTGATT CT AGAGAA T
 AC-- AG TTTC G
 GAM482 TGATAGAATAGGAAAATTTTAACATTTTTGTTTCTAAGGATAGTTTAAATTTTCTTATTTTTTTCA 7634
 TAGAATAGGAAAATTTTAACATTT 7635
 T- TT - T
 TGA AGAATAGGAAAATT AAC ATTTTTG T
 || ||||| || |||||
 ACT TTTTATTCTTTTAA TTG TAGGAAT T
 TT TT A C
 GAM483 TGATCTCCTGTGGGTCTGGTGCTATATTCTAGAGAAGTTTGCACCTGGACAATAGGAATTTCG 7637
 TCTCCTGTGGGTCTGGTGCTATAT 7638
 TC GG - TATA T
 TGA TCCTGT GTCT GGTGC TTC A
 || ||||| || ||||| |||
 GCT AGGATA CAGG CCACG AAG G
 TA A- T TTTG A
 GAM484 TGATCTGGAAGCCAACCTGGCTGTCCTGAAGCTGTACCAGTTCAACCCAGCCTTCTTTCAGACCA 7649
 TGGAAGCCAACCTGGCTGTCCTGA 7650
 A CCAACCT TCC G T
 TG TCTGGAAG GGCTG TGAA CTG A
 || ||||| || || |||||
 AC AGACTTTC CCGAC ACTT GAC /
 C TT----- CCA - C
 GAM485
 TGATGAAATGCACTTTCCCGTGCAGCAGTGTTCTTTTGCCTGTCAACTGCTGGGTGGTTTTTGCATTCATCA 7667
 TGAAATGCACTTTCCCGTGCAGCA 7668
 A CTTTC G GTTCTT
 TGATGAA TGCA CCGT CAGCAGT T
 ||||| || || |||||
 ACTACTT ACGT GGTG GTCGTCA G
 - TTTT- G ACTGTCC
 GAM486 TGATGAGAACACCGTGTACAGCATCGGCGAGGACGGGAAGGTAGGCGGCTGCAGGATTCA 7677
 TGAGAACACCGTGTACAGCATCGG 7678
 TGAGAA - G AGCA GCG
 TGA CA CCGT TAC TCG A
 || || |||| || |||
 ACT GT GGCG ATG GGC /

TAGGAC C G GAAG AGG
 GAM487 TGATGGTGTCTGTGCCGCTCCTTGTGGCCCTTATGCTTGGGCCCGGCCGCGCTCACCGTCA 7689
 TGGTGTCTGTGCCGCTCCTTGTGG 7690
 CTT C CCTT T TTA
 TGATGGTG GTGC GCT G GGCCC T
 ||||| ||||| | ||||
 ACTGCCAC CGCG CGG C CCGGG G
 T-- C ---- - TTC
 GAM488
 TGCACCTGGCACCTAGACATGTACAACAGGAACCGTGTGGATACATCCCCACACCTGTTTCTGTGGCATGGTCAT
 GTGTATGCA 7704 AGACATGTACAACAGGAACCGTGT 7705
 CTG CTAGA A A C- ATAC
 TGCA GCAC CATGT CA CAGGAAC GTGTGG A
 ||| ||| ||||| ||||| |||||
 ACGT TGTG GTACG GT GTCTTTG CACACC /
 A-- TACTG - - TC CCCT
 GAM489 TGCAGATGACACCAGGTTTCAGGAAAGAGGATGTCTACAGTTGCTTTCGCTTCCTACGTGGTGTGTTTGCA
 7719 TGACACCAGGTTTCAGGAAAGAGGA 7720
 TG G TC A A T CTA
 TGCAGA ACACCA GT AGGAA G GGA GT C
 ||||| ||||| || ||||| ||| ||
 ACGTTT TGTGGT CA TCCTT C CTT CG A
 -- G -- -G T TTG
 GAM490
 TGCATGAGGTTTGGTAACAGGCAAAGTCATCTGGTTAACGTGACTGATGCAAAAAGTCCAGGCCTGGGCA 7736
 TGAGGTTTGGTAACAGGCAAAGTC 7737
 ATG TAACAG- A- CTGG
 TGC AGGTTTGG GCA AGTCAT T
 ||| ||||| || |||||
 ACG TCCGGACC CGT TCAGTG /
 GG- TGAAAAA AG CAAT
 GAM491
 TGCCAGGCATAATCAACATTCCCTCATTACTTCTTCAACATCCTCTTGAAAGCTGTGCTCATTTTACAAATGAGAAAA
 CAGATTTAGAGAAATATAATGACTTGTATGAGGTCACATAGCTTATGAGTGGCA 7753
 TGAGAAAAACAGATTTAGAGAAATA 7754
 GG TCAACATT- T TTCT ACATCC- G G G-- T
 TGCCA CATAA CCTCAT AC TCA TCTT AAA CTGT CTCATTT A
 |||| |||| ||||| || ||| ||||| |||||
 ACGGT GTATT GGAGTA TG AGT AGAG TTT GACA GAGTAAA /
 GA CGATACACT - TTC- AATATAA A A AAA C
 GAM492
 TGCCCCTTCCATGACCAGCCACATCTGAAAAGGAAAGCATTCTGCTCTTTCCAGATCTACGCTGTGCCTTGGCAG
 GGCA 7778 TGACCAGCCACATCTGAAAAGGAA 7779
 CTT TGAC- CAC- A GAA AT
 TGCCC CCA CAGC ATCTG AAAG AGC T
 |||| ||| ||| ||||| ||| |||
 ACGGG GGT GTCG TAGAC TTTC TCG /
 AC- TCCGT CATC C --- TC
 GAM493
 TGCCCGCGTACATGGGCTGAGGAATGTTCAAGCAGAAGAAATGGTAGAGTTTTCTTCAGGCTTAAAGGGTA 7803
 AATGGTAGAGTTTTCTTCAGGCTT 7804

GCGTACAT G TG AAG GAA
 TGCCC GGCTGAGGAA TTC CA G
 |||| || ||||| || ||
 ATGGG TC GACTTCTT GAG GT /
 AAAT---- G TT ATG AAA
 GAM494 TGCCGACTCTATCGATCCCTTACCTTCAATGAGACCTACCAGGACATCAGTGAGTTGGTA 7821
 TACCAGGACATCAGTGAGTTGGTA 7822
 T C C- TACCT- AA
 TGCCGACTC AT GAT CCT TC T
 ||||| || || || ||
 ATGGTTGAG TG CTA GGA AG /
 - A CA CCATCC AG
 GAM495 TGCCTCTGCTTTTCAATTTCTATGGTTATTCGTGGAATGACTCATTGACCACGCGGAGAAGGCA 7835
 GACTCATTGACCACGCGGAGAAGG 7836
 --- TTTCATT T - G
 TGCC TCTGC TC ATG GTTATTC T
 ||| ||| || || |||||
 ACGG AGGCG AG TAC CAGTAAG /
 AAG CACC--- T T G
 GAM496 TGCCTGGAATGGCAGCATCTACATGTTCAACTGGCACCCAGTGCTTATGGTTGCTGGCATGGTGGTA
 7839 TGGCAGCATCTACATGTTCAACTG 7840
 TGGA G TCTA TTCA C
 TGCC ATG CAGCA CATG ACTGG A
 ||| || ||| ||| |||
 ATGG TAC GTCGT GTAT TGACC /
 TGG- G TG-- TCG- C
 GAM497
 TGCGGCCGATGGCGGGCTGCGGGCAAGCGTCACCCTGCTGGGTGCCGGGCTGCTGCTGAGCCTGCTGCCGGC
 CCTGCTGCG 7858 TGGCGGGCTGCGGGCAAGCGTCAC 7859
 CGAT G T A- T - T TG
 TGCGGC GGC GGC GCGGGC AGCG CA CCC GC G
 |||| || || |||| || || ||
 GCGTCG CCG CCG CGTCCG TCGT GT GGG CG /
 TC-- G T AG C C C TG
 GAM498 TGCTACAGGGTGTGACTGGCCCACTATCTAGGGTAGTGAGCCTATTTTGTGGCCCCTGTGTGCA
 7876 TCACAGGGTGTGACTGGCCCACTA 7877
 T T G T---- C CT
 TGC CACAGGG GT AC GGC CACTAT A
 || ||||| || || |||||
 ACG GTGTCCC CG TG CCG GTGATG /
 T - G TTTTAT A GG
 GAM499
 TGCTCCCGACCATCACCTGTGGGCACACCATCGAGATCCTCCGGGAGAAGGGCTTCGACCAGGCGCCCGTGGT
 GGATGAGGCGGGGGTA 7890 TCACCTGTGGGCACACCATCGAGA 7891
 AC- AC TG ACA A-- AT CCG
 TGCTCCCG CATC C TGGGC CC TCGAG CCT G
 ||||| ||| | ||| || |||||
 ATGGGGGC GTAG G GCCCG GG AGCTT GGA G
 GGA GTGT C-- ACC CG AGA
 GAM500 TGCTGGCATGCTAGGTTTCTGGGTTCTCTCTCCCTGAGCGGTCTGGTGACCCTGCTTGAAGCA 7896
 TGGCATGCTAGGTTTCTGGGTTCT 7897

GG T TA T TG TT T TC
TGCT CAGC GGTT C GG C CTC C
|||| ||| |||| | || | |||
ACGA GT CG CCAG G CC G GAG /
A- T TC T GT TG C TC
GAM501 TGCTGGGAATACCATAGCCACCTTTTAGGGAAACTTAAATTATGTTTTTGGATACCCTGTA 7909
TGGAATACCATAGCCACCTTTTA 7910
T A A T- CACCT G
TGC GGG AT CCA AGC TTTAGG A
|||| ||| ||| ||| |||||
ATG CCC TA GGT TTG AAATTC A
T A - TT TATT- A
GAM502
TGGAGTACCTTCTACTGCCTCAGTGGGCAAATCCAAAACCCCATTAGTGGCAAGGAAGAAAGTGTTCCG 7918
TTAGTGGCAAGGAAGAAAGTGTTTC 7919
C A- - TC- CAAAT
TGGAGTAC TTCT CT GCC AGTGGG C
|||||| ||| ||| |||||
GCCTTGTG AAGA GA CGG TTACCC C
A AG A TGA CAAAA
GAM503 TGGATAACAGTATAATAGCATTTACAATATTTCACTCTTTGTTCTCTTAATGTCTTATATAGTTATTTA
7924 TAACAGTATAATAGCATTTACAAT 7925
A TA TAC-- TTTC
TGGATAAC GTATAA GCATT AATA A
|||||| |||| |||| |||
ATTTATTG TATATT TGTA TTTGT C
A C- TTCTC TTCT
GAM504
TGGATTCCGGATGACACACACAGTCACCACCATCAGTTACCTGAACCTGGCCGTGGCTGACTTCTGTTTCACCTC
CA 7952 TGACACACACAGTCACCACCATCA 7953
TTCC A C CA--- CA --- T
TGGA GG TGA ACA CAGTCAC CCA TCAG T
|||| ||| ||| ||||| ||| |||
ACCT CC ACT TGT GTCGGTG GGT AGTC A
--- - T CTTCA CC CCA C
GAM505 TGGCAGGTGGTATTGGGGTCCCTCAGCCCACCTGGGCCGTGACCTCAAGTGTCCACTGCTG 7992
TGACCTCAAGTGTCCACTGCTG 7993
G TA-- CCTCA A
TGGCAG TGG TTGGGGTC GCCC C
|||| ||| ||||| |||
GTCGTC ACC AACTCCAG CGGG C
- TGTG TGC-- T
GAM506
TGGCCAAGGGCCGCGGCCGCGGAGGCCTGCAGCAGCAGAAGCAGCAGAAAGGCCGCGGCATGGGCGGCGCT
GGCCG 8026 GCAGAAAGGCCGCGGCATGGGCGG 8027
A G G--- AGGC- A AGC
TGGCCA G GCCGC GCCGCGG CTGC GC A
|||| | |||| ||||| ||| ||
GCCGGT C CGGCG CGGCGCC GACG CG /
- G GGTA GGAAA A AAG

GAM507

TGGGATGGCAAAGTTTGTGGCTCAGACTGTTGCTAACAGGAACTCTGAAGCCCGGGCTTTCAAGCCAGAAACAA
TCTCA 8051 TGGCAAAGTTTGTGGCTCAGACT 8052

----- --- TT - ---- G
TGGA TGGC AAAGTTTG GGCT CAGA CTGTT C
||||| ||| ||||| ||| ||| |||||
ACTCT ACCG TTTCGGGC CCGA GTCT GACAA /
AACAAAG AAC -- A CAAG T

GAM508 TGGGCAGGGTCCGCTGATCGTGGGCATCTTGCTGGTGTGATGGCTGTGGTCTATGCATCTCTGAATA
8071 TGGCTGTGGTCTATGCATCTCTGA 8072

GG TCC T-- TG G TT T
TG CAGGG GC GATCG G CATC GC G
|| |||| || |||| | |||| ||
AT GTCTC CG CTGGT C GTAG TG G
AA TA- TAT GT G T- T

GAM509

TGGGGCTGAGAGGCGAGACACTGATGGCACTCTTACTTCTGTCAGCTGCCGCAAAGTCTCGTCCACTTGCTGCA
8091 TGAGAGGCGAGACACTGATGGCAC 8092

G T A - AC A CT T T
TG GGC GAG GG CGAGAC TG TGGCA CT AC T
|| ||| || ||||| || |||| || ||
AC TCG TTC CC GCTCTG AC GCCGT GA TG C
G - A T AA - C- C T

GAM510

TGGGTCTGTTTACAGAGTGTGGTAATTTGTTCTTTAGATTTGCAGAATTTATAAAGAAAGAAAATTACAGCCTGCA
CACCCA 8109 TATAAAGAAAGAAAATTACAGCCT 8110

C TTTA AG AA G -- G
TGGGT TG CAG TGTGGT TTTC TTCTTTA GATTT C
||||| || || ||||| ||| ||||| |||||
ACCCA AC GTC ACATTA AAAG AAGAAAT TTAAG /
C ---- CG -- A AT A

GAM511 TGGTGAGGTATAGGAGTTGGAGTTTCGCAAATAGCCTGAGACCTTGAGAACATTTCTTCCTCACCA
8136 TGAGACCTTGAGAACATTTCTTC 8137

TAT ----- TG A -- AA
TGGTGAGG AGGAG T G GTTTC GC A
|||||| |||| | ||||| ||
ACCACTCC TCCTT A T CAGAG CG /
T-- TACAAG GT C TC AT

GAM512 TGGTGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACTACAGTTATGAAAAGCTGCTCTGGACCACCA
8149 TGAAAAGCTGCTCTGGACCACCA 8150

GCC CCCTCGT ATCATG T
TGGTGG CCAGG GCAG CGTAAC A
||||| |||| ||| |||||
ACCACC GGTCT CGTC GTATTG C
A-- ----- GAAAA- A

GAM513

TGGTTCATAGAAGCAGCCACCAGCAGATGACAAAGAAGCTTCAGTTCTCCTTAAAGAAGTTAGGGGTAGGACAAG
TATCTCGTGGTATTGAAGAGGTGAATATGTTTACAAACCA 8162 TGACAAAGAAGCTTCAGTTCTCCT 8163

CATAG GC-- AG-- - G AA A CA -- AG
TGTT AAGCA CACC CAG AT AC AGA GCTT GTTCT CCTTAA A

||||| ||||| ||||| ||||| ||||| ||||| |||||
ACCAA TTTGT GTGG GTT TG TG TCT TGAA CAGGA GGGATT /
ACA-- ATAA AGAA A G C- A -- TG GA
GAM514
TGGTTTTGGTGGCCCAGGCTGGGAGTGCAAGGGCGCAATCTCAGCTCAGTGAAACCTCGGCCTCCCGTGTCCA
8187 TCTCAGCTCAGTGAAACCTCGGCC 8188
TTT T- C ----- G AA
TGG TGG GGCC AG GCTGGGA TGC G
||| ||| ||||| ||||| ||||| |||||
ACC GCC CCGG TC CGACTCT ACG G
TGT CT C CAAAGTGACT A CG
GAM515
TGTCCCATAGAGCTTTTGCATCCTCTGGATGTATTGCGAAAGAAATGTCCAGACTTTGAGGGCTACAGGGTACA
8210 GTCCAGACTTTGAGGGCTACAGGG 8211
- ATAG GCATCC A GC
TGT CCC AGCTTTT TCTGGATGT TT G
||| ||| ||||| ||||| ||||| |||||
ACA GGG TCGGGAG AGACCTGTA AG A
T ACA- TTTC-- A AA
GAM516
TGTCTATGGAAATGTGAATAAAGGCAATCCATGAATAGGTCAACTTCTTCCTGGGTAACCTCCCCAGGTGTTTTGT
GGACA 8218 TGTGAATAAAGGCAATCCATGAAT 8219
TG - G AATAA CA T T T
TGTCTA GAA AT TG AGG ATCCA GAA AGG C
||||| ||| ||| ||| ||||| ||||| |||||
ACAGGT TTT TG AC TCC TGGGT CTT TTC A
GT G G CCC-- AA C C A
GAM517 TGTGAATCACCGGCAGAGCCTGGTGGAGCTGGAGGACCGGTTTCTGGGCCTGACAGACACA 8236
TCACCGGCAGAGCCTGGTGGAGCT 8237
AA ACCGG A GGT A
TGTG TC CAG GCCT GGAGCTGG G
||||| ||| ||| ||||| ||||| |||||
ACAC AG GTC CGGG CTTGGCC G
-- ACA-- - T-- A
GAM518
TGTGCATCCCAGCAGTAAGCAACAATGGCTGATCCAGAAGGTACAGACGGGGAGGGCACGGGTTGTAACGGCT
GGTTTTATGTACA 8254 TCCCAGCAGTAAGCAACAATGGCT 8255
C--- A AA AA- G GA AGAAGG
TGTGCAT CCAGC GT GCAAC TG CT TCC T
||||| ||||| ||||| ||||| ||||| |||||
ACATGTA GGTCG CA TGTTG AC GG GGG /
TTTT G A- GGC G AG CAGACA
GAM519 TGTGTGGTGATCGAGTGGTCTGTGTTCTATTGCTGGTGGGGTGATAGGGTGGGCTAAAAACCATGCA
8272 TAGGGTGGGCTAAAAACCATGCA 8273
GATCGAG TG GTT TG GG
TGTGTGGT TGGTC T CCTAT CT T
||||| ||||| ||||| ||||| ||||| |||||
ACGTACCA ATCGG G GGATA GG /
AAA---- GT --- GT GG
GAM520
TGTTCTTGGTGAGAAGGGCCGGCGGATTCGGGAACTGACTGCTGTAGTTCAGAAGAGGTTTGGCTTTCCAGAGG

GCA 8283 TGAGAAGGGCCGGCGGATTCGGGA 8284

- T AA GGCGGA GG A T
TGTTCT TGG GAG GGGCC TTC GAACTG C G
||||| ||| ||| |||| | ||| ||||| |
ACGGGA ACC TTC TTTGG AAG CTTGAT G C
G T GG AG---- A- - T

GAM521

TGTTGAGATGAGGGTTTCAGGGAAGCAGAAAAACCAAGTGCTGGATCATTTCTCCTTTGAGGGGCCTTTGTCCAA
TTCAGCA 8300 TGAGGGTTTCAGGGAAGCAGAAAA 8301

--- TG TT AGG C AA-- AG
TGTTGA GA AGGGT C GAAG AGAAA CCA T
||||| || ||||| | ||| ||||| |||
ACGACT CT TTCCG G TTTC TCTTT GGT /
TAAC GT GG AG- C ACTA CG

GAM522

TGTTGAGTGCAGATGAAGGGTTGTATGAGGCCCCATCCTGGGAGGGCTGTACACCTTCTTGGCACAGCAGCA
8319 TGAAGGGTTGTATGAGGCCCCATC 8320

A- AGAT GT GA CA C
TGTTG GTGC GAAGG TGTAT GGCCC TC T
||||| ||| ||||| ||||| ||||| ||
ACGAC CACG CTTCC ACATG TCGGG AG G
GA GTT- -- -- -- G

GAM523 TGTTTCATGACTGGTAACAGAGTAGTCTCGAGGGGATCCTTGGAGAACCTGTTCTGACTTTAGAAGCA
8335 TGA CTGTAACAGAGTAGTCTCGA 8336

A CT AA -- G G
TGTTTC TGA GGT CAGAGTAG TCTC AGGG A
||||| ||| ||| ||||| ||| |||||
ACGAAG ATT TCA GTCTTGTC AGAG TTCC /
- -- -- CA G T

GAM524

TTAAACATGTCACCTAAATGCACTTGATGGTGTGAAATGTGCACCTTCTTAAATTTAAGATGACTTAGTTTAA
8344 TGTCACCTAAATGCACTTGATGGT 8345

AT- C A TGCATT T TGA
TTAAAC GTCA CT AA GA GGTGT A
||||| ||| ||| || ||||| ||| |||||
AATTG CAGT GA TT CT CCACG A
ATT A A TTAAATT T TGT

GAM525

TTACTGTTTATGGAAGGGGAGACTTAGTATCATAATGATGTCAATCTTCTGCATACTGATCACTAATTCAATCAACA
ATAG 8355 TGGAAGGGGAGACTTAGTATCATA 8356

C T G GG A C - T T G
TTA TGTT AT GAA GG GA TTAGTAT CA AA GAT T
||| |||| || ||| || || ||||| || |||
GAT ACAA TA CTT TC CT AGTCATA GT TT CTA C
A C A AA A - C C - A

GAM526

TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAACTTTTCATAA
8366 TGAAAGGTGTGAACTTGCAATGTC 6904

G- ACTT A CTC GTCTT
TTATGAAAGGT TGA GCA TGTC CT A

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AATACTTTTCA ACT CGT ACAG GA A
AA CTCC G TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8367 TGAAAGGTGTGAACTTGCAATGTC 6904
G- ACTT A CTC GTCTT
TTATGAAAGGT TGA GCA TGTC CT A
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AATACTTTTCA ACT CGT ACAG GA A
AA CTCC G TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8368 TGAAAGGTGTGAACTTGCAATGTC 6904
G- ACTT A CTC GTCTT
TTATGAAAGGT TGA GCA TGTC CT A
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AATACTTTTCA ACT CGT ACAG GA A
AA CTCC G TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8369 TGAAAGGTGTGAACTTGCAATGTC 6904
G- ACTT A CTC GTCTT
TTATGAAAGGT TGA GCA TGTC CT A
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AATACTTTTCA ACT CGT ACAG GA A
AA CTCC G TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8370 TGAAAGGTGTGAACTTGCAATGTC 6904
G- ACTT A CTC GTCTT
TTATGAAAGGT TGA GCA TGTC CT A
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AA CTCC G TT- ACCCA
GAM526
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8371 TGAAAGGTGTGAACTTGCAATGTC 6904
G- ACTT A CTC GTCTT
TTATGAAAGGT TGA GCA TGTC CT A
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AATACTTTTCA ACT CGT ACAG GA A
AA CTCC G TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8372 TGAAAGGTGTGAACTTGCAATGTC 6904
G- ACTT A CTC GTCTT
TTATGAAAGGT TGA GCA TGTC CT A
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AATACTTTTCA ACT CGT ACAG GA A

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AA CTCC G TT- ACCCA

GAM526

TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8373 TGAAAGGTGTGAACTTGCAATGTC 6904

G- ACTT A CTC GTCTT

TTATGAAAGGT TGA GCA TGTC CT A

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AATACTTTTCA ACT CGT ACAG GA A

AA CTCC G TT- ACCCA

GAM526

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8374 TGAAAGGTGTGAACTTGCAATGTC 6904

G- ACTT A CTC GTCTT

TTATGAAAGGT TGA GCA TGTC CT A

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AATACTTTTCA ACT CGT ACAG GA A

AA CTCC G TT- ACCCA

GAM526

TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8375 TGAAAGGTGTGAACTTGCAATGTC 6904

G- ACTT A CTC GTCTT

TTATGAAAGGT TGA GCA TGTC CT A

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AATACTTTTCA ACT CGT ACAG GA A

AA CTCC G TT- ACCCA

GAM526

TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8376 TGAAAGGTGTGAACTTGCAATGTC 6904

G- ACTT A CTC GTCTT

TTATGAAAGGT TGA GCA TGTC CT A

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AATACTTTTCA ACT CGT ACAG GA A

AA CTCC G TT- ACCCA

GAM526

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8377 TGAAAGGTGTGAACTTGCAATGTC 6904

G- ACTT A CTC GTCTT

TTATGAAAGGT TGA GCA TGTC CT A

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AATACTTTTCA ACT CGT ACAG GA A

AA CTCC G TT- ACCCA

GAM526

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8378 TGAAAGGTGTGAACTTGCAATGTC 6904

G- ACTT A CTC GTCTT

TTATGAAAGGT TGA GCA TGTC CT A

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AATACTTTTCA ACT CGT ACAG GA A

AA CTCC G TT- ACCCA

GAM526

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8380 TGAAAGGTGTGAACTTGCAATGTC 6904

G- ACTT A CTC GTCTT
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AATACTTTTCA ACT CGT ACAG GA A
AA CTCC G TT- ACCCA

GAM526

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8381 TGAAAGGTGTGAACTTGCAATGTC 6904

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AA CTCC G TT- ACCCA

GAM526

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8382 TGAAAGGTGTGAACTTGCAATGTC 6904

G- ACTT A CTC GTCTT
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AATACTTTTCA ACT CGT ACAG GA A
AA CTCC G TT- ACCCA

GAM526

TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA

8383 TGAAAGGTGTGAACTTGCAATGTC 6904

G- ACTT A CTC GTCTT
TTATGAAAGGT TGA GCA TGTC CT A
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AATACTTTTCA ACT CGT ACAG GA A
AA CTCC G TT- ACCCA

GAM526

TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA

8384 TGAAAGGTGTGAACTTGCAATGTC 6904

G- ACTT A CTC GTCTT
TTATGAAAGGT TGA GCA TGTC CT A
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AATACTTTTCA ACT CGT ACAG GA A
AA CTCC G TT- ACCCA

GAM526

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8385 TGAAAGGTGTGAACTTGCAATGTC 6904

G- ACTT A CTC GTCTT
TTATGAAAGGT TGA GCA TGTC CT A
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AATACTTTTCA ACT CGT ACAG GA A
AA CTCC G TT- ACCCA

GAM526

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8386 TGAAAGGTGTGAACTTGCAATGTC 6904

G- ACTT A CTC GTCTT

TTATGAAAGGT TGA GCA TGTC CT A

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AATACTTTTCA ACT CGT ACAG GA A

AA CTCC G TT- ACCCA

GAM526

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8387 TGAAAGGTGTGAACTTGCAATGTC 6904

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TTATGAAAGGT TGA GCA TGTC CT A

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AA CTCC G TT- ACCCA

GAM526

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8388 TGAAAGGTGTGAACTTGCAATGTC 6904

G- ACTT A CTC GTCTT

TTATGAAAGGT TGA GCA TGTC CT A

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AATACTTTTCA ACT CGT ACAG GA A

AA CTCC G TT- ACCCA

GAM526

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8389 TGAAAGGTGTGAACTTGCAATGTC 6904

G- ACTT A CTC GTCTT

TTATGAAAGGT TGA GCA TGTC CT A

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AATACTTTTCA ACT CGT ACAG GA A

AA CTCC G TT- ACCCA

GAM527

TTATGAAGACATACTGGATGGCAGTGGGTACTTCGATGTGAGGGACAAGGAGGACCAGTGGATCCGGATCTTCA

TGG 8390 AACTGGATGGCAGTGGGTACTTC 8391

CATA GG G GTA GA GA

TTATGAAGA CTGGAT CA TGG CTTC TGT G

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GGTACTTCT GGCCTA GT ACC GAGG ACA /

A--- G- G AG- A- GG

GAM528 TTCGGGCTGTGCAAGGAGGGGATCAAGGACGGTGCCACCATGAAGACCTTTTGCGGCACACCTGAG

8394 TGAAGACCTTTTGCGGCACACCTG 8395

C AA- GA- A ACGG

TTCGGG TGTGC GGAGGG TCA GG T

||||| ||||| ||||| ||| ||

GAGTCC ACACG TTTTCC AGT CC /

- GCG AGA A ACCG

GAM529 TTCTGTGGAGAGAGGTCTAATATAATATGTAGTATTTTATGTAAGGCACTGTTATACAGAA 8403

TGTAAGGCACTGTTATACAGAA 8404

GA G - A TATGT

TTCTGTG GA AG GTCT ATATAA A

||||| || || ||| |||||

AAGACAT TT TC CGGA TGTATT /

A- G A A TTATG

GAM530 TTCTTTGGCATTATTCACCTAGATCTCTAAACAGGAGATCACTGTTTCGTATGCTCTAGAG 8432
 TCACTGTTTCGTATGCTCTAGAG 8433
 TT TTATTC TA- AA
 TTCT GGCAT AC GATCTCT A
 |||| |||| || |||||
 GAGA TCGTA TG CTAGAGG /
 TC TGCTT- TCA AC
 GAM531 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTACACTCATGTTTCATGCCTCTTGCATCGTTAA 8440
 CATTGTAGGCTGGCGCTGGCATCA 8441
 AT CT CT C GTT
 TTGAC TGTAGG GGCG GGCAT AG C
 |||| |||| || |||| ||
 AATTG ACGTTC CCGT TTGTA TC /
 CT TC AC C ACA
 GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTACACTCATGTTTCATGCCTCTTGCATCGTTAA 8449
 CATTGTAGGCTGGCGCTGGCATCA 8441
 AT CT CT C GTT
 TTGAC TGTAGG GGCG GGCAT AG C
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 AATTG ACGTTT CCGT TTGTA TC /
 CT CT AC C ACA
 GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTACACTCATGTTTCATGCCTCTTGCATCGTTAA 8451
 CATTGTAGGCTGGCGCTGGCATCA 8441
 AT CT CT C GTT
 TTGAC TGTAGG GGCG GGCAT AG C
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 CT CT AC C ACA
 GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTACACTCATGTTTCATGCCTCTTGCATCGTTAA 8452
 CATTGTAGGCTGGCGCTGGCATCA 8441
 AT CT CT C GTT
 TTGAC TGTAGG GGCG GGCAT AG C
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 CT CT AC C ACA
 GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTACACTCATGTTTCATGCCTCTTGCATCGTTAA 8453
 CATTGTAGGCTGGCGCTGGCATCA 8441
 AT CT CT C GTT
 TTGAC TGTAGG GGCG GGCAT AG C
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 CT CT AC C ACA
 GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTACACTCATGTTTCATGCCTCTTGCATCGTTAA 8454
 CATTGTAGGCTGGCGCTGGCATCA 8441
 AT CT CT C GTT
 TTGAC TGTAGG GGCG GGCAT AG C
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 CT CT AC C ACA
 GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTACACTCATGTTTCATGCCTCTTGCATCGTTAA 8455
 CATTGTAGGCTGGCGCTGGCATCA 8441

AT CT CT C GTT
TTGAC TGTAGG GGCG GGCAT AG C
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CT CT AC C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTTCACTCATGTTTCATGCCTCTTTGCATCGTTAA 8456
CATTGTAGGCTGGCGCTGGCATCA 8441
AT CT CT C GTT
TTGAC TGTAGG GGCG GGCAT AG C
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CT CT AC C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTTCACTCATGTTTCATGCCTCTTTGCATCGTTAA 8457
CATTGTAGGCTGGCGCTGGCATCA 8441
AT CT CT C GTT
TTGAC TGTAGG GGCG GGCAT AG C
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AATTG ACGTTT CCGT TTGTA TC /
CT CT AC C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTTCACTCATGTTTCATGCCTCTTTGCATCGTTAA 8458
CATTGTAGGCTGGCGCTGGCATCA 8441
AT CT CT C GTT
TTGAC TGTAGG GGCG GGCAT AG C
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CT CT AC C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTTCACTCATGTTTCATGCCTCTTTGCATCGTTAA 8459
CATTGTAGGCTGGCGCTGGCATCA 8441
AT CT CT C GTT
TTGAC TGTAGG GGCG GGCAT AG C
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CT CT AC C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTTCACTCATGTTTCATGCCTCTTTGCATCGTTAA 8460
CATTGTAGGCTGGCGCTGGCATCA 8441
AT CT CT C GTT
TTGAC TGTAGG GGCG GGCAT AG C
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CT CT AC C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTTCACTCATGTTTCATGCCTCTTTGCATCGTTAA 8461
CATTGTAGGCTGGCGCTGGCATCA 8441
AT CT CT C GTT
TTGAC TGTAGG GGCG GGCAT AG C
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CT CT AC C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTTCACTCATGTTTCATGCCTCTTTGCATCGTTAA 8462
CATTGTAGGCTGGCGCTGGCATCA 8441
AT CT CT C GTT

TTGAC TGTAGG GGCG GGCAT AG C
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 CT CT AC C ACA
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 CATTGTAGGCTGGCGCTGGCATCA 8441
 AT CT CT C GTT
 TTGAC TGTAGG GGCG GGCAT AG C
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 AT CT CT C GTT
 TTGAC TGTAGG GGCG GGCAT AG C
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 CATTGTAGGCTGGCGCTGGCATCA 8441
 AT CT CT C GTT
 TTGAC TGTAGG GGCG GGCAT AG C
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 CT CT AC C ACA
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 CATTGTAGGCTGGCGCTGGCATCA 8441
 AT CT CT C GTT
 TTGAC TGTAGG GGCG GGCAT AG C
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 CT CT AC C ACA
 GAM533 TTGAGATGGGCACGTGGAAGTCAAAGGGTTTCTCTTTTTTTTTTTTTTTTTTCCCCTTTTAG 8469
 TGAGATGGGCACGTGGAAGTCAAA 8470
 T CACGT TC T
 TTGAGA GGG GGAAG AAAGGG T
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 GATTTT CCC TTTT TTTTCT T
 C TTTT TT C
 GAM534
 TTGAGTGTTTGATAAGAGTAGCATTAGGTATTAGTGGGAAATGATTGGATTTTTTCATTTAAGCATTGTTGGGACAA
 CTTGTTAACCATTTGG 8493 TAAGAGTAGCATTAGGTATTAGTG 8494
 TG T A- AG T - ATT GG GA
 T AGTG TTGATAAG GT CA TAG GT AGTG AAAT T
 | ||| |||| || || || || ||| |||
 G TTAC AATTGTTC CA GT GTT CG TTAC TTTA T
 GT C AA GG T A AAT TT GG
 GAM535 TTGATGTCATGTGTCAAGTGCTTACTGATTTGATTGATGAAGAAGTAAAAAGTGGCATCAA 8508
 TGTCATGTGTCAAGTGCTTACTGA 8509
 GTGTCAAG A G- TG

TTGATGTCAT TGCTT CT ATT A
 ||||| |||| || ||
 AACTACGGTG ATGAA GA TAG /
 AAAA---- - AG TT
 GAM536 TTGGATGAGGCCCGCACACATTATGGAGGGCAATTTTCTCTACTGATTAAGGTTAATTTTCATCCAA
 8519 TGAGGCCCGCACACATTATGGAGG 8520
 C--- GCACAC - CA
 TTGGATGAGG CC ATTA TGGAGGG A
 ||||| || |||||
 AACCTACTTT GG TAGT ATCTCTT /
 AATT AAAAT- C TT
 GAM537 TTGTACAGACCTTAGTAAAGTCTTCAATTTAATAAAAATCAAAAAGCCAAAAGTCAAGCAA
 8528 TCAAAAAGCCAAAAGTCAAGGTC 8529
 ACA -- AAAGT CA-- AA
 TTGT GACCT TAGT CTT ATTT T
 |||| |||| |||| ||
 AACG CTGGA ATCA GAA TAAA /
 AA- AA AAACC AAAC AA
 GAM538
 TTGTGTCTTACTAAAGCAGCTTATTGTAGGTGTGGCGTTCTAAAACGTTTCCTGCCTGCGATGGTTCACAAAATAA
 ACACAA 8549 AAGCAGCTTATTGTAGGTGTGGCG 8550
 C CTAAAGC T GT-- C
 TTGTGT TTA AGCT ATTGTAGGT GGC GTT T
 ||||| |||| ||||| |||||
 AACACA AAT TTGG TAGCGTCCG TTGCAA A
 - AAAACAC - TCCT A
 GAM539 TTGTTTTTTCGGTTGGGCATGCTGCTTACCGCAGGATGATGGAAGCGACGGCCCGTACAAAGACAG
 8564 TGGAAGCGACGGCCCGTACAAAGA 8565
 TCG - A C A - AG
 TTGTTTTT GT TGGGC TG TGCTT CCG C G
 ||||| || |||| || |||| ||
 GACAGAAA CA GCCCG GC GCGAA GGT G /
 --- T - A - ATA
 GAM540
 TTTCAATTTGACAATGTCCGGCCCTTGAAATTTTCATACCCGGTGGGAAAATTTTAAATGGCCGGGACCTTG GTTGG
 TTTGAGA 8567 TGTCCGGCCCTTGAAATTTTCATAC 8568
 T TG AATG-- C- CATA G
 TTTCAA T AC TCCGGCC TTGAAATTT CCC G
 ||||| || ||||| ||||| ||
 AGAGTT G TG GGGCCGG AATTTTAAA GGG /
 T GT GTTCCA TA A--- T
 GAM541 TTTCAATTTAAAAAATGGTTTCAGCAAATATGAAAATAGAAAGTCCGTTATTTGTCCATTTGTAATATGAGA
 8573 TCATTTAAAAAATGGTTTCAGCAA 8574
 TTAAA TTTCA TGAAAATA
 TTTCAT AAATGG GCAAATA G
 ||||| ||||| |||||
 AGAGTA TTTACC TGTTTAT A
 TAATG ----- TGCCTGAA
 GAM542
 TTTTCGGATACTTACATAGTTTTGCGGGAAGCCAGATCGAAGATGTATCCCAGCAAGCACACTAGGCAGGTGGCTG
 AGA 8579 CAGCAAGCACACTAGGCAGGTGGC 8580

A ACA --- - A CAGAT
 TTTCGG TACTT TAGT TTTGC GGA GC C
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 AGAGTC GTGGA ATCA GAACG CCCT TG G
 G CGG CAC A A TAGAA
 GAM543 TTTCGGCGCTGGGTGCGCCCAAAGCAAAATGGAAACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
 8608 TAGAGTGGTGGCTCCCAGAATCCC 8609
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 GAM544 TTTCGGCGCTGGGTGCGCCCAAAGCAAAATGGAGACGGATAGAGTGGTGGCTCCCAAATCCCGAAA
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GAM547

TTTGAATGACTTGTAATGATGGCTGCTAAGCATATCCTGTACTGTGGCTATGTCAATTTGCGAATCCTCCTCAAA
8715 TGACTTGTAATGATGGCTGCTAAG 8716

AT-- C -- -- TG TAA TA

TTTGA GA TTGTAA TGAT GGC C GCA T

|||| || ||||| |||| ||| | |||

AAACT CTAGCGTT ACTG TCG G TGT /

CCTC A TA TA GT TCA CC

GAM548

TTTGAGATGTACGACCTGGACGGCGACGGGCGCATCACGCGCCTGGAGATGCTGGAGATCATCGAGGCAATCT
ACAAG 8724 TGTACGACCTGGACGGCGACGGGC 8725

- - A- CCTGGA- A--- AT

TTTG AGAT GT CGA CGGCG CGGGCGC C

|||| ||||| || ||| ||||| |||||

GAAC TCTA CG GCT GTCGT GTCCGCG /

A A GA ACTAGAG AGAG CA

GAM549 TTTGTTAATGTTTCAAACATACTTTCTTGTTTTCTAATGGAGTATATAGTTTAGTCATTTACAGA 8728
GGAGTATATAGTTTAGTCATTTCA 8729

T- TTTC --- TC T

TTTGT AATG AAAC ATACTT TTGG T

|||| |||| |||| ||||| ||||

AGACA TTAC TTTG TATGAG AATC T

CT TGA- ATA GT T

GAM550

TTTTTTTCAGTGAACATGTTTTTATTGAACACCACTTAATTTTCAGGAACATTTTCAGGTACATTGTCAGAAA 8744
TTTCAGGAACATTTTCAGGTACATT 8745

TT A ---- --- ACA

TTTTT CAGTG AC ATGTTTTT ATTGA C

|||| ||||| || ||||| |||||

AAAGA GTTAC TG TACAAGGA TAATT C

CT A GACTT CTT CAA

GAM-NAME	TARGET-GENE	TAREGT-SEQ	TARGET-ID	TARGET-DRAW
GAM24	A1BG	CACGCCATTGCACTCCAG-CCT 3 AACA C	CT	<p>CGCCA TGCCTCCAGTC</p> <p> </p> <p>GCGGT ACGTGAGGTCGG</p> <p>_____ A AC</p>
GAM24	APPL	CACACCACTGCACTCCAG-CCT 4 AACA	CT	<p>CGCCACTGCACTCCAGTC</p> <p> </p> <p>GTGGTGACGTGAGGTCGG</p> <p>_____ AT</p>
GAM24	ATP6V1A1	CACGCCATTGCACTCCAG-CCT 3 AACA C	CT	<p>CGCCA TGCCTCCAGTC</p> <p> </p> <p>GCGGT ACGTGAGGTCGG</p> <p>_____ A AC</p>
GAM24	CASP8	CACGCCACTGCACTCCAG-CCT 5 AACA	CT	<p>CGCCACTGCACTCCAGTC</p> <p> </p> <p>GCGGTGACGTGAGGTCGG</p> <p>_____ AC</p>
GAM24	CNN2	CGCCACTGCACTCCAG-CCT 6 AACACGCC	C	<p>ACTGCACTCCAGTC</p> <p> </p> <p>TGACGTGAGGTCGG</p> <p>_____ A</p>
GAM24	CR1	ACGCCACTGCACTCCAG-CCT 7 AACACG	C	<p>CCACTGCACTCCAGTC</p> <p> </p> <p>GGTGACGTGAGGTCGG</p> <p>_____ A</p>
GAM24	CYP1A2	CGCCACTGCACTCCAG-CCT 6 AACACGCC	C	<p>ACTGCACTCCAGTC</p> <p> </p> <p>TGACGTGAGGTCGG</p> <p>_____ A</p>
GAM24	CYP2B6	CACGCCACTGCACTCCAG-CCT 5 AACA	CT	<p>CGCCACTGCACTCCAGTC</p> <p> </p> <p>GCGGTGACGTGAGGTCGG</p> <p>_____ AC</p>
GAM24	EIF2S3	CACGCCACTGCACTCCAG-CCT 5 AACA	CT	<p>CGCCACTGCACTCCAGTC</p> <p> </p> <p>GCGGTGACGTGAGGTCGG</p> <p>_____ AC</p>
GAM24	EVC	CACGCCACTGCACTCCAG-CCT 5 AACA	CT	<p>CGCCACTGCACTCCAGTC</p> <p> </p> <p>GCGGTGACGTGAGGTCGG</p>

GAM24	F2RL3	<div style="text-align: center;">AC</div> <div style="text-align: center;">_____</div> CACGCCACTGCACTCCAG-CCT 5 AACACCT CGCCACTGCACTCCAGTC GCGGTGACGTGAGGTCGG	CT
GAM24	FCAR	<div style="text-align: center;">AC</div> <div style="text-align: center;">_____</div> GCCACTGCACTCCAG-CCT 8 AACACGCCAC TGCCTCCAGTC ACGTGAGGTCGG	
GAM24	FUT1	<div style="text-align: center;">AC</div> <div style="text-align: center;">_____</div> CACGCCACTGCACTCCAG-CCT 5 AACACCT CGCCACTGCACTCCAGTC GCGGTGACGTGAGGTCGG	CT
GAM24	LZTS1	<div style="text-align: center;">AC</div> <div style="text-align: center;">_____</div> CATGCCACTGCACTCCAG-CCT 9 AACACCT GCCACTGCACTCCAGTC CGGTGACGTGAGGTCGG	CT
GAM24	PAICS	<div style="text-align: center;">A_____AC</div> CACGCCACTGCACTCCAG-CCT 5 AACACCT CGCCACTGCACTCCAGTC GCGGTGACGTGAGGTCGG	CT
GAM24	PCDHB9	<div style="text-align: center;">AC</div> <div style="text-align: center;">_____</div> CGCCACTGCACTCCAG-CCT 6 AACACGCC ACTGCACTCCAGTC TGACGTGAGGTCGG	C
GAM24	PPP1R12B	<div style="text-align: center;">A</div> <div style="text-align: center;">_____</div> CACACCACTGCACTCCAG-CCT 4 AACACCT CGCCACTGCACTCCAGTC GTGGTGACGTGAGGTCGG	CT
GAM24	PSMB2	<div style="text-align: center;">AC</div> <div style="text-align: center;">_____</div> ACGCCACAGCACTCCAG-CCT 10 AACACG T CCAC GCACTCCAGTC GGTG CGTGAGGTCGG	C
GAM24	RABL2B	<div style="text-align: center;">T A</div> <div style="text-align: center;">_____</div> CGCCACTGCACTCCAG-CCT 6 AACACGCC ACTGCACTCCAGTC TGACGTGAGGTCGG	C
GAM24	TBXA2R	<div style="text-align: center;">A</div> <div style="text-align: center;">_____</div> CGCCACTGCACTCCAG-CCT 6 AACACGCC ACTGCACTCCAGTC TGACGTGAGGTCGG	C

GAM24	TERF1	<div>_____A</div> <div>CGCCACTGCACTCCAG-CCT 6 AACACGCC C</div> <div>ACTGCACTCCAGTC</div> <div> </div> <div>TGACGTGAGGTCGG</div>
GAM24	TERF2	<div>_____A</div> <div>CACGCCACTGCACTCCAG-CCT 5 AACACCT CT</div> <div>CGCCACTGCACTCCAGTC</div> <div> </div> <div>GCGGTGACGTGAGGTCGG</div>
GAM24	TMPRSS3	<div>_____AC</div> <div>CGCCACTGCACTCCAG-CCT 6 AACACGCC C</div> <div>ACTGCACTCCAGTC</div> <div> </div> <div>TGACGTGAGGTCGG</div>
GAM24	VHL	<div>_____A</div> <div>CGCCACTGCACTCCAG-CCT 6 AACACGCC C</div> <div>ACTGCACTCCAGTC</div> <div> </div> <div>TGACGTGAGGTCGG</div>
GAM25	AMACR	<div>_____A</div> <div>ACAGGCAACCCTA-AACTG 21 TGAACA ACAAAA</div> <div>GGCAACCT TGG</div> <div> </div> <div>CCGTTGGG ACT</div>
GAM25	ATRX	<div>_____ATTTTG</div> <div>AACAGGT---TACAAAATG 18 TGAA CAACC</div> <div>CAGG TACAAAAT</div> <div> </div> <div>GTCC ATGTTTTA</div>
GAM25	BMP1	<div>_____A_____</div> <div>ACAGACACCAT-CAAAATGGG 23 TGAACA A TA</div> <div>GGCA CC CAAAATGG</div> <div> </div> <div>CTGT GG GTTTTACC</div>
GAM25	CBR1	<div>_____TA</div> <div>CAGGACAAGGTACAAAATGGG 27 TGAACAG CC</div> <div>GCAA TACAAAATGGG</div> <div> </div> <div>TGTT ATGTTTACC</div>
GAM25	COL14A1	<div>_____CC</div> <div>TGAACAGGCAA---ACAAAA 34 CCT TG</div> <div>TGAACAGGCAA AAAAA</div> <div> </div> <div>ACTTGTCCGTT TGTTTT</div>
GAM25	CRKL	<div>_____ </div> <div>AATAGCCACAGCAACAAAATGG 13 TGAACA A CT__ G</div> <div>GGC AC ACAAATGG</div> <div> </div> <div>TCG TG TGTTTACC</div>

GAM25	FKBP6	<p> A_____ G TCGT G AACAGAGAACCCTACAAAAT 14 TGAA CAA_ G CAGG CCTACAAAATG GTCT GGATGTTTTAT _____ CTTG G </p>
GAM25	IGF2R	<p> GAACAGGCAAACCTCTCCAAAA 28 TG __ A GGG AACAGGCAA C CT CAAAAT TTGTCCGTT G GA GTTTTG _____ T A G </p>
GAM25	IKBKAP	<p> GAACAATCATTCTCACAAAATGG 30 TG G AC _ GI AACAG CA CT ACAAATGG TTGTT GT GA TGTTTTACC _____ A AA G AI </p>
GAM25	ITGB1	<p> AACAGGCAA-ATAGCAAAAT 15 TGAA CCTA CAGGCAA CAAAATGG GTCCGTT GTTTTATT _____ TATC </p>
GAM25	LIMK1	<p> AGGCAAAGTGACAAAATGG 24 TGAAC_____ CAA AGG CCTACAAAATGG TCC GGATGTTTTACC TTCAGTGTGTTTACCGGGAGIIIGGGTAAAACA AAC AGGCAACCTAGTCACCATGG 25 TGAACAGGCA __ AA ACCTA CA ATGG TGGAT GT TACC _____ CA GG </p>
GAM25	MEN1	<p> AAAAGGCAACCTATAAACTGG 19 TGAAC C A AGGCAACCTA AAA TGGG TCCGTTGGAT TTT ACCT T_____ A G </p>
GAM25	NPR2L	<p> AAAAAGCAAATACAAAATG 16 TGAAC CC G AGGCAA TACAAAATG TTCGTT ATGTTTTAC T_____ TT A </p>
GAM25	PLAG1	<p> AACTGGC--CCTACAAAAGG 20 TGAACA AA T GGC CCTACAAA GG CCG GGATGTTTT CC GA_____ T </p>
GAM25	PPP2R2B	<p> GAGCGGGCAGCCGCGACAAAATGG 29 TGAACA A T__ GI GGCA CC ACAAATGG </p>

		CCGT GG TGTTTTACC	
		TCGC__ C CGC AI	
GAM25 RAD1		ACATGCCCTCTACAAAATGG 22 TGAACAG AAC	
		GC CTACAAAATGG	
		CG GATGTTTTACC	
		A_____ GGA	
GAM25 RRM2B		AAAAGGAAATGTACAAAATG 17 TGAAC C CC	
		AGG AA TACAAAATGG	
		TCC TT ATGTTTTACT	
		T_____ T AC	
GAM25 SLC12A7		TGACCA--CAACCTACAAA 33 A AG ATG	
		TGA C GCAACCTACAAA	
		ACT G TGTTGGATGTTT	
		G III	
GAM25 SLC14A1		TGAA-AGGAAAA-TACAAAATG 35 C C CC G	
		TGAA AGG AA TACAAAATG	
		ACTT TCC TT ATGTTTTAC	
		_ _ TT I	
GAM25 SLC6A5		TGACACAGGCAACAGACTGAACTGG 32 _ CT AAAA_ GII	
		TGA ACAGGCAAC AC TGG	
		ACT TGTCCGTTG TG ACC	
		G TC ACTG	
GAM25 SYT1		AGGAATTCTACAAAATTGG 26 TGAACAGGCAAC _	
		CTACAAAAT GG	
		GATGTTTTA CC	
		AA_____ A	
GAM25 TBXAS1		GAACAGGCAACCAAGCAAA 31 TG TA_ ATGG	
		AACAGGCAACC CAAA	
		TTGTCCGTTGG GTTT	
		_ TTC G	
GAM26 CSPG3		AGACCTTTGTTCAAAGGAATA 38 TATTAGAC _ T TA	
		CTTTGT CAGA GGA	
		GAAACA GTTT CCT	
		_____ A _ TA	
GAM26 DTNB		TATTAGCCCTTTGTCAGATG 44 A GAT	
		TATTAG CCTTTGTCAGATG	
		ATAATC GGAAACAGTCTAC	
		G	
GAM26 NPHP1		TACTAGACCTTTATCAGTTAGAT 45 A AI	
		TATTAGACCTTTGTCAG TGGAT	

ATGATCTGGAAATAGTC ATCTA

A II

GAM26	NYX	TATTAGGAAACCCTTTGTCAG	43	A____	ATGGATA
		TATTAG CCTTTGTCAG			
		ATAATC GGAAACAGTC			
		CTTTG IIIATAG			
GAM26	RDX	TACACATTTGTCAGACGTGATA	42	TATTAG C	_
		AC TTTGTCAGATG GATA			
		TG AAACAGTCTGC CTAT			
		_____ T A			
GAM26	RPL10	TAGACCTTTGGTCAGGTGG	41	TATTAG _	A AT
		ACCTTTG TCAG TGG			
		TGGAAAC AGTC ACC			
		_____ C C AC			
GAM26	SHC1	ATTAGACCTAAG--AGATGG	40	TA TTGTC	A
		TTAGACCT AGATGG			
		AATCTGGA TCTACC			
		_ TTC_ A			
GAM26	SLC22A5	AGGCCTTTGTCACTGAAGGA	39	TATTAGAC	_ T
		CTTTGTCA GA GGAT			
		GAAACAGT CT CCTG			
		_____ GA T			
GAM27	APPBP2	AAAAAAAAAAAAATTTCTGGC	53	CT	TT
		AAAAAAGA GAATTTCTGGC			
		TTTTTTT TTTAAAGGACCG			
		TT II			
GAM27	MYO6	AAAAAAGACACTAGGAATTC	48	T____	CTGGCTT
		AAAAAAGAC GAATTC			
		TTTTTTCTG CTTAAAG			
		TGATC IIITCG			
GAM27	RABL2A	AAAAAACACCTAAATTCCTG	49	G _	GCTT
		AAAAAA AC TGAATTCCTG			
		TTTTTT TG ATTTAAAGGAC			
		G G IIIT			
GAM27	RABL2B	AAAAAACACCTAAATTCCTG	49	G _	GCTT
		AAAAAA AC TGAATTCCTG			
		TTTTTT TG ATTTAAAGGAC			
		G G IIIT			
GAM27	SET	AAAAAAGACTGCAACTTGCT	50	_ C	GGCT
		AAAAAAGACTG AATTT CT			

		TTTTTTCTGAC TTGAA GA		
		G C III T		
GAM27	SLC4A8	AAAAAAGACAGAAAGTCCT 51	T TT	GGCT
		AAAAAAGAC GAA TCCT		
		III		
		TTTTTTCTG CTT AGGA		
		T TC III T		
GAM27	SLC6A3	AACATAAACAGAATTTTCCTGG 52	AAAAA T	CTT
		AGAC GAATTTTCCTGG		
		TTTG CTAAAGGACC		
		TTGTA T III		
GAM28	AASS	TATTTATAAAATACAGGGT 58	ACC_	TTTGG
		TATTTA ATACAGGGT		
		ATAAAT TATGTCCCA		
		ATTT III TG		
GAM28	CYP19	ATTCACCA--CAGGGTTT 57	TATTTA AT	G
		ACC ACAGGGTTTT		
		TGG TGTCCCAAAG		
		AAAG_ _ I		
GAM28	DAAM1	TTTAACCATAC--GTATAGGT 66	TATT A_	TGG
		TAACCATAC GGGTTT		
		ATTGGTATG TCCAGA		
		_ CATA III		
GAM28	HIF1A	TAATAAACCATACAGCATTT 60	TATTT G	TGG
		AACCATACAG GTTT		
		TTGGTATGTC TAAA		
		ATTAT G III		
GAM28	KCNAB1	TTTAACCATGCAGCTTCTGTGGT 63	TATT A GG _ I	
		TAACCAT CAG TTT TGGT		
		ATTGGTA GTC AGA ACCA		
		_ C GA C A		
GAM28	MBNL	TTAATTCAAAGAGG-TTTTGGT 61	TATTTAAC TACA	
		CA GGGTTTTGGT		
		GT TCCAAAACCA		
		TAA_ TTC_		
GAM28	PRKY	TTTAA--TACAGGGTCTTG 64	TATTTAAC C	
		C ATACAGGGTTTTG		
		A TATGTCCCAGAAC		
		_ T		
GAM28	PRPS2	TAATTAATTCTATACAGGGTTTT 59	TATTTAACC_	GGTI
		ATACAGGGTTTT		

		TATGTCCCAAAA			
		ATTAATTAAGA III			
GAM28	RAI14	ATATTACCATATCAGGGTTTT	56	TATTTA _	GGT
		ACCATA CAGGGTTTT			
		TGGTAT GTCCCAAAA			
		ATAA_ A AII			
GAM28	SFRS2IP	TTTAATAGAGACAGGGTTTTG	62	TATTTAACCAT	GT
		ACAGGGTTTTG			
		TGTCCCAAAAC			
		ATTATCTC_ GG			
GAM28	ZNF264	TTTATAGTAGACAGGGTTTTG	65	TATTTAACCAT	G
		ACAGGGTTTTG			
		TGTCCCAAAAC			
		AATCATC_ G			
GAM29	ABCC2	AAGTACCT-G-GTGACATTT	76	A CGTC	C
		AAG ACCT GTGACATTT			
		TTC TGGA CACTGTAAA			
		A C_ I			
GAM29	ANK3	ACTTCCTGCTGACATTTCT	80	AAGAA C CG	
		CCT GT TGACATTTCT			
		GGA CG ACTGTAAAGA			
		_____ - -			
GAM29	APOH	AAGAAACAAGT-GTGACATTT	75	CCTC C	CT
		AAGAA GT GTGACATTT			
		TTCTT CA CACTGTAAA			
		TGTT _ II			
GAM29	ARHGEF7	AGGACATTGTCTGTGACATTT	82	AAGAACCTC _	CTC
		GTC GTGACATTT			
		CAG CACTGTAAA			
		CCTGTAA_ A TII			
GAM29	ASGR1	CCCTGCGGCAGGTCGAGGCATT	84	TG_ CTIII	
		CCCTGCGGC GAGGC			
		GGGACGCCG CTCCG			
		TCCAG TAAII			
GAM29	ASGR1	CCCTGCGGCAGGTCGAGGCATT	84	TGTCCC TG_ CTTTI	
		TGCGGC GAGGC			
		ACGCCG CTCCG			
		_____ TCCAG TAACT			
GAM29	CLCN6	TCCCTGCGGCACAGGAGGCC	89	T_ III	
		TCCCTGCGGC GGAGGC			

		AGGGACGCCG CCTCCG			
		TGT GII			
GAM29	CLCN6	TCCCTGCGGCACAGGAGGCC 89 TGTC T__ T			
		CCTGCGGC GGAGGCCTT			
		GGACGCCG CCTCCGGGA			
		____ TGT I			
GAM29	FXD7	TCCCAGGAGCTGGAGGCCT 90 TGC II			
		TCCC GGCTGGAGGCC			
		AGGG TCGACCTCCGG			
		TCC AI			
GAM29	FXD7	TCCCAGGAGCTGGAGGCCT 90 TGTC TGC T			
		CC GGCTGGAGGCCT			
		GG TCGACCTCCGGA			
		____ TCC C			
GAM29	GGA3	TGTCCCCACGGCTGGAGGCACGCTTT 94 TG CTTTIII			
		TGTCCC CGGCTGGAGGC			
		ACAGGG GCCGACCTCCG			
		GT TGCGAAA			
GAM29	GGA3	TGTCCCCACGGCTGGAGGCACGCTTT 94 C TG CTTI			
		CC CGGCTGGAGGC			
		GG GCCGACCTCCG			
		_ GT TGCG			
GAM29	HMGCL	AAGAACCTC--CATGACCTGTGTC 77 GT ATTTCTC			
		AAGAACCTC CGTGAC			
		TTCTTGGAG GTACTG			
		____ GACACAG			
GAM29	JRKL	AAGAACCTCCGTCTTCAAGTTTCT 73 _ GTGACA CI			
		AAGAACCTC GTC TTTCT			
		TTCTTGGAG CAG AAAGA			
		G AAGTTC II			
GAM29	LAMC2	AAGAACCTCAGTTGAGAAAT 74 TCG CATTTCT			
		AAGAACCTCG TGA			
		TTCTTGGAGT ACT			
		CA_ CTTTII			
GAM29	LIPE	GTCCCTGCGGC-GGTGCGC 88 T AG I			
		GTCCCTGCGGC GG GC			
		CAGGGACGCCG CC CG			
		_ AG G			
GAM29	LIPE	GTCCCTGCGGC-GGTGCGC 88 TG T AG TT			
		TCCCTGCGGC GG GCC			

		AGGGACGCCG CC CGG		
		— _ AG CI		
GAM29	LMO1	AATAAAATCG-CATTACATTTCTC 78	AAGAACC T G	I
		TCG CGT ACATTTCTC		
		AGC GTA TGTAAGAG		
		TTATTTT _ A I		
GAM29	LTBP2	CCTGTGACTGGAGGCCATT 85	C	TTII
		CCTG GGCTGGAGGCC		
		GGAC CTGACCTCCGG		
		A TAAI		
GAM29	LTBP2	CCTGTGACTGGAGGCCATT 85	TGTCCCTGC	TT
		GGCTGGAGGCC		
		CTGACCTCCGG		
		A TA		
GAM29	MGAT1	AAGCTCAGGACGTGGACATTTCT 69	AAGAAC T_ _	CI
		CTCG CGTG ACATTTCT		
		GAGT GCAC TGTAAGA		
		— CCT C CC		
GAM29	MLC1	TGTCCCTGCAGCCTGGCAGG 91	_ _ CCTTT	
		TGTCCCTGCGGC TGG AGG		
		ACAGGGACGTCG ACC TCC		
		G G IIIT		
GAM29	MLC1	TGTCCCTGCAGCCTGGCAGG 91	_ AGIII	
		TGTCCCTGCGGC TGG		
		ACAGGGACGTCG ACC		
		G GTCCI		
GAM29	NEUROD2	TGTCCCTGCGCTCTGGGGGC 92	G_ A CTTT	
		TGTCCCTGCG CTGG GGC		
		ACAGGGACGC GACC CCG		
		GA C IIIT		
GAM29	NEUROD2	TGTCCCTGCGCTCTGGGGGC 92	G_ A II	
		TGTCCCTGCG CTGG GG		
		ACAGGGACGC GACC CC		
		GA C GI		
GAM29	PAX5	TGCCCCTCCCTCAGGAGGCCTT 96	GCGGCT	TI
		TGTCCCT GGAGGCCTT		
		ACGGGGA CCTCCGAA		
		GGGAGT II		
GAM29	PAX5	TGCCCCTCCCTCAGGAGGCCTT 96	GCGGCT	I
		GTCCCT GGAGGCCT		

		CGGGGA CCTCCGGA		
		GGGAGT I		
GAM29	PPP2R5C	AAGACACTTGGAATAGTGACATTTCT 72	AC C__ C	CII
		AAGA CT GT GTGACATTTCT		
		TTCT GA TA CACTGTAAAGA		
		GT ACCT T III		
GAM29	PSD	ACCTCGTCGTCCACATCTTCT 79	AAGAACCT GA T C	
		CGTCGT CAT TCT		
		GCAGCA GTG AGA		
		_____ G_ T A		
GAM29	RGS19IP1	TGTCCCT---GCTGGGGGCC 95	GGC A T	
		TGTCCCTGC TGG GGCC		
		ACAGGGACG ACC CCGG		
		_____ C I		
GAM29	RGS19IP1	TGTCCCT---GCTGGGGGCC 95 _	GGC A	
		GTCCCTGC TGG GGC		
		CAGGGACG ACC CCG		
		A _____ C		
GAM29	RNPEPL1	GTCCCAG--GCTGGAGGCC 87	TGC I	
		GTCCC GGCTGGAGGC		
		CAGGG CCGACCTCCG		
		T_____ G		
GAM29	RNPEPL1	GTCCCAG--GCTGGAGGCC 87	TG TGC	
		TCCC GGCTGGAGGCCT		
		AGGG CCGACCTCCGGG		
		_____ T_____		
GAM29	ROR2	AGGACCTCGTCGTCGTCCTCTTCTC 83	AAGA GACA__ II	
		ACCTCGTCGT TTTCTC		
		TGGAGCAGCA GAAGAG		
		CC_____ GCAGGA GI		
GAM29	SFTPC	TGTCCCTGCGG-TGTGGGC 93	C GA CTT	
		TGTCCCTGCGG TG GGC		
		ACAGGGACGCC AC CCG		
		_____ AC III		
GAM29	SFTPC	TGTCCCTGCGG-TGTGGGC 93	C GA I	
		TGTCCCTGCGG TG GG		
		ACAGGGACGCC AC CC		
		_____ AC G		
GAM29	SORD	AACCTCA-CATGACATTTCT 71	AAGAAC T	
		CTCG CGTGACATTTCT		

GAGT GTACTGTAAAG

GAM29	SRRM1	GAACAGAGCCATGACATTTTC	86	AAGAACCTC	T
		GTCTGTGACATTTTC			
		CGGTACTGTAAAG			
		TGTCT_____T			
GAM29	TBXAS1	AATCACTTCAGTGACATTTTTC	70	AAGA C TC	CTC
		AC TCG GTGACATTT			
		TG AGT CACTGTAAA			
		G__ A __ AAG			
GAM29	TM4SF4	AGAACCTCGATGGCAATGGACATTT	81	AA TC_ ____	CTCII
		GAACCTCG GT GACATTT			
		CTTGGAGC CG CTGTAAA			
		__ TAC TTAC TIIIC			
GAM30	ADAMTS5	GTTGAATGTGTTGGACATGATAG	106	AA IIIC	
		GTTGAATGTGTT GATA			
		CAACTTACACAA CTGT			
		C_ ACTA			
GAM30	ADH7	TAATAGTTTCAATGTGTTAAG	111	G_ ATAG	
		TAATAGTT AATGTGTTAAG			
		ATTATCAA TTACACAATTC			
		AG IIIG			
GAM30	ADH7	TAATAGTTTCAATGTGTTAAG	111	A G_ I	
		ATAGTT AATGTGTTAA			
		TATCAA TTACACAATT			
		_ AG I			
GAM30	AF1Q	TAATAGTAGGAATGCATGTTAAGAT	110	T_ __ AGII	
		TAATAGT GAATGT GTTAAGAT			
		ATTATCA CTTACG CAATTCTA			
		TC TA IIIG			
GAM30	AF1Q	TAATAGTAGGAATGCATGTTAAGAT	110	AAT T_ __ I	
		AGT GAATGT GTTAAGA			
		TCA CTTACG CAATTCT			
		__ TC TA I			
GAM30	AKT1	TAA-AGTTGAATGTTGTAA	113	TAAT GTTAAGAT	
		AGTTGAATGT			
		TCAACTTACA			
		ATT_ ACATTIII			
GAM30	AKT1	TAA-AGTTGAATGTTGTAA	113	TAAT GTTAI	
		AGTTGAATGT			

		TCAACTTACA		
		ATT_ ACATT		
GAM30	C8orf1	TAATAGTTGAATTTATTTAGA 115	G A TAG	
		TAATAGTTGAAT TGTT AGA		
		ATTATCAACTTA ATAA TCT		
		A A		
GAM30	C8orf1	TAATAGTTGAATTTATTTAGA 115	G AAGI	
		AATAGTTGAAT TGTT		
		TTATCAACTTA ATAA		
		A ATCI		
GAM30	CSN2	TACTAGTTGAA---TTAAGAT 116 AA_ ATGT		
		TAGTTGA GTTAAGA		
		ATCAACT TAATTCT		
		ATG _		
GAM30	CSN2	TACTAGTTGAA---TTAAGAT 116 TAA ATGT		
		TAGTTGA GTTAAGAT		
		ATCAACT TAATTCTA		
		ATG _		
GAM30	CYBB	TAATAGTTGAGCACAGTTTAAAGA 112 AT__ G TAGI		
		TAATAGTTGA GT TTAAGA		
		ATTATCAACT CA AATTCT		
		CGTGT A G		
GAM30	DAZ	AACAGTTTCA-GTGTTAAGATA 102 _ GAAT I		
		ATAGTT GTGTTAAGAT		
		TGTCAA CACAATTCTA		
		T AGT_ I		
GAM30	DAZ	AACAGTTTCA-GTGTTAAGATA 102 TA GAAT		
		ATAGTT GTGTTAAGATAG		
		TGTCAA CACAATTCTATT		
		_ AGT_		
GAM30	GALR1	TTGAATTCTTGTTAAGATA 118 G__		
		TTGAAT TGTTAAGAT		
		AACTTA ACAATTCTA		
		AGA T		
GAM30	HGF	TAGTTGAATGT-TGAATGATA 117 GTTAA I		
		AGTTGAATGT GAT		
		TCAACTTACA CTA		
		ACTTA I		
GAM30	HGF	TAGTTGAATGT-TGAATGATA 117 TAATAG GTTAA		
		TTGAATGT GATA		

		AACTTACA CTAT	
		_____ ACTTA	
GAM30 HMGE	TA	ACTAGTTGAATATGATTTAAATA 107 A	TTAAGATI
		TAGTTGAATGTG	
		ATCAACTTATAC	
		G TAAATTTI	
GAM30 HMGE	TA	ACTAGTTGAATATGATTTAAATA 107 TAA_	_ A GII
		TAGTTGAATGTG TT AGATA	
		ATCAACTTATAC AA TTTAT	
		ATTG T A III	
GAM30 IL1RAP	A	ATAGTTGAGCACTGAGGTTAACATAG100 TA	A__ T_ G III
		ATAGTTGA TG GTTAA ATAG	
		TATCAACT AC CAATT TATC	
		___ CGTG TC G GII	
GAM30 LMO2	A	ATAGTTGAACAACTTTTAAAGAT 99 TA	TG__ AGI
		ATAGTTGAATG TTAAGAT	
		TATCAACTTGT AATTCTA	
		___ TGAAA AII	
GAM30 MEF2A	A	TAGCAGAATGTGTTCAAAAGTAG 104 A T	_ TAI
		GT GAATGTGT TAAGA	
		CG CTTACACA GTTTT	
		_ T A CAI	
GAM30 MEF2A	A	TAGCAGAATGTGTTCAAAAGTAG 104 TAAT T	_ _ I
		AGT GAATGTGT TAAGA TAG	
		TCG CTTACACA GTTTT ATC	
		___ T A C A	
GAM30 PAFAH1B2	T	AATAATTCAATGAATGTGTTACACATA109	___ AG GIII
		TAATAGT TGAATGTGTTA ATA	
		ATTATTA ACTTACACAAT TGT	
		AGTT G_ ATII	
GAM30 PAFAH1B2	T	AATAATTCAATGAATGTGTTACACATA109 AATAGT	AI
		TGAATGTGTTA	
		ACTTACACAAT	
		TT___ GT	
GAM30 PPP1CB	T	AATAGTTGGTGAATGTCTGTAAAG 108	AAT_ AAGATAGII
		TAATAGTTG GTGTT	
		ATTATCAAC TACAG	
		CACT ACATTTCI	
GAM30 SCG3	T	AATAG--GAA-GTGTAAAGA 114 TT T	T
		TAATAG GAA GTGTAAAGA	

		ATTATC CTT CACAATTCT	
		— — I	
GAM30	SCG3	TAATAG--GAA-GTGTTAAGA 114 _ TT T	
		AATAG GAA GTGTTAAG	
		TTATC CTT CACAATTC	
		A — —	
GAM30	SNX5	ATGGTTAAATG--TTAAGAT 105 TA_ AT I	
		GTTGA GTGTTAAGA	
		CAATT TACAATTCT	
		TAC — — I	
GAM30	SNX5	ATGGTTAAATG--TTAAGAT 105 TAATA AT	
		GTTGA GTGTTAAGAT	
		CAATT TACAATTCTA	
		C — —	
GAM30	TNFSF4	ATAGTTGAAGGTGTACTTAAGA 103 T TAAGIII	
		ATAGTTGAA GTGT	
		TATCAACTT CACA	
		C TGAATTC	
GAM30	TNFSF4	ATAGTTGAAGGTGTACTTAAGA 103 TAAT T _ TAG	
		AGTTGAA GTGT TAAGA	
		TCAACTT CACA ATTCT	
		— — C TGA CCI	
GAM30	TOB1	AATAGTTG-ATGTCTTTAAGAT 101 A G_ I	
		ATAGTTGA TGT TTAAGA	
		TATCAACT ACA AATTCT	
		— GA I	
GAM30	TOB1	AATAGTTG-ATGTCTTTAAGAT 101 TA A G_ AG	
		ATAGTTGA TGT TTAAGAT	
		TATCAACT ACA AATTCTA	
		— — GA CI	
GAM31	AF3P21	GCGCCGAGCCGCGCCGCGGT 123 _ AAC II	
		GCGC GAG CGCCGCGG	
		CGCG CTC GCGGCGCC	
		G GGC AI	
GAM31	AF3P21	GCGCCGAGCCGCGCCGCGGT 123 TATGCG AAC G	
		CGAG CGCCGCGGT	
		GCTC GCGGCGCCA	
		G — — GGC A	
GAM31	AKAP13	GCCCGAGCA--GCCGCGGTG 127 G AACC I	
		GC CGAG GCCGCGG	

		CG GCTC CGGCGCC			
		G GT__ A			
GAM31 AKAP13		GCCCGAGCA--GCCGCGGTG	127	TATGCG	AACC
		CGAG GCCGCGGT			
		GCTC CGGCGCCA			
		_____ GT__			
GAM31 CDKN2C		TGCTGGGAGAGC-GCCGCGGTG	130	GC_ AC	I
		GC GAGA CGCCGCGGT			
		CG CTCT GCGGCGCCA			
		ACC C_ I			
GAM31 CDKN2C		TGCTGGGAGAGC-GCCGCGGTG	130	TATGCGC AC	T
		GAGA CGCCGCGGTG			
		CTCT GCGGCGCCAC			
		GACC__ C_ C			
GAM31 CYP7B1		GCGCGCGCTAGGCCGCGGTG	129	AGAACC	I
		GCGCG GCCGCGG			
		CGCGC CGGCGCC			
		GATC__ A			
GAM31 CYP7B1		GCGCGCGCTAGGCCGCGGTG	129	TAT G AACC	
		GCGC AG GCCGCGGTG			
		CGCG TC CGGCGCCAC			
		G__ A _____			
GAM31 DTNB		ATGGG-GAGAACCGCTGGGG	121	ATGCGC	CGCI
		GAGAACCGC			
		CTCTTGGCG			
		ACCC__ ACCC			
GAM31 DTNB		ATGGG-GAGAACCGCTGGGG	121	TATGCGC	CGC TG
		GAGAACCGC GG			
		CTCTTGGCG CC			
		ACCC__ ACC CI			
GAM31 ECEL1		GCGCCGAGG-CCGCCGCGGTG	124	_ AA	I
		CGC GAG CCGCCGCGGT			
		GCG CTC GGCGGCGCCA			
		G C_ I			
GAM31 ECEL1		GCGCCGAGG-CCGCCGCGGTG	124	TATGCG	AA
		CGAG CCGCCGCGGTG			
		GCTC GGCGGCGCCAC			
		G_____ C_			
GAM31 FBXL4		GCGCGAGAA-GGCCTGGGTG	128	_ CC GC	I
		CGCGAGAA GCC GGT			

		GCGCTCTT CGG CCA			
		C C_ AC I			
GAM31	FBXL4	GCGCGAGAA-GGCTGGGTG	128	TATGCG	CC GC
		CGAGAA GCC GGTG			
		GCTCTT CGG CCAC			
		_____ C_ AC			
GAM31	MAPRE3	CGCTGAGG-CCGCCGCGGT	122	_ AA	II
		CGC GAG CCGCCGCGG			
		GCG CTC GGCGGCGCC			
		A C_ AI			
GAM31	MAPRE3	CGCTGAGG-CCGCCGCGGT	122	TATGCGC	AA
		GAG CCGCCGCGGT			
		CTC GGCGGCGCCA			
		_____ C_			
GAM31	MARK3	GCGCAAGACAGGCCGCGCGG	125	A____	III
		GCGCGAGA CCGCCGCG			
		CGCGTTCT GGCGGCGC			
		GTCC CII			
GAM31	MF12	GCGCGAGAGGCCGCGCGG	126	A_	II
		GCGCGAGA CCGCCGCG			
		CGCGCTCT GGCGGCGC			
		CC CI			
GAM31	MF12	GCGCGAGAGGCCGCGCGG	126	TATGCG	A_ TG
		CGAGA CCGCCGCGG			
		GCTCT GGCGGCGCC			
		_____ CC TT			
GAM31	PRKCI	TGCCGAGAAACCGCGGCCGT	132	TATG C	C G G
		CG GAGAACCGC GC GT			
		GC CTCTTGGCG CG CA			
		G_ _ C G G			
GAM31	PRKCI	TGCCGAGAAACCGCGGCCGT	132	TG C	C GI
		CG GAGAACCGC GC			
		GC CTCTTGGCG CG			
		G_ _ C GC			
GAM31	RPS6KA1	TGCGACCCGAACCGCCGCG	131	_ GA	II
		TGCG C GAACCGCCGCG			
		ACGC G CTTGGCGGCG			
		T GG CI			
GAM31	RPS6KA1	TGCGACCCGAACCGCCGCG	131	TAT C GA	GTG
		G GC GAACCGCCGCG			

		G TG CTTGGCGGCGC			
		___ C GG GGI			
GAM31	SLC18A3	TGGGCG-GAGGCGCCGCGGTG	133	___ C AAC	I
		GCG GAG CGCCGCGGT			
		CGC CTC GCGGCGCCA			
		ACC _ C_ I			
GAM31	SLC18A3	TGGGCG-GAGGCGCCGCGGTG	133	TAT C AAC	
		GCG GAG CGCCGCGGTG			
		CGC CTC GCGGCGCCAC			
		C_ _ C_			
GAM32	B3GALT3	TCACTATCCTTTTTATCTTGTA	155	AT A AA	
		TCAC TTCTTTTTATC TGTA			
		AGTG AGGAAAAATAG ACAT			
		AT A II			
GAM32	B3GALT3	TCACTATCCTTTTTATCTTGTA	155	AT A I	
		CAC TTCTTTTTATC TGT			
		GTG AGGAAAAATAG ACA			
		AT A I			
GAM32	BACH1	CATTTCTTTGTCTCTTGTA	145	TTA A II	
		CATTTCTTT TC TGT			
		GTAAAGAAA AG ACA			
		CAG A TI			
GAM32	CAPZA1	CACCTTTCTTTTTTTGACATGTA	141	ACA AT_ I	
		TTTCTTTT CATGT			
		AAAGAAAA GTACA			
		G_ AACT I			
GAM32	CAPZA1	CACCTTTCTTTTTTTGACATGTA	141	TC A AT_ AAI	
		AC TTTCTTTT CATGTA			
		TG AAAGAAAA GTACAT			
		_ G AACT AII			
GAM32	COG3	TCACATTTCTTGTGACCATTTAAA	157	TTT G I	
		TCACATTTCTT ATCAT TAAA			
		AGTGTAAGAA TGGTA ATTT			
		CAC A I			
GAM32	COG3	TCACATTTCTTGTGACCATTTAAA	157	TTT GTAAI	
		CACATTTCTT ATCAT			
		GTGTAAAGAA TGGTA			
		CAC AATTI			
GAM32	COL4A4	CACATTTTCTTTTTACCA-GAAAA	139	ACA TGI	
		TTTCTTTTTATCA			

		AAAGAAAAATGGT		
		A__ CTT		
GAM32 COL4A4		CACATTTTCTTTTACCA-GAAAA	139 TC	__ TGTAAGI
		ACATT TCTTTTATCA		
		TGTAA AGAAAAATGGT		
		__ AA CTTTAT		
GAM32 COX15		ACATTTCTTTCTCTACAT-TAAA	136	AT_ GTAAGI
		CATTTCTTTT CAT		
		GTAAAGAAAGA GTA		
		GAT ATTII		
GAM32 EIF5A2		CATTGCATAGTATCATGTAAA	146 ATTTCTTTT	I
		TATCATGTAA		
		ATAGTACATT		
		TAACGTATC I		
GAM32 EIF5A2		CATTGCATAGTATCATGTAAA	146 TCACATTTCTTTT	
		TATCATGTAAA		
		ATAGTACATTT		
		ACGTATC_____		
GAM32 FANCD2		TCACATTTCTATTTTGTATGT	149	_ ATC AAA
		TCACATTTCT TTTT ATGT		
		AGTGTAAGA AAAA TACA		
		T ACA		
GAM32 FZD6		CACATTTCTGTTT-TCAGGTA	144 _	T A T I
		ACATTTCT TTT TCA GT		
		TGTAAAGA AAA AGT CA		
		G C _ C I		
GAM32 FZD6		CACATTTCTGTTT-TCAGGTA	144 TC	T A T A
		ACATTTCT TTT TCA GTA		
		TGTAAAGA AAA AGT CAT		
		_ C _ C A		
GAM32 GPR23		CACATTTCTTATTAATAATGT	140 TC	T TC_ AAA
		ACATTTCTT TTA ATGT		
		TGTAAAGAA AAT TACA		
		_ T TAT AII		
GAM32 LTBR		TCCCATT-CTTTTATTTGCATGT	150 A T	_ AAAI
		TC CATT CTTTTTAT CATGT		
		AG GTAA GAAAAATA GTACA		
		G _ AAC IIIA		
GAM32 MS4A3		TCACATTTTCTTTTATTTTCATTAA	147	_ _ GTAAAI
		TCACATTT CTTTTTA TCAT		

		AGTGTAAGAAAAAT AGTA		
		A AAA AATTIIIA		
GAM32 MS4A3		TCACATTTTCTTTTATTTTCATTAA147 CA	___	GTAI
		TTTCTTTTTA TCAT		
		AAAGAAAAAT AGTA		
		A_ AAA AIII		
GAM32 NEDD4		TCACATTTTCAGATTTCTATCAGGT 148	___	T AAAl
		TCACATTTTC TTTTATCA GT		
		AGTGTAAG AAAGATAGT CA		
		TCT C IIIA		
GAM32 PDK4		TCACATTTCTCTGTA-CAT 151		T CAI
		TCACATTTCTTT TAT		
		AGTGTAAGAGA ATG		
		C TAI		
GAM32 PDK4		TCACATTTCTCTGTA-CAT 151		T CATGTA
		TCACATTTCTTT TAT		
		AGTGTAAGAGA ATG		
		C TAIIA		
GAM32 PGK1		TCAC-TTCTTTTAAACAGGCAAA 156	A	T T I
		TCAC TTTCTTTTTA CA GTAAA		
		AGTG AAAGAAAAAT GT CGTTT		
		_ T C I		
GAM32 PGK1		TCAC-TTCTTTTAAACAGGCAAA 156	_ A	T T I
		CAC TTTCTTTTTA CA GTAA		
		GTG AAAGAAAAAT GT CGTT		
		A _ T C I		
GAM32 PIGA		ATTTCTTTTATATCAGTGCAA 137	_ _	III
		ATTTCTTTT TATCA TGTA		
		TAAAGAAAA ATAGT ACGT		
		T C TII		
GAM32 PLS3		CACATTTCTTTGTTTCAGGTGTAAA 143	TC	TTA ___ II
		ACATTTCTTT TCA TGTA		
		TGTAAAGAAA AGT ACATTT		
		_ CAA CC TI		
GAM32 PRPF18		TTTCTTTTAAATCATCTAA 159	_	G II
		TTTCTTTTTA TCAT TA		
		AAAGAAAAAT AGTA AT		
		T G TI		
GAM32 RAI14		TCACATTTCTTTGGAGCAT 152		TTATCAII
		TCACATTTCTTT		

		AGTGTAAGAAA		
		CCTCGTAI		
GAM32	RAI14	TCACATTTCTTTGGAGCAT	152	TTATCATGTAA
		TCACATTTCTTT		
		AGTGTAAGAAA		
		CCTCGTAIIIA		
GAM32	RASGRP1	ATGTCT-TTTATCATATAAA	138	TCACATTTCT
		TTTTATCATGTAA		
		AAAATAGTATATT		
		G_____		
GAM32	RASGRP1	ATGTCT-TTTATCATATAAA	138	TTTC I
		TTTTATCATGTAA		
		GAAAATAGTATATT		
		TACA I		
GAM32	SLC21A9	TCCCTTTTCTTTT-ATCATGT	153	ACA T AA
		TC TTTCTTTT ATCATGT		
		AG AAAGAAAA TAGTACA		
		GGA _ II		
GAM32	SLC21A9	TCCCTTTTCTTTT-ATCATGT	153	CACA_ T I
		TTTCTTTT ATCATG		
		AAAGAAAA TAGTAC		
		AGGGA _ I		
GAM32	TFAP2C	CACTTTTCTTTTTTCAAGGTAAA	142	TC A A T_ I
		AC TTTCTTTT TCA GTAAA		
		TG AAAGAAAA AGT CATTT		
		_ A A TC A		
GAM32	TFAP2C	CACTTTTCTTTTTTCAAGGTAAA	142	ACA A T_ I
		TTTCTTTT TCA GTAA		
		AAAGAAAA AGT CATT		
		GA_ A TC I		
GAM32	TIMM23	TCATGTTTCTTTTTCTCCTTTAAA	158	CA A ATG I
		TCA TTTCTTTT TC TAAA		
		AGT AAAGAAAA AG ATTT		
		AC G GAA I		
GAM32	ZNF253	TCACATTTCTTTATAT-TTGTA	154	T CA AA
		TCACATTTCTTT TAT TGTA		
		AGTGTAAGAAA ATA ACAT		
		T A_ II		
GAM32	ZNF253	TCACATTTCTTTATAT-TTGTA	154	_ T CATGTI
		CACATTTCTTT TAT		

		GTGTAAAGAAA ATA	
		A T AACAI	
GAM33 ALEX3		AGCATTGATGATACAA---TATGA 163 A_ GTATI	
		AGCA GATGATACAATG	
		TCGT CTACTATGTTAT	
		AA ACTII	
GAM33 ALEX3		AGCATTGATGATACAA---TATGA 163 TA A_ ATG	
		GCA GATGATACA GTATGA	
		CGT CTACTATGT TATACT	
		__ AA __	
GAM33 ATRX		CAGGAAGA---AATGGTATG 167 TAGC TGATAC	
		AAGA AATGGTAT	
		TTCT TTACCATA	
		C__ ____	
GAM33 DPP4		AAGATGATA---GGTATGA 162 _ CAAT	
		AGATGATA GGTATG	
		TCTACTAT CCATAC	
		T ____	
GAM33 LARS2		TAGCCTAATGTGCCAATGGTATGA 176 AA ATA I	
		TAGC GATG CAATGGTATGA	
		ATCG TTAC GTTACCATACT	
		GA ACG I	
GAM33 LARS2		TAGCCTAATGTGCCAATGGTATGA 176 AA ATA I	
		AGC GATG CAATGGTATG	
		TCG TTAC GTTACCATAC	
		GA ACG I	
GAM33 MLLT7		TAGCAC-ATGATACAATCTGGGTA 173 AG ____ TGAI	
		TAGCA ATGATACAAT GGTA	
		ATCGT TACTATGTTA CCAT	
		G_ GAC IIIA	
GAM33 MLLT7		TAGCAC-ATGATACAATCTGGGTA 173 AGCAAG ____ I	
		ATGATACAAT GGT	
		TACTATGTTA CCA	
		GTG__ GAC I	
GAM33 MYO1D		AGGAAGATGATACCAAAGG 164 C AATGII	
		AG AAGATGATAC	
		TC TTCTACTATG	
		C GTTTCC	
GAM33 MYO1D		AGGAAGATGATACCAAAGG 164 TAGC AAT_ ATG	
		AAGATGATAC GGT	

		TTCTACTATG CCG		
		CC__ GTTT III		
GAM33	NEK2	AGCAAGATG-T-C-ATGGTAT 165 _	ATACA	
		GCAAGATG ATGGTA		
		CGTTCTAC TACCAT		
		T AG__		
GAM33	NEK2	AGCAAGATG-T-C-ATGGTAT 165 TA	ATACA	
		GCAAGATG ATGGTAT		
		CGTTCTAC TACCATA		
		__ AG__		
GAM33	NFE2	CAAGATGATGACAGT-ATATG 166	ACA I	
		AAGATGAT ATGGTAT		
		TTCTACTA TGTCATA		
		C__ T		
GAM33	OTC	GCAAGATGATAGAGAAGGTAT 168 C	CAAT_ I	
		AAGATGATA GGTA		
		TTCTACTAT CCAT		
		_ CTCTT I		
GAM33	OTC	GCAAGATGATAGAGAAGGTAT 168 TAGC	CAAT_ A	
		AAGATGATA GGTATG		
		TTCTACTAT CCATAT		
		__ CTCTT C		
GAM33	PTGIS	TAGTAACAATAATCACAATGGTA 170 _	GATGA I	
		AGCAA TACAATGGT		
		TTGTT GTGTTACCA		
		A ATTA_ I		
GAM33	PTGIS	TAGTAACAATAATCACAATGGTA 170 __	GATGA TGAI	
		TAGCAA TACAATGGTA		
		ATTGTT GTGTTACCAT		
		ATC ATTA_ IIIA		
GAM33	PYGB	TAGCAAGATGTGTGCAAAGTTCTG 172	ATA_ T ATGAI	
		TAGCAAGATG CAA GGT		
		ATCGTTCTAC GTT TCA		
		ACAC _ AGACI		
GAM33	PYGB	TAGCAAGATGTGTGCAAAGTTCTG 172 A	ATA_ T ATI	
		GCAAGATG CAA GGT		
		CGTTCTAC GTT TCA		
		_ ACAC _ AGA		
GAM33	RAI3	GCAAGATGAGAGAA--GTAT 169	TACAATGGTI	
		GCAAGATGA		

		CGTTCTACT		
		CTCTTCATAI		
GAM33	RAI3	GCAAGATGAGAGAA--GTAT	169 TAGC	TACAAT
		AAGATGA GGTAT		
		TTCTACT TCATA		
		____ CTCT__		
GAM33	TFRC	TACCAAGATGATGGGATGGAAT	174 G	ACA TATGA
		TA CAAGATGAT ATGG		
		AT GTTCTACTA TACC		
		G CCC TTAII		
GAM33	TFRC	TACCAAGATGATGGGATGGAAT	174 G	ACA TI
		CAAGATGAT ATGG		
		GTTCTACTA TACC		
		G CCC TI		
GAM33	UBQLN2	TAGCAAAAAAGAT-CAATGGTAT	171 T_ A	GA
		TAGCAAGA GAT CAATGGTAT		
		ATCGTTTT CTA GTTACCATA		
		TT _ II		
GAM33	UBQLN2	TAGCAAAAAAGAT-CAATGGTAT	171 T_ A	I
		AGCAAGA GAT CAATGGTA		
		TCGTTTT CTA GTTACCAT		
		TT _ I		
GAM33	VIPR1	TATCCAGATGATAC-ATGAGATG	175 GCA	A TI
		AGATGATACA TGG		
		TCTACTATGT ACT		
		AGG _ CT		
GAM33	VIPR1	TATCCAGATGATAC-ATGAGATG	175 TAGCA	A GT A
		AGATGATACA TG ATG		
		TCTACTATGT AC TAC		
		ATAGG _ TC I		
GAM34	BTC	GCTATCAAAC----AAATCA	184	TTGGAAAT
		GCTATCAAAC		
		CGATAGTTTG		
		TTTAGTII		
GAM34	CYBB	TATCAAACCTTTAAGAAATC	185 _	III
		TATCAAACCTT GGAAAT		
		ATAGTTTGAA TCTTTA		
		AT GII		
GAM34	DAAM1	TCAGCTATCAA-----AAATCAT	187	CTTGGA
		TCAGCTATCAAA		

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AGTCGATAGTTT
      TTAGTAI
GAM34 DAAM1 TCAGCTATCAA-----AAATCAT 187 AACTTG
      TCAGCTATCA GAAATC
      ||||| ||||
      AGTCGATAGT TTTTAG

      -----
GAM34 ECT2 CTATCAAAC---AAATCA 183 TGG
      CTATCAAAC AAATC
      ||||| ||||
      GATAGTTTGA TTTAG

      -----
GAM34 FACL5 TATTAAGGTTTGGAATCAT 186 TATCAAAC II
      TTGGAAATCA
      |||||
      AACCTTTAGT
      ATAATTCC AI
GAM34 FZD3 CAGCTATCAGTCATGCAAA 182 AACTTGGAII
      CAGCTATCA
      |||||
      GTCGATAGT
      CAGTACGTTT
GAM34 FZD3 CAGCTATCAGTCATGCAAA 182 TC AACT G TCA
      AGCTATCA TG AAA
      ||||| ||||
      TCGATAGT AC TTT
      CAGT G TII
GAM34 GAS7 CAGCAACCAA-CTTGGAACACCAT 181 T A _ I
      AGC ATCAA CTTGGAA ATCA
      || |||| ||||| ||||
      TCG TGGTT GAACCTT TGGT
      T _ G I
GAM34 GAS7 CAGCAACCAA-CTTGGAACACCAT 181 TC T A _ I
      AGC ATCAA CTTGGAA ATCAT
      || |||| ||||| ||||
      TCG TGGTT GAACCTT TGGTA
      _ T _ G A
GAM34 GDF8 AGCTCAAAAACCTCTGGAAATCAT 179 _ CTATC _ I
      TCAG AAAC TGGAAATCAT
      ||| |||| |||||
      AGTT TTTGA ACCTTTAGTA
      G _ _ G T
GAM34 GDF8 AGCTCAAAAACCTCTGGAAATCAT 179 GCTA _ _ I
      TCAA ACT TGGAAATCA
      ||| || |||||
      AGTT TGA ACCTTTAGT
      G _ TT G I
GAM34 STK4 CAGCTATCACTCAACTAGGA 180 _ T III
      CAGCTATCA AACT GG
      ||||| |||| ||

```

		GTCGATAGT TTGA CC		
		GAG T TII		
GAM34	STK4	CAGCTATCACTCAACTAGGA 180 TC	___	T AATCA
		AGCTATCA AACT GGA		
		TCGATAGT TTGA CCT		
		___ GAG T CIIIT		
GAM35	ANXA9	CCCAGCATCTCTTCTCCAG 197 TACC	AAA_	CT
		CAGCATCTTT CCAG		
		GTCGTAGAGA GGTC		
		___ AGAG CT		
GAM35	COG6	TACCCA---TCTTTAAACACCAGGCTT206	GCA	___ _ I
		TACCCA TCTTTAA ACCAG CTT		
		ATGGGT AGAAATT TGGTC GAA		
		___ TG C I		
GAM35	DDB2	CCCAGGGCTTGTTCAAACCAGCTT 196 TACCCA ATC		I
		GC TTAAACCAGCTT		
		CG AAGTTTGGTCGAA		
		GTCC_ AAC C		
GAM35	DHCR24	TACCCAGCACCTTCAATGTGACCAG 205	___	CTTII
		TACCCAGCATCTTTAA ACCAG		
		ATGGGTCGTGGAAGTT TGGTC		
		ACAC IIIT		
GAM35	EPHB6	CCCAGCATCTAGACTCCAG 198 TACC	TTAAA	CT
		CAGCATCT CCAG		
		GTCGTAGA GGTC		
		___ TCTGA AC		
GAM35	GALNT7	TACCAACATCATCTTTAAAACA 200	___ G	C GCTT
		TACC CA CATCTTTAAA CA		
		ATGG GT GTAGAAATTT GT		
		TT A T IIIT		
GAM35	GBP1	TACACAGCATCTTTTAAAGTCCATCTT203	C	_ _ G III
		TAC CAGCATCTTT AAA CCA CTT		
		ATG GTCGTAGAAA TTT GGT GAA		
		T A CA A III		
GAM35	ICOS	TACCCCTGGCATCTTTAAAACA 201	A_	C GCTT
		TACCC GCATCTTTAAA CA		
		ATGGG CGTAGAAATTT GT		
		GAC T IIIT		
GAM35	KCNJ16	TACCCAGCATCATCATAAAACA 204	TT_	C GCTT
		TACCCAGCATC TAAA CA		

		ATGGGTCGTAG	ATTT GT	
		TAGT	T IIIT	
GAM35	MSH3	CCAACAATCTTTAAA-CTGCTT	195 TACCCA	_ CA
		GCA TCTTTAAAC GCTT		
		III IIIIIII IIII		
		TGT AGAAATTTG	CGAA	
		_____ T	A_	
GAM35	NCAM2	GACTAGTTTTAGTACACTGG	199	A GAG CGA
		GACTAGTTT AG	ACTGG	
		IIIIIIII II IIII		
		CTGATCAAA TC	TGACC	
		A ATG	III	
GAM35	NOS1	ACCTCATCCACTTTA-ACCAGCTT	190 TA	_ G_ T A I
		CC CA CA CTTTAA CCAGCTT		
		II II II IIIII IIIIIII		
		GG GT GT GAAATT	GGTCGAA	
		_ A AG _ _	G	
GAM35	PACE	ACCCAGCATCTTACAAAACCAGC	191 TA	T_ TI
		CCCAGCATCTT	AAACCAGCT	
		IIIIIIII IIIIIII		
		GGGTCGTAGAA	TTTGGTCGG	
		_ TGT	II	
GAM35	PCDHA9	ACTAGCTCTAAGGAGACTGG	194 GA	_ CGA
		CTAGTTT AAGGAGACTGG		
		IIIIII IIIIIIIII		
		GATCGAG TTCCTCTGACC		
		_ A	TII	
GAM35	RCV1	TACCCAGCACTCCACAAAGGAGCTT	202	_ T CC II
		TACCCAGCA TCT TAAA	AGCTT	
		IIIIIIII III IIII IIII		
		ATGGGTCGT AGG GTTT	TCGAA	
		G T CC	II	
GAM35	SUV39H1	TACCCAGCA-CTGTAAGCACGAGC	207	CTTTAA_ C TTI
		TACCCAGCAT	AC AGC	
		IIIIIIII II III		
		ATGGGTCGTG	TG TCG	
		ACATTTCG C	III	
GAM35	USP9Y	ACCCAGTCTCATTCAAACCAGCT	193 TA	CA _ I
		CCCAG TC TTTAAACCAGCTT		
		IIII II IIIIIIIIIII		
		GGGTC AG AAGTTTGGTCGAG		
		_ AG T	I	
GAM35	VCAM1	ACCCGGCATCTTTACAAAACC	192 TA	A _ AGCTT
		CCC GCATCTTTA	AACC	
		III IIIIIII IIII		
		GGG CGTAGAAAT	TTGG	
		_ C	GTT AIIIT	
GAM36	ABP1	GGGTCGTTCTGGTGGTAGAT	212	_ II
		GGGTT TTCTGGTGGTGGA		
		IIII IIIIIIIIIII		

		CCCAG AAGACCACCATCT		
		C AI		
GAM36	ABP1	GGGTCGTTCTGGTGGTAGAT 212	TAGCGGGTT	
		TTCTGGTGGTGGAT		
		AAGACCACCATCTA		
		GC_____		
GAM36	APM1	GGGTTTTCT-GTTGTGAAT 213	GTG I	
		GGGTTTTCTG GTGGA		
		CCCAAAGAC CACTT		
		AA_ A		
GAM36	APM1	GGGTTTTCT-GTTGTGAAT 213	TAGCGGGT GTG	
		TTTCTG GTGGA		
		AAAGAC CACTT		
		_____ AA_		
GAM36	INPP5A	GCAGGTTTTCTGGGTCGTCGA 211	C _G GGI	
		GGGTTTTCTGG T GT		
		TCCAAAAGACC A CA		
		_ C G GCI		
GAM36	INPP5A	GCAGGTTTTCTGGGTCGTCGA 211	TAGC _G G TC	
		GGGTTTTCTGG T GT GA		
		TCCAAAAGACC A CA CT		
		_____ C G G TC		
GAM36	TIRAP	GCTGCTTTCTCTT-TGGTGGATC 210	CGG GG_ I	
		GTTTTCT TGGTGGAT		
		CGAAAGA ACCACCTA		
		GA_ GAA I		
GAM36	TIRAP	GCTGCTTTCTCTT-TGGTGGATC 210	TAGCGG GG_	
		GTTTTCT TGGTGGATC		
		CGAAAGA ACCACCTAG		
		A_____ GAA		
GAM37	ADAT1	TGACCTCAAGT-GATCTGCCTGCC 231	ATA I	
		TGACCTCAAGTGG TGCCTGCC		
		ACTGGAGTTCACT ACGGACGG		
		AG_ I		
GAM37	C21orf5	TGACCTCAAGT-GATCTGCCTGCC 231	ATA I	
		TGACCTCAAGTGG TGCCTGCC		
		ACTGGAGTTCACT ACGGACGG		
		AG_ I		
GAM37	CASP10	TGACCTCAAGT-GATCTGCCTGCC 231	ATA I	
		TGACCTCAAGTGG TGCCTGCC		

		ACTGGAGTTCACT ACGGACGG		
		AG_ I		
GAM37 CPT2		TGACCTCAAGT-GATCCACCCGCC 227	ATA	I
		TGACCTCAAGTGG TGCCTGCC		
		ACTGGAGTTCACT GTGGGCGG		
		AG_ I		
GAM37 CTSS		TGGCCTCAAGTTGATATGCCTGCC 234 A	G	I
		TG CCTCAAGT GATATGCCTGCC		
		AC GGAGTTCA CTATACGGACGG		
		C A I		
GAM37 DAPP1		TGACCTCAAGT-GATCTGCTTG 222	ATA C CC	
		TGACCTCAAGTGG TGC TG		
		ACTGGAGTTCACT ACG AC		
		AG_ A II		
GAM37 DMC1		TGACCTCAAGT-GATCCACCTGCC 228	ATA	I
		TGACCTCAAGTGG TGCCTGCC		
		ACTGGAGTTCACT GTGGACGG		
		AG_ I		
GAM37 DNASE2		TGACCTCAAGT-GATCTGCC 220	ATA TGC	
		TGACCTCAAGTGG TGCC		
		ACTGGAGTTCACT ACGG		
		AG_ III		
GAM37 FCMD		TGGCCTCAAGT-GATCCACCTGCC 232 A	ATA	I
		TG CCTCAAGTGG TGCCTGCC		
		AC GGAGTTCACT GTGGACGG		
		C AG_ I		
GAM37 FPRL1		TGACCTCAAGGCTGCAAATGC 218	TGGATA C_ C	
		TGACCTCAAG TGC TGC		
		ACTGGAGTTC ACG ACG		
		CG_ TTT I		
GAM37 GGCX		TGGCCTCAAGT-GATCTGCC 221 A	ATA TGC	
		TG CCTCAAGTGG TGCC		
		AC GGAGTTCACT ACGG		
		C AG_ III		
GAM37 HCS		GACCTCAAGT-GATCTGCCTGCC 217 TG	ATA	
		ACCTCAAGTGG TGCCTGCC		
		TGGAGTTCACT ACGGACGG		
		_ AG_		
GAM37 HOXB5		TGACCTCAAGAGGTAATTCATGC 223	T A_ CTGCC	
		TGACCTCAAG GG TATGC		

		ACTGGAGTTC CC GTACG		
		T ATTA IICCG		
GAM37 IL10		TGACCTCAAGT-GATCCACCCGCC 227	ATA	I
		TGACCTCAAGTGG TGCCTGCC		
		ACTGGAGTTCACT GTGGGCGG		
		AG_ I		
GAM37 MSL3L1		TGGCCTCAAGT-GATCCTCCTGCC 233 A	G ATG	I
		TG CCTCAAGTG AT CCTGCC		
		AC GGAGTTCAC TA GGACGG		
		C _ GGA I		
GAM37 NUP62		TGACCTCAAGT-CATCTGCCCCGCC 226	GGATA	I
		TGACCTCAAGT TGCCTGCC		
		ACTGGAGTTCA ACGGGCGG		
		GTAG_ I		
GAM37 OPA3		TGACCTCAAGT-GATCCGCCCGCC 229	ATA	I
		TGACCTCAAGTGG TGCCTGCC		
		ACTGGAGTTCACT GCGGGCGG		
		AG_ I		
GAM37 PAICS		TGACCTCAAGT-GATCTGCTTGC 224	ATA C C	
		TGACCTCAAGTGG TGC TGC		
		ACTGGAGTTCACT ACG ACG		
		AG_ A I		
GAM37 PHKB		ACCTCAAGT-GATCCACCTGCC 216 TGAC	ATA	
		CTCAAGTGG TGCCTGCC		
		GAGTTCACT GTGGACGG		
		____ AG_		
GAM37 POLK		TGACCTCAAGT-GATCTGCC 220	ATA TGC	
		TGACCTCAAGTGG TGCC		
		ACTGGAGTTCACT ACGG		
		AG_		
GAM37 SUDD		TGACCTCAAGT-GATCCACCCGCC 227	ATA	I
		TGACCTCAAGTGG TGCCTGCC		
		ACTGGAGTTCACT GTGGGCGG		
		AG_ I		
GAM37 TNFRSF10A		TGACCTCAAGT-GATCCACCCGCC 227	ATA	I
		TGACCTCAAGTGG TGCCTGCC		
		ACTGGAGTTCACT GTGGGCGG		
		AG_ I		
GAM37 TPM4		TGACCTCAAGT-GATCTGTCCTG 219	ATA _ CC	
		TGACCTCAAGTGG TG CCTG		

		ACTGGAGTTCACT AC GGAC		
		AG_ A II		
GAM37	TRPM8	TGACCTCAAGT-GATCTGCC 220	ATA	TGC
		TGACCTCAAGTGG TGCC		
		ACTGGAGTTCACT ACGG		
		AG_ III		
GAM37	ZNF136	TGACCTCAAGT-GATCCTCCTGCC 230	G ATG	I
		TGACCTCAAGTG AT CCTGCC		
		ACTGGAGTTCAC TA GGACGG		
		_ GGA I		
GAM37	ZNF14	TGACCTCAAAT-GATCTGCCCGCC 225	ATA	I
		TGACCTCAAGTGG TGCCTGCC		
		ACTGGAGTTTACT ACGGGCGG		
		AG_ I		
GAM38	ANK1	TCTGGCAGCCAG---GTCCCCGGC 243	AAAA	AGC
		TCTG CCAG GTCCCCGGC		
		AGAC GGTC CAGGGGCCG		
		CGTC _		
GAM38	ANK1	TCTGGCAGCCAG---GTCCCCGGC 243	_ AAAA	AGC
		CTG CCAG GTCCCCGG		
		GAC GGTC CAGGGGCC		
		A CGTC _		
GAM38	CD3Z	AAACCAGAGGGCCCAAGGC 238	C CC	II
		AAACCAGAG GTCC GG		
		TTTGGTCTC CGGG CC		
		C TT GI		
GAM38	DPH2L1	TCTGAAAACCAACAGCCTC 241	G_ G	CCCGG
		TCTGAAAACCA AGC TC		
		AGACTTTTGGT TCG AG		
		GG G ICG		
GAM38	DPH2L1	TCTGAAAACCAACAGCCTC 241	G_ GTII	
		TCTGAAAACCA AGC		
		AGACTTTTGGT TCG		
		GG GAGI		
GAM38	HAS3	TCTGAAAA-CACAGAATCCCCTGC 242	_ GC	G I
		TCTGAAAAC CAGA GTCCCC GC		
		AGACTTTTG GTCT TAGGGG CG		
		T _ A I		
GAM38	HAS3	TCTGAAAA-CACAGAATCCCCTGC 242	_ _ GC	GGI
		CTGAAAAC CAGA GTCCCC		

GACTTTTG GTCT TAGGGG
 A T _ ACI
 GAM38 JAM2 TGAAAACCAGACGAGGCGTCCGCCGG 244 TCTG _ _ CII
 AAAACCAGA GCGTCC CCGG
 ||||| |||||
 TTTTGGTCT CGCAGG GGCC
 _ GCTC C CAI
 GAM38 SLBP GAAACCC---GCGTCCCCG 240 GA AGA
 AAACC GCGTCCCC
 |||| |||||
 TTTGG CGCAGGGG
 C_ G_
 GAM38 TGFB3 GAAAACCAGGCGGCCTCCCC 239 A_ G III
 GAAAACCAG GC TCCC
 ||||| |||||
 CTTTGGTCT CG AGGG
 CGC G GII
 GAM38 TGFB3 GAAAACCAGGCGGCCTCCCC 239 TCTGAA A_ G
 AACCAG GC TCCCCGG
 |||| |||||
 TTGGTC CG AGGGGTC
 _ CGC G
 GAM38 TRPV3 AAAACCAGAGGCTTCACCCGG 237 _ G _ III
 AAAACCAGAG C TC CCCG
 ||||| |||||
 TTTTGGTCTC G AG GGGC
 C A T CII
 GAM39 ADAR AGTCTGGCTGGTTCTAGACTTC 252 GT AC CTTI
 CTGGCTG TCTG
 ||||| |||||
 GACCGAC AGAT
 _ CA CTGA
 GAM39 ARCN1 GTGTGAGTG-CTCTGCTTC 254 C GC A I
 GT TG TG CTCTGCTT
 || || |||||
 CA AC AC GAGACGAA
 C TC _ G
 GAM39 CNGB3 GAAAG-CTTCATGATCTCTGCTTC 253 T GGC _ I
 AAAG CT TGA CTCTGCTT
 |||| || |||||
 TTTC GA ACT GAGACGAA
 _ AGT A I
 GAM39 CNGB3 GAAAG-CTTCATGATCTCTGCTTC 253 TG T GGC _ I
 AAAG CT TGA CTCTGCTTC
 |||| || |||||
 TTTC GA ACT GAGACGAAG
 _ _ AGT A G
 GAM39 DAPK1 TGACAGCTCCTGGCTGACTC 255 A _ TGCTT
 TGA AGT CTGGCTGACTC
 |||| |||||

		ACT TCG GACCGACTGAG			
		G AG IIICT			
GAM39	DAPK1	TGACAGCTCCTGGCTGACTC	255	A _	III
		TGA AGT CTGGCTGACT			
		III III IIIIIIIII			
		ACT TCG GACCGACTGA			
		G AG GII			
GAM39	EPB41	TGAAAGTCTGAAGTCTGACTATG	256	_	C CTTCI
		TGAAAGTCTGG CTGACT TG			
		IIIIIIII IIIII II			
		ACTTTCAGACT GACTGA AC			
		TCA T IIICT			
GAM39	EPB41	TGAAAGTCTGAAGTCTGACTATG	256	_ A	ACTCI
		TGAA GTCTGGCTG			
		III IIIIIII			
		ACTT CAGACTGAT			
		CAG _ ACIII			
GAM39	FMOD	AAAGTCTGGCCTTTCTCTTCT	248	AA GA_	GCI
		GTCTGGCT CTCT			
		IIIIII III			
		CAGACCGG GAGA			
		_ AAAG AGI			
GAM39	FMOD	AAAGTCTGGCCTTTCTCTTCT	248	TGAA GA_	G TC
		AGTCTGGCT CTCT CT			
		IIIIII III II			
		TCAGACCGG GAGA GA			
		_ AAAG A CT			
GAM39	IDH3A	AAGTACTAGCT--CTCTGCTTC	251	_ _ GA	I
		AGT CTGGCT CTCTGCTT			
		III IIIII IIIIIII			
		TCA GATCGA GAGACGAA			
		T T _ I			
GAM39	IDH3A	AAGTACTAGCT--CTCTGCTTC	251	TGAAAGT GA	
		CTGGCT CTCTGCTT			
		IIIIII IIIIIII			
		GATCGA GAGACGAA			
		AT_ _			
GAM39	IL5RA	TGAAAGTCTGAGGTGAGTC	257	_ C C	TGCTT
		TGAAAGTCTG G TGA TC			
		IIIIIIII I III II			
		ACTTTCAGAC C ACT AG			
		T C C IIICT			
GAM39	IL5RA	TGAAAGTCTGAGGTGAGTC	257	_ C	CTII
		TGAAAGTCTG G TGA			
		IIIIIIII I III			
		ACTTTCAGAC C ACT			
		T C CAGI			
GAM39	RNMT	TGAAATTCAAGTCTTATCTGCTTC	258	G T _ GA_	II
		TGAAA TC GG CT CTCTGCTTC			
		IIII II II II IIIIIII			

		ACTTT AG TC GA GAGACGAAG	
		A T A ATA II	
GAM39 RNMT		TGAAATTCAAGTCTTATCTCTGCTTC 258 GA__ GGCTGA I	
		AAGTCT CTCTGCTT	
		TTCAGA GAGACGAA	
		TTAAG ATA__ I	
GAM39 TMEM2		AAAGACCTCAGGCTGACTCT 247 T __ III	
		AAAG CT GGCTGACTC	
		TTTC GG CCGACTGAG	
		T AGT AII	
GAM39 TMEM2		AAAGACCTCAGGCTGACTCT 247 T AAG T GCTT	
		GA TC GGCTGACTCT	
		CT AG CCGACTGAGA	
		T GG_ T GTII	
GAM39 WARS		AAAGCCACCCTGACTCTGC 250 TGG II	
		AAAGTC CTGACTCTG	
		TTTCGG GACTGAGAC	
		TGG GI	
GAM39 WARS		AAAGCCACCCTGACTCTGC 250 TGAA TGG TT	
		AGTC CTGACTCTGC	
		TCGG GACTGAGACG	
		__ TGG TC	
GAM39 ZNF144		AAAGTCTGG--GATCTGTGCTT 249 _ CT _ C I	
		AAGTCTGG GA CT TGCT	
		TTCAGACC CT GA ACGA	
		T _ A C I	
GAM39 ZNF144		AAAGTCTGG--GATCTGTGCTT 249 TGAA CT _ C	
		AGTCTGG GA CT TGCTT	
		TCAGACC CT GA ACGAA	
		__ _ A C	
GAM40 GNRH1		AAAAAGCTAGCATCTGTATCA 261 AC__ GTTCIII	
		AAAAAGCTA CTG	
		TTTTTCGAT GAC	
		CGTA ATAGTII	
GAM40 GNRH1		AAAAAGCTAGCATCTGTATCA 261 TA AC__ GT AAAT	
		AAAAGCTA CTG TCA	
		TTTTTCGAT GAC AGT	
		_ CGTA AT GIII	
GAM40 MNDA		AAAGCTAACAAGG--AAAAAT 262 CT TTCAAAI	
		AAAGCTAAC GG	

		TTTCGATTG CC		
		TT TTTTAT		
GAM41	AGTR1	AATTTGTTGCAAACACTATATCAA	276	TAAAATTTCTCAA TI
		ACTATATCAA		
		TGATATAGTT		
		AACAACGTTTG__ TA		
GAM41	BCAT1	AAATTTTCTCAAATTAGCTTTCAA	269	TAAAA C TA__ TI
		TTTCTCAAA TA TCAA		
		AAAGAGTTT AT AGTT		
		TTA__ A CGAA TI		
GAM41	FACL4	AAATTCCTCAAACACTACAT	274	TAAAA CAA
		TTTCTCAAACACTATAT		
		AAGGAGTTTGATGTA		
		TA__ AGI		
GAM41	GALNT2	AAAATTAC-CAAACACTATAT	271	TA T T CA
		AAATT C CAAACACTATAT		
		TTTAA G GTTTGATATA		
		_ T _ AI		
GAM41	ITIH2	TATAATTTCCCAAACACTATA	281	TAA TCAA
		AATTTCTCAAACACTATA		
		TTAAAGGGTTTGATAT		
		ATA IIIT		
GAM41	LHCGR	AAAATTTCT-AAACACTCTCAA	273	TA C TATA
		AAATTTCT AAAC TCAAT		
		TTTAAAGA TTTG AGTTG		
		_ _ TGAG		
GAM41	MDM1	AAAATTTCTATTCAAACCTTTTAAA	265	TA _ ATATCAATII
		AAATTTCT TCAAAC		
		TTTAAAG AGTTTGA		
		_ ATA AAAATTTTII		
GAM41	NDUFA5	AAAATTTCTCCAATAACCTGTATGCAAT	267	TA AAA__ A _ III
		AAATTTCTC CT TAT CAAT		
		TTTAAAGAG GA ATA GTTA		
		_ GTTATTG C C CII		
GAM41	PDGFRA	TAAAAGTTTCTCTCAAAC	277	TAAAA__ ATATCAA
		TTTCTCAAAC		
		AGAGAGTTTGA		
		ATTTTCAA IIITAAC		
GAM41	PITPNB	AAAATGTCATCACTAACTATATC	266	TA T _ _ AATI
		AAAT TC TCA AACTATATC		

		TTTA AG AGT TTGATATAG	
		___ C T GA GIII	
GAM41	RANBP2L1	AAAATTTCTCAACAATTTATAACAAT 268 TA	AC___ T II
		AAATTTCTCAA TATA CAAT	
		TTTAAAGAGTT ATAT GTTA	
		___ GTTAA T GI	
GAM41	RAX	AAAGTTTCTCAAACCTCTAT 272 TAAAA	A CAA
		TTTCTCAAACCT TAT	
		AAAGAGTTTGA ATA	
		TTC___ G AII	
GAM41	RNF6	AAAATAGTTCAAACCTATAT 270 TAAAATTTC	CAA
		TCAAACCTATAT	
		AGTTTGATATA	
		TTTATCA___ TII	
GAM41	SAS	TAAACTTTCTCAAACCTGGATC 282 A	AT AAT
		TAAA TTTCTCAAACCT ATC	
		ATTT AAAGAGTTTGA TAG	
		G CC III	
GAM41	SCN3A	TATAAATTCTCAATAACTATATCA 280 TAAAAT	___ ATI
		TTCTCAA ACTATATCA	
		AAGAGTT TGATATAGT	
		ATATTT AT III	
GAM41	SIP1	TAAAATTTTCATCATACAATTTCTAT 279	_ A T A AATII
		TAAAATTTTC TCA AC AT TC	
		ATTTTAAAG AGT TG TA AG	
		T A T A ATAI	
GAM41	SMARCC1	AAAAGTCTCAAACCTTTACCA 275 TAAAATT	A A
		TCTCAAACCT TATCA	
		AGAGTTTGA ATGGT	
		TTC___ A A	
GAM41	SORCS1	TACAATGGTTCTCAAACCTTTA 278 TAAAAT___	ATATCAAT
		TTCTCAAACCT	
		AAGAGTTTGA	
		ATGTTACC AATIIITA	
GAM42	ACTN2	AAGGCTT---TTTTTTTTTCCCC 288	CAG C
		AGGGTT TTT TTTTTCCC	
		TTCCGA AAA AAAAAGGG	
		AA_ _	
GAM42	ACTN2	AAGGCTT---TTTTTTTTTCCCC 288 TAA	CAG C
		GGGT TTT TTTTTCCC	

		TCCGA AAA AAAAGGGG		
		___ AA_ A		
GAM42	ADD2	GGGTTCGGAATTTCTTTTC	292	___ III
		GGGTTC AGTTTCTTTT		
		CCCAAG TTAAAGAAAAA		
		CC GII		
GAM42	ADD2	GGGTTCGGAATTTCTTTTC	292	TAA TTCA CC
		GGG GTTTCTTTTC		
		CCT TAAAGAAAAAG		
		AAG ___ AA		
GAM42	BCRP2	GGGTT-ATTTT-TTTTCCCC	294	_ CA C I
		GGTT GTTT TTTTCCC		
		CCAA TAAA AAAAAGGG		
		C _ A I		
GAM42	BCRP2	GGGTT-ATTTT-TTTTCCCC	294	TAAGGGTTCA C
		TTTT TTTTCCC		
		TAAA AAAAAGGG		
		AA_____ A		
GAM42	CDH13	AGGGTTCAGGTGTCTTAGTTTCC	290	_ _ C_ TTTTI
		AGG GTT AGTTTCT		
		TCC CAG TCAAAGG		
		AG A AA IIIT		
GAM42	CDH13	AGGGTTCAGGTGTCTTAGTTTCC	290	TAAG TT_ _ CCI
		GGTTCAG TCTT TTTCC		
		CCAAGTC AGAA AAAGG		
		___ CAC TC TGI		
GAM42	CLCA3	GGGTTCAGTATAATTTTTC	293	TTC_ II
		GGGTTCAGT TTTTC		
		CCCAAGTCA AAAAAG		
		TATT GI		
GAM42	CLCA3	GGGTTCAGTATAATTTTTC	293	TAAGGG TTC_ C
		TTCAGT TTTTTC		
		AAGTCA AAAAAGG		
		___ TATT T		
GAM42	CSPG3	TAAGGGTTCAGTTTACACTTCTT	298	CTT CCCI
		TAAGGGTTCAGTTT TTTC		
		ATTCCCAAGTCAAA GAAG		
		TGT AAI		
GAM42	CSPG3	TAAGGGTTCAGTTTACACTTCTT	298	AAG _ I
		GGTTCAGTTT CTTT		

CCAAGTCAAA GAAGA
 _____ TGT I

GAM42 CSPG3 AAGGTGTTGTGCTTTCTTTT 285 TA _ CAG_ CCCC
 AGG GTT TTTCTTTT
 ||| ||| |||||
 TCC CAA AAAGAAAA
 _ A CACG AIII

GAM42 PLA2G2A GGATCTGTTGCTCTTTTCC 295 TAAGGGTTCA T C
 GTT CTTTTTCC
 ||| |||||
 CGA GAAAAAGG
 GACAA_____ A

GAM42 RGL AGGTTCTCAGTTTCTTCTATTTCCC 289 GGGT _____ I
 TCAGTTTCTTT TTCC
 ||||| |||
 AGTCAAAGAAG AAGG
 G_____ ATA I

GAM42 RGL AGGTTCTCAGTTTCTTCTATTTCCC 289 TAA GG _____ CII
 G TTCAGTTTCTTT TTCCC
 | ||||| |||
 C GAGTCAAAGAAG AAGGG
 _____ AA ATA ACI

GAM42 SET AAGGGAGCAGGTTTTTCTTTTCCC 286 A_____ CAG _ CI
 GGGTT TTTCTTTT CC
 |||| ||||| ||
 TCCAA AAAGAAAA GG
 CTCG _____ A II

GAM42 SET AAGGGAGCAGGTTTTTCTTTTCCC 286 TA TT _____ CII
 AGGG CAG TTTCTTTT CCC
 ||| ||| ||||| |||
 TCCC GTC AAAGAAAA GGG
 _____ TC CAA A TII

GAM42 STAU TAGGGGTTATGCTTTCTTTT 297 AA CA _ I
 GGGTT GTTT CTTTT
 |||| ||| ||||
 CCCAA CGAA GAAAA
 C_ TA A I

GAM42 STAU TAGGGGTTATGCTTTCTTTT 297 TAA CA _ CCCC
 GGGTT GTTT CTTTT
 |||| ||| ||||
 CCCAA CGAA GAAAA
 ATC TA A IIIC

GAM42 TIMM23 TTCATGTTTCTTTTCTCC 299 _ _ II
 TTCA GTTTCTTTTCC CC
 ||| ||||| ||
 AAGT CAAAGAAAAAG GG
 A A II

GAM42 TMEM2 GTTCACATTTTTTTCCC 296 _ C II
 GTTCA GTTT TTTTCCC
 |||| ||| |||||

		CAAGT TAAA AAAAGGGG			
		G A II			
GAM42	TMEM2	G TTCACATTTTTTTTCCCC	296	TAAGGGTTCA	C
		GTTT TTTTCCC			
		TAAA AAAAGGGG			
		G_____ A			
GAM42	XKRY	AAAGGT--AGTTTCTTTTT	287	TC	I
		AAGGGT AGTTTCTTTT			
		TTCCA TCAAAGAAAA			
		_____ A			
GAM42	XKRY	AAAGGT--AGTTTCTTTTT	287	TA TC	CC
		AGGGT AGTTTCTTTTT			
		TTCCA TCAAAGAAAA			
		_____ AI			
GAM42	ZNF135	AGGGTTCAGACTTATGTTTTCCC	291	GG _ CT_	I
		GTTTCAG TTT TTTTCC			
		CAAGTC GAA AAAAGG			
		_____ T TAC I			
GAM42	ZNF135	AGGGTTCAGACTTATGTTTTCCC	291	TAAG _ CT_	CI
		GGTTCAG TTT TTTTCCC			
		CCAAGTC GAA AAAAGGG			
		_____ T TAC AA			
GAM43	ADCY9	ACACTCTTTGAAACGTTGAGCTTG	302	TGACACCG _____	TCAI
		TTGA TTGAGCTTG			
		AACT AACTCGAAC			
		TGAGA_____ TTGC CAII			
GAM43	DYRK1A	GAC-CCGTTGATT--GCTTCTCA	305	TG A GA G	
		AC CCGTTGATT GCTT TC			
		TG GGCAACTAA CGAA AG			
		_____ G			
GAM43	FUS1	ACACC-TTGATTGAGCCTG	303	TGAC G T	
		ACC TTGATTGAGCTTG			
		TGG AACTAACTCGGAC			
		_____ C			
GAM43	KRT15	GACACTGTACAAATGAGCTTGT	304	TG C _ T CA	
		ACAC GT TGA TGAGCTTGT			
		TGTG CA GTT ACTCGAACA			
		_____ A T T AI			
GAM43	PHYH	TGACACCGTTCCTATGCCCTTG	307	GA A GTCA	
		TGACACCGTT TTG GCTT			

		ACTGTGGCAA GAT CGGG	
		G_ A AACI	
GAM43	RGL	TGGCAC--TTGATTGAGAAAGTCA 308 A CG CTT	
		TG CAC TTGATTGAG GTCA	
		AC GTG AACTAACTC CAGT	
		C _ TTT	
GAM43	SCD	TGTCAC--TTGAATTGAGCTT 306 TGA CG _ GTC	
		CAC TTGA TTGAGCTT	
		GTG AACT AACTCGAA	
		ACA _ T	
GAM44	BCL2	GTTTCTTACTCAGACAGAGC 328 AG	
		GTTTCTTACTCGGG	
		CAAAGAATGAGTCT	
		GTCTC	
GAM44	BCL2	GTTTCTTACTCAGACAGAGC 328 TGAGTT _ TG	
		TCTTACTCGG GAGC G	
		AGAATGAGTC CTCG C	
		_ TGT GT	
GAM44	CIAS1	GCTACTCAGGAAGTTGAGGT 320 TGGC T _ C	
		TACTC GGA GTTGAGGTG	
		ATGAG CCT CAACTCCAT	
		_ T T C	
GAM44	CRYAA	GCTA-TCTAAAGGAGTGTGAGGTGCG 318 TGG CTCT _	
		CTA GGAGT TGAGGTGCG	
		GAT CCTCA ACTCCACGC	
		ATA TT_ C CA	
GAM44	CX3CR1	GCTACT--GGAGTTGGGGT 323 TGGCTACT A G	
		CTGGAGTTG GGT	
		GACCTCAAC CCA	
		AT_ C A	
GAM44	FUS1	GAGTTTCTTGC-CGGG-GCAGG 316 TG A T A T	
		AGTTTCTT C CGGG GC GG	
		TCAAAGAA G GCCC CG CC	
		_ C _ _ T	
GAM44	FUS1	GAGTTTCTTGC-CGGG-GCAGG 316 A T A TI	
		GAGTTTCTT C CGGG GC	
		CTCAAAGAA G GCCC CG	
		C _ _ TC	
GAM44	GFAP	TGAGTTTCTTGTAGTTGGAGTTG 331 ACTCG_ C GCI	
		TGAGTTTCTT GGAG TG	

		ACTCAAAGAA	CCTC AC		
		CAATCAA	A III		
GAM44	GFAP	TGAGTTTCTTGT	TTAGTTGGAGTTG	331 A	ACTCG__ CTI
		GTTTCTT	GGAG		
		CAAAGAA	CCTC		
		_	CAATCAA AII		
GAM44	GNGT2	CTACTCTGGCGT	GGAATGC	314 TGGCTA	A T
		CTCTGG	GT GAGGTGC		
		GAGACC	CA CTTTACG		
		_____	G C		
GAM44	HEM1	TGGCTA-T-TGGAGTT	GAGG	335 CTC	TG
		TGGCTA	TGGAGTTGAGG		
		ACCGAT	ACCTCAACTCC		
		A__	II		
GAM44	HSPB2	GCTACCTCTGGAGT	TGGTGG	317 TGGCTA	TGA T
		CTCTGGAGT	GG GC		
		GAGACCTCA	CC CG		
		ATG__	CCA _		
GAM44	HTR1D	GCTACTCTGGAGGCT	GAGG	319 TGGC	_ C
		TACTCTGGAG	TTGAGGTG		
		ATGAGACCTC	GACTCCGT		
		_____	C I		
GAM44	IMPA2	ACTTTGCAAGGCT	GAGGTGCG	311 TGGCTACTCT	A
		GG GTTGAGGTGCG			
		TC CGACTCCACGC			
		CGT_____	_		
GAM44	LTF	TGAGGCTTTCTTG---	GGGAGCTGG	330 _	ACTC C
		TGAG TTTCTT	GGGAGCTGG		
		ACTC AAAGAA	CCCTCGACC		
		CG	C__ I		
GAM44	LTF	TGAGGCTTTCTTG---	GGGAGCTGG	330 _ _	ACTC I
		GAG TTTCTT	GGGAGCTG		
		CTC AAAGAA	CCCTCGAC		
		A CG	C__ I		
GAM44	MAFF	TGGACACTGACAGGGG	TTGAGGTG	333 C	CT__ A CGI
		TGG TACT	GG GTTGAGGTG		
		ACC GTGA	CC CAACTCCAC		
		T	CTGT C III		
GAM44	METTL1	CTCCTC---	AGTTGAGGTGC	315 TGGCTA	TGG
		CTC	AGTTGAGGTG		

GAG TCAACTCCAC

GAM44	MME	GTTTCTTA--CAGGTGCTGGC	329	_	TC	A	I
		TTTCTTAC GGG GCTGG					
		AAAGAATG TCC CGACC					
		C _ A I					
GAM44	MME	GTTTCTTA--CAGGTGCTGGC	329	TGAGTT	TC	A	
		TCTTAC GGG GCTGG					
		AGAATG TCC CGACC					
		_ _ A					
GAM44	MPP2	TGGCGCCTCTGGAGTTGTGTGTG	334	TA	AG	CGI	
		TGGC CTCTGGAGTTG GTG					
		ACCG GAGACCTCAAC CAC					
		CG A_ ACI					
GAM44	MTR	GCTACTCTGGAGGCTGAGG	319	TGGC	_	C	
		TACTCTGGAG TTGAGGTG					
		ATGAGACCTC GACTCCGT					
		_ C I					
GAM44	NFRKB	GCTGCTG-GGAGTTGAGGTAGCG	324	TG	ACTCT	_	
		GCT GGAGTTGAGGT GCG					
		CGA CCTCAACTCCA CGC					
		A_ C_ T					
GAM44	PPP2R2B	AGTTTCTTAGAACTGGGGAGCTGG	313	GTT	_	C	I
		TCTT ACT GGGAGCTG					
		AGAA TGA CCCTCGAC					
		_ TCT C I					
GAM44	PPP2R2B	AGTTTCTTAGAACTGGGGAGCTGG	313	TGAG	_	C	CI
		TTTCTT ACT GGGAGCTGG					
		AAAGAA TGA CCCTCGACC					
		_ TCT C CT					
GAM44	RENT1	GGCTACTCT-GAGATGAGG	326	TG	G T	TG	
		GCTACTCTG AG TGAGG					
		CGATGAGAC TC ACTCC					
		_ _ T CI					
GAM44	REQ	GCCACTCTGGAGGAAAGAGGTG	321	TGGC	TT_	CG	
		TACTCTGGAG GAGGTG					
		GTGAGACCTC CTCCAC					
		_ CTTT TC					
GAM44	SIM2	AGTCTGCGTCCTGGGGAGCTGGC	312	_	T	ACTC	I
		GT TCTT GGGAGCTGG					

		CG AGGA CCCTCGACC			
		AGA C C_____ I			
GAM44	SLC24A1	GGCTACTCTGGGATTGAGGT	327	TG	AG G GC
		GCTACTCTGG TT AGGT			
		CGATGAGACC AA TCCA			
		_____ CT G AI			
GAM44	SLC6A3	GGC-ACACTGGGAGTTGAGG	325	TG T T _	TGC
		GC AC CTGG AGTTGAGG			
		CG TG GACC TCAACTCC			
		_____ T C TII			
GAM44	TCF2	TGAGTCGATGACTCGGGAGC	332	TCTT	TGG
		TGAGTT ACTCGGGAGC			
		ACTCAG TGAGCCCTCG			
		CTAC III			
GAM44	TCF2	TGAGTCGATGACTCGGGAGC	332	TCTT	I
		GAGTT ACTCGGGAG			
		CTCAG TGAGCCCTC			
		CTAC I			
GAM44	TEM5	TGGC-AGTCAGCTGTTGAGGTGC	336	TAC TGGA	G
		TGGC TC GTTGAGGTGC			
		ACCG AG CAACTCCACG			
		TC_ TCGA I			
GAM44	TNFRSF11A	GCTACTCCGAAGGTTGAGGTG	322	TGGC	_ CG
		TACTCTGGAG TTGAGGTG			
		ATGAGGCTTC AACTCCAC			
		_____ C CC			
GAM45	ADORA1	AGTGTTCTCCTCTCCATCAG	349	TACAGT	GTA A
		GTTCTC TCCA CAG			
		CAAGAG AGGT GTC			
		_____ GAG A			
GAM45	BTG3	TACAGGGTTCTCGTATCCAACAGA	358	T	I
		TACAG GTTCTCGTATCCAACAGA			
		ATGTC CAAGAGCATAGGTTGTCT			
		C I			
GAM45	BTG3	TCAAAGGGGCTAAAACAAATCGTC	363	T	I
		TCAAAGG GCTAGAACAAATCGTC			
		AGTTTCC CGATTTTGTTTAGCAG			
		C I			
GAM45	CLASP1	ACAGTGTTCCCAAGGATCTCAGCAG	344	TA	T_ _ A All
		CAGTGTTCTCG ATC CA CAG			

		GTCACAAGGGT TAG GT GTC	
		___ TCC A C All	
GAM45 CPD		CAGTGTTC---CCAAGAG 355 TACA GTAT C	
		GTGTTCTC CCAA A	
		CACAAGAG GGTT T	
		___ C	
GAM45 DGKI		CACTGTATCCTGTATCCAACAG 351 TACA C A	
		GTGTTCT GTATCCAACAG	
		CATAGGA CATAGGTTGTC	
		GA___ A	
GAM45 FAAH		CAGT-TTCTGGTGCATCCAACAGA 353 TACAGTG C___ I	
		TTCT GTATCCAACAGA	
		AAGA CGTAGGTTGTCT	
		CA___ CCA C	
GAM45 FCMD		TCAAAGGTGCATGAAACAAT 360 TA_ ATCGT	
		TCAAAGGTGC GAACAA	
		AGTTTCCACG TTTGTT	
		TAC AIIIC	
GAM45 FZD4		AAAGGTGCT-GAACAGAATC 340 TCAA A _ GT	
		AGGTGCT GAACA AATC	
		TCCACGA CTTGT TTAG	
		___ C AG	
GAM45 GNRHR		GTGTATTGGTAATCCAACAGA 356 TACAGTGTTC _	
		GTA TCCAACAGA	
		CAT AGGTTGTCT	
		TAAC___ T	
GAM45 HGF		ACAGTGTTC--T-TTCAAGAGA 346 TA CGTATC C	
		CAGTGTTC CAA AG	
		GTCACAAGA GTT TC	
		___ AAA___ C	
GAM45 HNRPDL		TCAAAGGTG-TGGTAGAAATC 362 C___ CAA GT	
		TCAAAGGTG TAGAA ATC	
		AGTTTCCAC ATCTT TAG	
		ACC ___ II	
GAM45 HS2ST1		AGTGATTATC-TCTCCAACAGA 347 TACAGTGT GTA	
		TCTC TCCAACAGA	
		AGAG AGGTTGTCT	
		CTAAT___	
GAM45 MEN1		CAAATGAG---GAACAAATC 350 TCAA CTA G	
		AGGTG GAACAAATC	

		TTTAC CTTGTTTAG		
		____ TC_ G		
GAM45	MLLT2	ACAGTGTTCTTCCATTTCTAC	343 TA	__ A A AGA
		CAGTGTTCT CGT TCC AC		
		GTCACAAGA GTA AGG TG		
		__ AG A A A		
GAM45	NAB1	TCAAAGGTG-TAGAA-AAAT	359 C	CAAATCG
		TCAAAGGTG TAGAA		
		AGTTTCCAC ATCTT		
		__ TTTA		
GAM45	NPTX2	AGAGTTCTCGTAGCATACA	348 TACAGT	TC _
		GTTCTCGTA CA ACAG		
		CAAGAGCAT GT TGTT		
		____ C_ A		
GAM45	SH3BP2	AAGGTGCTAAGAA-AAATC	342 TCAAAG	_ C G
		GTGCTA GAA AAATC		
		CACGAT CTT TTTAG		
		____ T _ T		
GAM45	SNRP70	TCCAAGGGGCCAGAACAAAT	361 A T	CGT
		TC AAGG GCTAGAACAAAT		
		AG TTCC CGGTCTTGTTTA		
		G C		
GAM45	SOX11	AAAGGTGTCACAGAACAAAT	339 TCAA	C__ CGT
		AGGTG TAGAACAAAT		
		TCCAC GTCTTGTTTA		
		____ AGT CGI		
GAM45	TMEM2	TCCAAGGTGCTACAATAGCTGGTC	364 A	G CAAATC I
		TC AAGGTGCTA AA GTC		
		AG TTCCACGAT TT CAG		
		G G ATCGAC I		
GAM45	UBQLN1	TACAGTGTTCTTCAGTCTGCACAAAGA	357	CG _ CA_
		TACAGTGTCT TA TC ACAGA		
		ATGTCACAAGG GT AG TGTTT		
		AA C ACG CTI		
GAM45	VAT1	AAGGCACTGAGAACAAATC	341 TCAAAG TG	_ GT
		G CT AGAACAAATC		
		I		
		C GA TCTTGTTTAG		
		____ GT C GT		
GAM45	VSX1	AACTGTTTCCAGCTATCCAACA	345 TA G	CT _ AI
		CA TGTT CG TATCCAACAG		

		GT ACAA GT ATAGGTTGTT		
		___ G AG CG II		
GAM45	WNT2	CAGTGTTCTTGCAGATCCAA 352 TACA C ___ CAG		
		GTGTTCT GT ATCCAA		
		II		
		CACAAGA CG TAGGTT		
		___ A TC ACI		
GAM45	ZNF137	CAGTGTTCT---TATACAAC 354 TACA CGT___ AAC		
		GTGTTCT ATCC		
		CACAAGA TGGG		
		___ TATGT III		
GAM46	AQP6	TGACTGG-GACCCTCTCTTGGCC 384 T G C		
		TGACTGG GG TCTCTCTTGGCC		
		II		
		ACTGACC CT GGAGAGAACCGG		
		_ G I		
GAM46	AQP6	TGACTGG-GACCCTCTCTTGGCC 384 _ T G I		
		GACTGG GG TCTCTCTTGGC		
		II		
		CTGACC CT GGAGAGAACCG		
		A _ G I		
GAM46	ATP4A	ACTGGTGGGGCTGGGACTCTTGG 370 T ___ IIIC		
		ACTGGTGGG CT CTCTTG		
		II		
		TGACCACCC GA GAGAAC		
		C CCCT CIII		
GAM46	ATP4A	ACTGGTGGGGCTGGGACTCTTGG 370 TGAC T ___ CCCI		
		TGGTGGG CT CTCTTG		
		II		
		ACCACCC GA GAGAACC		
		___ C CCCT AAI		
GAM46	C8G	ACTGGTGGGGTCGTCTCTCGG 368 _ _ III		
		ACTGGTGGG TC TCTCTTG		
		II		
		TGACCACCC AG AGAGAGC		
		C C CII		
GAM46	C8G	ACTGGTGGGGTCGTCTCTCGG 368 TGAC _ _ CCC		
		TGGTGGG TC TCTCTTG		
		II		
		ACCACCC AG AGAGAGCC		
		___ C C CCI		
GAM46	CALM3	CTGGAATGCCTCTCTTGGC 374 TGG II		
		CTGG GTCTCTCTTGG		
		GACC CGGAGAGAACC		
		TTA GI		
GAM46	CALM3	CTGGAATGCCTCTCTTGGC 374 TGACTGGTGG _		
		GTCTCTCTTGGC C		
		I		

		CGGAGAGAACCG G		
		CTTA_____ T		
GAM46	CUTL1	CTGGCTGGGGCTCTCTCTTTGG	372	_ _ _ _ _ IIIC
		CTGG TGGG TCTCTCTTG		
		GACC ACCC AGAGAGAAC		
		G CGAG CIII		
GAM46	CUTL1	CTGGCTGGGGCTCTCTCTTTGG	372	TGA T G_ _ CCCI
		CTGG GG TCTCTCTTG		
		GACC CC AGAGAGAACC		
		C_ _ GAG CCAI		
GAM46	ELAVL3	TGCCTG-TGCTGTCTCTCTTGGGCC	380	A _ GG CI
		CTG GT GTCTCTCTTG		
		GAC CG CAGAGAGAACC		
		G A A_ CI		
GAM46	ELAVL3	TGCCTG-TGCTGTCTCTCTTGGGCC	380	TGA _ GG _ CI
		CTG GT GTCTCTCTTG CC		
		GAC CG CAGAGAGAACC GG		
		ACG A A_ C II		
GAM46	HTR2A	GGTTGGTCTCAAACCTTTGGCC	377	G _ _ _ _ IIIG
		GGT GGTCTC TCTTGGC		
		CCA CCAGAG AGAACCG		
		A TTTG GIII		
GAM46	ITGAM	TGGTTGGGTCTCTTCTGCCCC	385	GG CT G I
		TGGGTCTCT TG CC		
		ACCCAGAGA AC GG		
		CA AG G I		
GAM46	ITGAM	TGGTTGGGTCTCTTCTGCCCC	385	TGACTGG CT G
		TGGGTCTCT TG CCC		
		ACCCAGAGA AC GGG		
		_____ AG G		
GAM46	KCNQ1	GGTGGGGCCACTCTTGGCC	376	_ T II
		GGTGGG TC CTCTTGGC		
		CCACCC GG GAGAACCG		
		C T GI		
GAM46	KCNQ1	GGTGGGGCCACTCTTGGCC	376	TGACTGGTG T
		GGTC CTCTTGGCC		
		CCGG GAGAACCGG		
		_____ T		
GAM46	MDK	ACTGGTGGGTCACATCTCGGGCC	371	TC_ CCI
		TGGTGGGTC TCTTGG		

		ACCACCCAG AGAGCC		
		TGT CII		
GAM46 MDK		ACTGGTGGGTACATCTCGGGCC 371 TGAC TC_ _ CI		
		TGGTGGGTC TCTTGG CC		
		II		
		ACCACCCAG AGAGCC GG		
		_____ TGT C AC		
GAM46 NFATC3		TGGTGGGTCCCCTCCTGGGCC 386 GG _ I		
		TGGGTCT CTCTTGGCC		
		ACCCAGG GAGGACCGG		
		_ GT I		
GAM46 NRAP		CTGCTGGCTC-CTCTTGGCC 375 _ G G T I		
		TG TGG TC CTCTTGGC		
		II III II		
		AC ACC AG GAGAACCG		
		G G G _ I		
GAM46 NRAP		CTGCTGGCTC-CTCTTGGCC 375 TGA CTGG G T		
		TGG TC CTCTTGGCC		
		III II		
		ACC AG GAGAACCGG		
		G_____ G _		
GAM46 PAIP2		TGA CTGGT GCTTCTTTCTTGC 382 GG C G CC		
		TGA CTGGTG TCT TCTT GC		
		III II		
		ACTGACCAC AGA AGGA CG		
		GA A A II		
GAM46 PAIP2		TGA CTGGT GCTTCTTTCTTGC 382 GG C GGI		
		GACTGGTG TCT TCTT		
		III		
		CTGACCAC AGA AGGA		
		GA A ACI		
GAM46 POLR2E		ACAGGTGGCTTCTCTCTTG 369 T G_ II		
		AC GGTGG TCTCTCTT		
		II		
		TG CCACC AGAGAGAA		
		T GA CI		
GAM46 POLR2E		ACAGGTGGCTTCTCTCTTG 369 TGA CT G_ G		
		GGTGG TCTCTCTTG CC		
		CCACC AGAGAGAAC GG		
		T_____ GA _		
GAM46 PTGS1		CTGTTGGGTCTCTGGTCTTG 373 G CTTIII		
		CTG TGGGTCTCT		
		III		
		GAC ACCCAGAGA		
		A CCAGAA		
GAM46 PTGS1		CTGTTGGGTCTCTGGTCTTG 373 TGA CTGG _ CC		
		TGGGTCTC TCTTGG		

		ACCCAGAG AGAACT		
		A _____ ACC CT		
GAM46	RAD17	TGACTGGTAC-TATAATCTTGGCCC 381	GGTCTC	I
		TGACTGGTG TCTTGGCCC		
		ACTGACCAT AGAACCGGG		
		GATATT I		
GAM46	RAD17	TGACTGGTAC-TATAATCTTGGCCC 381	GGTCTC	I
		GACTGGTG TCTTGGCC		
		CTGACCAT AGAACCGG		
		GATATT I		
GAM46	SLC21A9	ACTGCTGTGGCTGCTACTCTTGGCC 367	A G _ CT	CII
		TG CTG TGG GT CTCTTGGCC		
		AC GAC ACC CG GAGAACCGG		
		_ _ GA AT TCI		
GAM46	SLC21A9	ACTGCTGTGGCTGCTACTCTTGGCC 367	C_ GG CT	I
		TGGT GT CTCTTGGC		
		ACCG CG GAGAACCG		
		AC A_ AT I		
GAM46	TBL1X	TGATCTGTTGATTCTCTCTTG 379	_ G GG	GCCC
		TGA CTG TG TCTCTCTTG		
		ACT GAC AC AGAGAGAAC		
		A A TA IIIC		
GAM46	TBL1X	TGATCTGTTGATTCTCTCTTG 379	GA G GG	I
		CTG TG TCTCTCTT		
		GAC AC AGAGAGAA		
		TA A TA I		
GAM46	TBX5	TGTCTGTGGGGT-TCTCTTGGC 383	GA_ G TC	I
		CTG TGGG TCTCTTGG		
		GAC ACCC AGAGAACC		
		ACA _ CA I		
GAM46	TBX5	TGTCTGTGGGGT-TCTCTTGGC 383	TGA G TC	CC
		CTG TGGG TCTCTTGGC		
		GAC ACCC AGAGAACCG		
		ACA _ CA II		
GAM46	TNFRSF6B	GGTGGGT---TCTTGGCCC 378	CTC	
		GGTGGGT TCTTGGCC		
		CCACCCA AGAACCGG		

GAM47	ATM	TGAGCCGCTGCGCCCAGCC 415	A	II
		TGAGCC CTGCGCCCAGC		

		ACTCGG GACGCGGGTCG		
		C GI		
GAM47	ATM	TGAGCCGCTGCGCCAGCC 415	CATG	A
		AGCC CTGCGCCCAGCCTG		
		TCGG GACGCGGGTCGGGC		
		____ C		
GAM47	CHST5	CATGAGCCACCGCACCCGGCCTGG 401		A I
		CATGAGCCACTGCGCCC GCCTGG		
		GTACTCGGTGGCGTGGG CGGACC		
		C I		
GAM47	CHST5	CATGAGCCACCGCACCCGGCCTGG 401		A I
		ATGAGCCACTGCGCCC GCCTG		
		TACTCGGTGGCGTGGG CGGAC		
		C I		
GAM47	CLECSF12	GCCGTTGCACTCCAGCCTGG 408	AC _	II
		GCC TCGC CCAGCCTG		
		CGG ACGTG GGTCGGAC		
		CA A CI		
GAM47	CLECSF12	TGTGCCACTGCACTCCAGCCTGG 413	CATGA _	I
		GCCACTGCGC CCAGCCTG		
		CGGTGACGTG GGTCGGACC		
		A____ A C		
GAM47	CLECSF12	TGTGCCACTGCACTCCAGCCTGG 413	GA _	I
		GCCACTGCGC CCAGCCTG		
		CGGTGACGTG GGTCGGAC		
		A_ A I		
GAM47	CROT	CATGAGCCACTGCACCCAGCC 393		TGG
		CATGAGCCACTGCGCCCAGCC		
		GTACTCGGTGACGTGGGTCGG		
GAM47	CROT	CATGAGCCACTGCACCCAGCC 393		I
		ATGAGCCACTGCGCCCAGC		
		TACTCGGTGACGTGGGTCG		
		I		
GAM47	DFFB	GCCACTACACTCCAGCCTGG 406	_	II
		GCCACTGCGC CCAGCCTG		
		CGGTGATGTG GGTCGGAC		
		A CI		
GAM47	FANCC	TGAGCCACTGCACCCAGCCAGG 420		TGI
		GAGCCACTGCGCCCAGCC		

		CTCGGTGACGTGGGTCGG		
		TCI		
GAM47	FANCC	TGAGCCACTGCACCCAGCCAGG 420 CATG		T
		AGCCACTGCGCCCAGCC GG		
		TCGGTGACGTGGGTCGG CC		
		_____ T		
GAM47	FANCD2	CATGAGCCACTGCG-CCAGCC 394	C	TG
		CATGAGCCACTGCGCC AGCC		
		GTA		
		CTCGGTGACGCGG TCGG		
		_____ II		
GAM47	FANCD2	CATGAGCCACTGCG-CCAGCC 394 _	C	I
		ATGAGCCACTGCGCC AGC		
		TACTCGGTGACGCGG TCG		
		G _ I		
GAM47	FGF2	CATGAGCCACTGCACCCGGCCT 398	A	GG
		CATGAGCCACTGCGCCC GCCT		
		GTA		
		CTCGGTGACGTGGG CGGA		
		C II		
GAM47	FGF2	CATGAGCCACTGCACCCGGCCT 398	A	I
		ATGAGCCACTGCGCCC GCC		
		TACTCGGTGACGTGGG CGG		
		C I		
GAM47	FUT1	GCCACTGCACTCCAGCCTGG 407 _		II
		GCCACTGCGC CCAGCCTG		
		CGGTGACGTG GGTCGGAC		
		A CI		
GAM47	GNE	TGAGCCACTGCACTCCAGCCTGG 409 CATG	_	I
		AGCCACTGCGC CCAGCCTGG		
		TCGGTGACGTG GGTCGGACC		
		_____ A C		
GAM47	GNE	TGAGCCACTGCACTCCAGCCTGG 409 G	_	I
		AGCCACTGCGC CCAGCCTG		
		TCGGTGACGTG GGTCGGAC		
		_ A I		
GAM47	GNE	TGAGCCACTGTGCCCGGCCTGG 421	C	A I
		GAGCCACTG GCCC GCCTG		
		CTCGGTGAC CGGG CGGAC		
		A C I		
GAM47	GNE	TGAGCCACTGTGCCCGGCCTGG 421 CATG	C	A
		AGCCACTG GCCC GCCTG		

		TCGGTGAC CGGG CGGACC		
		_____ A C		
GAM47 GP2		CATGAGCCACTGCGCCCAGCC 395	C CA I	
		GAGCCACTG GCC GCC		
		III III		
		CTCGGTGAC CGG CGG		
		A AC I		
GAM47 GP2		CATGAGCCACTGCGCCCAGCC 395 CATG	C CA	
		AGCCACTG GCC GCCTG		
		III		
		TCGGTGAC CGG CGGAC		
		_____ A AC		
GAM47 IFIT4		CATGAGCCACTGCGCCCGGCC 396	A TGG	
		CATGAGCCACTGCGCCC GCC		
		III		
		GTA CTCTCGGTGACGCGGG CGG		
		C III		
GAM47 IFIT4		CATGAGCCACTGCGCCCGGCC 396	A I	
		ATGAGCCACTGCGCCC GC		
		II		
		TACTCTCGGTGACGCGGG CG		
		C I		
GAM47 IL18		TGAGCCACTGCGCCCGGCATG 417	A CTI	
		GAGCCACTGCGCCC GC		
		II		
		CTCGGTGACGCGGG CG		
		C TAI		
GAM47 IL18		TGAGCCACTGCGCCCGGCATG 417 CATG	A C	
		AGCCACTGCGCCC GC TGG		
		III		
		TCGGTGACGCGGG CG ACT		
		_____ C T		
GAM47 IPP		TGAGCCACCATGCCCAGCCT 416 GC	I	
		GAGCCACT GCCCAGCC		
		CTCGGTGG CGGGTCGG		
		TA I		
GAM47 IPP		TGAGCCACCATGCCCAGCCT 416 CATG	GC	
		AGCCACT GCCCAGCCTG		
		TCGGTGG CGGGTCGGAT		
		_____ TA		
GAM47 IPP		CATGAGGCCACTGCGCCCAGCCT 390	GGI	
		CATGAG CCACTGCGCCCAGCCT		
		GTA CTCTGGTGACGCGGGTCGGA		
		C III		
GAM47 IPP		CATGAGGCCACTGCGCCCAGCCT 390 A	I	
		TGAG CCACTGCGCCCAGCC		

		ACTC GGTGACGCGGGTCGG		
		— C I		
GAM47	KCNA7	CATGAGCCACCGCGCCCGGCCT 397	A	GG
		CATGAGCCACTGCGCCC GCCT		
		GTACTCGGTGGCGCGGG CGGA		
		C II		
GAM47	KCNA7	CATGAGCCACCGCGCCCGGCCT 397	A	I
		ATGAGCCACTGCGCCC GCC		
		TACTCGGTGGCGCGGG CGG		
		C I		
GAM47	MEFV	CCACTGCACTCCAGCCTGG 402	—	II
		CCACTGCGC CCAGCCTG		
		GGTGACGTG GGTCGGAC		
		A CI		
GAM47	MEFV	GCCACTGCACTCCAGCCTGG 407	—	II
		GCCACTGCGC CCAGCCTG		
		CGGTGACGTG GGTCGGAC		
		A CI		
GAM47	MIR16	CATGAGCCACTGTGCCCAGC 391	C	CTG
		CATGAGCCACTG GCCCAGC		
		GTACTCGGTGAC CGGGTCG		
		A III		
GAM47	MIR16	CATGAGCCACTGTGCCCAGC 391	C	I
		ATGAGCCACTG GCCCAG		
		TACTCGGTGAC CGGGTC		
		A I		
GAM47	OPTN	CATGAGCCACTGTGCCCCGGCCTG 399	C	A GI
		CATGAGCCACTG GCCC GCCTG		
		GTACTCGGTGAC CGGG CGGAC		
		A C II		
GAM47	OPTN	CATGAGCCACTGTGCCCCGGCCTG 399	C	A I
		ATGAGCCACTG GCCC GCCT		
		TACTCGGTGAC CGGG CGGA		
		A C I		
GAM47	PCDHB9	ATGAGCCACTGAGCCCTGCCT 389	C	A I
		TGAGCCACTG GCCC GCC		
		ACTCGGTGAC CGGG CGG		
		T A I		
GAM47	PCDHB9	ATGAGCCACTGAGCCCTGCCT 389	CA	C A GG
		TGAGCCACTG GCCC GCCT		

		ACTCGGTGAC CGGG CGGA			
		___ T A GI			
GAM47 PDE6B		GCCACGGCACTCCAGCCTGG	405	T _	II
		GCCAC GCGC CCAGCCTG			
		CGGTG CGTG GGTCGGAC			
		C A CI			
GAM47 PPEF2		GCCAATGCACTCCAGCCTGG	404	C _	II
		GCCA TGCGC CCAGCCTG			
		CGGT ACGTG GGTCGGAC			
		T A CI			
GAM47 PRKR		TGTGTCATTGCACTCCAGCCTGG	414	CATGAGC C _	I
		CA TGCGC CCAGCCTGG			
		GT ACGTG GGTCGGACC			
		ACA___ A A C			
GAM47 PRKR		TGTGTCATTGCACTCCAGCCTGG	414	GAGC C _	I
		CA TGCGC CCAGCCTG			
		GT ACGTG GGTCGGAC			
		ACA_ A A I			
GAM47 RABL2B		TGCGCCACTGCACTCCAGCCTGG	410	GA _	I
		GCCACTGCGC CCAGCCTG			
		CGGTGACGTG GGTCGGAC			
		G_ A I			
GAM47 RABL2B		TGCGCCACTGCACTCCAGCCTGG	410	CATGA _	I
		GCCACTGCGC CCAGCCTGG			
		CGGTGACGTG GGTCGGACC			
		G___ A C			
GAM47 RHD		TGCGGCACTGCACTCCAGCCTGG	411	_A C _	I
		G GC ACTGCGC CCAGCCTG			
		C CG TGACGTG GGTCGGAC			
		G_ _ A I			
GAM47 RHD		TGCGGCACTGCACTCCAGCCTGG	411	CATGAGC _	I
		CACTGCGC CCAGCCTGG			
		GTGACGTG GGTCGGACC			
		GCC___ A A			
GAM47 SIM2		TGAGCCACTGAGCCCGGCCTGG	419	C A I	
		GAGCCACTG GCCC GCCTG			
		CTCGGTGAC CGGG CGGAC			
		T C I			
GAM47 SIM2		TGAGCCACTGAGCCCGGCCTGG	419	CATG C A	
		AGCCACTG GCCC GCCTG			

		TCGGTGAC CGGG CGGACC	
		_____ T C	
GAM47	SLC17A5	CATGAGCCACCGTGCCCGGCC 392	C A TGG
		CATGAGCCACTG GCCC GCC	
		GTACTCGGTGGC CGGG CGG	
		A C III	
GAM47	SLC17A5	CATGAGCCACCGTGCCCGGCC 392	C A I
		ATGAGCCACTG GCCC GC	
		TACTCGGTGGC CGGG CG	
		A C I	
GAM47	TRIM14	TGAGCCACCGCGCCCAGCCAGG 418	TGI
		GAGCCACTGCGCCCAGCC	
		CTCGGTGGCGCGGGTCGG	
		TCI	
GAM47	TRIM14	TGAGCCACCGCGCCCAGCCAGG 418	CATG T
		AGCCACTGCGCCCAGCC GG	
		TCGGTGGCGCGGGTCGG CC	
		_____ T	
GAM47	TRPM1	CATGAGCCACTGTGCCCAGC 391	C CTG
		CATGAGCCACTG GCCCAGC	
		GTACTCGGTGAC CGGGTCG	
		A III	
GAM47	TRPM1	CATGAGCCACTGTGCCCAGC 391	C I
		ATGAGCCACTG GCCCAG	
		TACTCGGTGAC CGGGTC	
		A I	
GAM47	VENTX2	TGCGTCATTGCACTCCAGCCTGG 412	GAGC C _ I
		CA TGCGC CCAGCCTG	
		GT ACGTG GGTGGAC	
		GCA_ A A I	
GAM47	VENTX2	TGCGTCATTGCACTCCAGCCTGG 412	CATGAGC C _ I
		CA TGCGC CCAGCCTG	
		GT ACGTG GGTGGACC	
		GCA_ A A C	
GAM47	VHL	CATGAGCCACTGTGCTCGGCCTG 400	C CCA GI
		CATGAGCCACTG GC GCCTG	
		GTACTCGGTGAC CG CGGAC	
		A AGC II	
GAM47	VHL	CATGAGCCACTGTGCTCGGCCTG 400	C CCA I
		ATGAGCCACTG GC GCCT	

		TACTCGGTGAC CG CGGA				
		A AGC I				
GAM47	VHL	CCTCTGCACTCCAGCCTGG 403 A _ II				
		CC CTGCGC CCAGCCTG				
		II IIIII IIIIIII				
		GG GACGTG GGTCGGAC				
		A A CI				
GAM47	VHL	GCCACTGCACTCCAGCCTGG 407 _ II				
		GCCACTGCGC CCAGCCTG				
		IIIIIIII IIIIIII				
		CGGTGACGTG GGTCGGAC				
		A CI				
GAM47	YES1	GCCACTGCACTCCAGCCTGG 407 _ II				
		GCCACTGCGC CCAGCCTG				
		IIIIIIII IIIIIII				
		CGGTGACGTG GGTCGGAC				
		A CI				
GAM48	AP2B1	GTGGTGTAATGGTTTCCTGC 427 T_ II				
		GTGGTGT TGGTTTCCTG				
		IIIIII IIIIIIIII				
		CACCACA ACCAAAGGAC				
		TT GI				
GAM48	AP2B1	GTGGTGTAATGGTTTCCTGC 427 TG T_ CC				
		TGGTGT TGGTTTCCTGCT				
		IIIIII IIIIIIIIIII				
		ACCACA ACCAAAGGACGG				
		_ TT II				
GAM48	GALGT	GTGGTGTTCTGGCCGTTTCCTGC 426 _ _ IIIG				
		GTGGTG TTTGGT TTCCTG				
		IIIIII IIIII IIIII				
		CACCAC AGACCG AAGGAC				
		CA GCA GIII				
GAM48	GALGT	GTGGTGTTCTGGCCGTTTCCTGC 426 T_ G _ CCTI				
		GTGGT TTTGGT TTCCTGCT				
		IIII IIIII IIIIIII				
		CACCA AGACCG AAGGACGG				
		AC _ GCA IIIT				
GAM48	HK1	GGTGTTTGACTCTTTTCCTTCTC 424 _ GCTIIIG				
		GGTGTTTG TTTCT				
		IIIIII IIIII				
		CCACAAACC AAAGGA				
		TGAGA AGAGIII				
GAM48	SPTBN2	GTGGTAGGCGGCTTCCTGCTCCT 428 TT I				
		TGGTG TGGTTTCCTGCTCC				
		IIII IIIIIIIIIII				
		ACCAT GCCGAAGGACGAGG				
		CC I				
GAM48	SPTBN2	GTGGTAGGCGGCTTCCTGCTCCT 428 TG TT I				
		TGGTG TGGTTTCCTGCTCCT				
		IIII IIIIIIIIIIIII				

		ACCAT GCCGAAGGACGAGGA		
		___ CC C		
GAM48	TAL1	GGTGTTTGGAGCCTTTCCT	425	___ IIIA
		GGTGTTTGG TTTCC		
		CCACAAACC AAAGG		
		TCGG AIII		
GAM48	TAL1	GGTGTTTGGAGCCTTTCCT	425	TGTGGT TTT GC
		GTTTGG CCT TCC		
		CAAACC GGA AGG		
		___ TC_ A_		
GAM49	ACVR1B	AACGAGCCTTCAGAATGGT	432	AT_ A II
		AAC CCT CAGAATGG		
		TTG GGA GTCTTACC		
		CTC A AI		
GAM49	ACVR1B	AACGAGCCTTCAGAATGGT	432	TAACAT A GAAA
		CCT CAGAATGGT		
		GGA GTCTTACCA		
		TGCTC_ A AIII		
GAM49	APOL1	CATCCTGGCCAACATGGTGAAA	446	AT A__ A I
		CCT CAG ATGGTGAA		
		GGA GTT TACCACTT		
		___ CCG G I		
GAM49	APOL1	CATCCTGGCCAACATGGTGAAA	446	TAACAT A__ A G
		CCT CAG ATGGTGAAA		
		GGA GTT TACCACTTT		
		___ CCG G G		
GAM49	DAPP1	ACTTTCTATCAGAATGGTGA	438	ACATC _ II
		CTA CAGAATGGTG		
		GAT GTCTTACCAC		
		TGAAA A TI		
GAM49	DAPP1	ACTTTCTATCAGAATGGTGA	438	TAACATC _ AA
		CTA CAGAATGGTGA		
		GAT GTCTTACCACT		
		AAA___ A AA		
GAM49	FGF5	CATCCTGACCAACATGGTGAAA	444	AT _ AGA_ I
		CCT AC ATGGTGAA		
		GGA TG TACCACTT		
		___ C GTTG I		
GAM49	FGF5	CATCCTGACCAACATGGTGAAA	444	TAACAT _ AGA_ G
		CCT AC ATGGTGAAA		

		GGA TG TACCACTTT		
		_____ C GTTG G		
GAM49 FMN2		TAACATCCTAGA-AAAATTGAAA 451	C TGG G	
		TAACATCCTA AGAA TGAAA		
		ATTGTAGGAT TTTT ACTTT		
		C TA_ I		
GAM49 FMN2		TAACATCCTAGA-AAAATTGAAA 451 _	C TGG I	
		AACATCCTA AGAA TGAA		
		TTGTAGGAT TTTT ACTT		
		A C TA_ I		
GAM49 GDF8		ATGCTACAGAAT--TGAAAG 442 TC_	GG I	
		CTACAGAAT TGAAA		
		GATGTCTTA ACTTT		
		TAC _ I		
GAM49 GRM7		CATCCTGGCCAACATGGTGAAA 446 AT A__ A I		
		CCT CAG ATGGTGAA		
		GGA GTT TACCACTT		
		_ CCG G I		
GAM49 GRM7		CATCCTGGCCAACATGGTGAAA 446 TAACAT A__ A G		
		CCT CAG ATGGTGAAA		
		GGA GTT TACCACTTT		
		_____ CCG G A		
GAM49 MCP		ACATTCTATAGT-TGGTGAAAG 440 _ C C AA I		
		CAT CTA AG TGGTGAAA		
		GTA GAT TC ACCACTTT		
		T A A A_ I		
GAM49 MCP		ACATTCTATAGT-TGGTGAAAG 440 TAACATC C AA		
		CTA AG TGGTGAAAG		
		GAT TC ACCACTTTC		
		TAA_____ A A_		
GAM49 NRIP1		TAACCTTT-TACAAGAGATGGTGAAA 448 ATCC _ _ GI		
		TAAC TACA GA ATGGTGAAA		
		ATTG ATGT CT TACCACTTT		
		AAA_ T C II		
GAM49 NRIP1		TAACCTTT-TACAAGAGATGGTGAAA 448 AACATCC _ _ I		
		TACA GA ATGGTGAA		
		ATGT CT TACCACTT		
		TGAAA_ T C I		
GAM49 PPARGC1		AAAATCCTACAGATCTATGCTGAAA 436 ACA _ G I		
		TCCTACAGA ATG TGAA		

AGGATGTCT TAC ACTT
 ____ AGA G I
 GAM49 PPARGC1 AAAATCCTACAGATCTATGCTGAAA 436 TAAC ____ G GII
 ATCCTACAGA ATG TGA
 ||||| |||||
 TAGGATGTCT TAC ACTTT
 TT__ AGA G AII
 GAM49 PRKWNK3 ACATTTCTACAGAATGATGA 437 C_ II
 ACAT CTACAGAATGGTG
 ||| |||||
 TGTA GATGTCTTACTAC
 AA TI
 GAM49 PRKWNK3 ACATTTCTACAGAATGATGA 437 TAACATC AA
 CTACAGAATGGTG
 |||||
 GATGTCTTACTACT
 TAAA__ CG
 GAM49 RHD AACTATCCTAGCCAACATGGTGAAA 431 AC _ A I
 ATCCTA CAG ATGGTGAA
 |||| | |||||
 TAGGAT GTT TACCACTT
 _ CG G I
 GAM49 RHD AACTATCCTAGCCAACATGGTGAAA 431 TAAC _ A GII
 ATCCTA CAG ATGGTGAAA
 |||| | |||||
 TAGGAT GTT TACCACTTT
 TGA_ CG G GII
 GAM49 RPE TAACGTTCTTAAGAATGGTG 450 A_ C C AAA
 TAAC TC TA AGAATGGTG
 ||| || |||||
 ATTG AG AT TCTTACCAC
 CA A _ III
 GAM49 RPE TAACGTTCTTAAGAATGGTG 450 AACA_ C C I
 TC TA AGAATGGT
 || || |||||
 AG AT TCTTACCA
 TTGCA A _ I
 GAM49 RYR2 TCCTTCCAGGATGGTGAAA 452 A_ A II
 TCCT CAG ATGGTGAA
 ||| || |||||
 AGGA GTC TACCACTT
 AG C TI
 GAM49 RYR2 TCCTTCCAGGATGGTGAAA 452 TAACATCCTA A
 CAG ATGGTGAAA
 ||| |||||
 GTC TACCACTTT
 G_____ C
 GAM49 SBF1 ACACACT-CAGGAATGGTG 439 TC A _ II
 ACA CT CAG AATGGTG
 ||| || |||||

		TGT GA GTC TTACCAC	
		GT _ C TI	
GAM49	SBF1	ACACACT-CAGGAATGGTGA 439 TAACATC A _ AA	
		CT CAG AATGGTGA	
		GA GTC TTACCACT	
		TGT____ _ C GG	
GAM49	TERF1	AACATCCTGACCAGCATGGTGAAA 433 AC A__ A I	
		ATCCT CAG ATGGTGAA	
		TAGGA GTC TACCACTT	
		_ CTG G I	
GAM49	TERF1	AACATCCTGACCAGCATGGTGAAA 433 TA A__ A GI	
		ACATCCT CAG ATGGTGAAA	
		TGTAGGA GTC TACCACTTT	
		_ CTG G GI	
GAM49	TLX1	TAAAATCCTACAG---GGTTCGAAAG 449 C AAT _ I	
		TAA ATCCTACAG GGT GAAAG	
		ATT TAGGATGTC CCA CTTTC	
		T _ _ AG I	
GAM49	TLX1	TAAAATCCTACAG---GGTTCGAAAG 449 AC AAT GI	
		ATCCTACAG GGT	
		TAGGATGTC CCA	
		T_ _ AG	
GAM49	TUFT1	CAGCCTAGCCAGTATGGTGAAA 445 AT _ A I	
		CCTA CAG ATGGTGAA	
		GGAT GTC TACCACTT	
		_ CG A I	
GAM49	TUFT1	CAGCCTAGCCAGTATGGTGAAA 445 TAACAT _ A G	
		CCTA CAG ATGGTGAAA	
		GGAT GTC TACCACTTT	
		_____ CG A G	
GAM49	UBE4A	AACATCCTACTAGATTGGGTTTGGGAAG435 T _ A TGAAAI	
		CCTAC AGA TGG	
		GGATG TCT ACC	
		_ A A CAAACI	
GAM49	UBE4A	AACATCCTACTAGATTGGGTTTGGGAAG435 TA _ A TGAAAGIII	
		ACATCCTAC AGA TGG	
		TGTAGGATG TCT ACC	
		_ A A CAAACCTTC	
GAM49	UC28	ATCCAAACAGAATGG-GAAAG 441 T_ T I	
		TCC ACAGAATGG GAAA	

		AGG TGTCTTACC CTTT	
		TT _ I	
GAM49 UC28		ATCCAAACAGAATGG-GAAAG 441 TAACATCCT T	
		ACAGAATGG GAAA	
		TGTCTTACC CTTT	
		TT_____ _	
GAM49 VHL		CATCCTGGACAACATGGTGAAA 443 AT _ A I	
		CCT ACAG ATGGTGAA	
		GGA TGTT TACCACTT	
		_ CC G I	
GAM49 VHL		CATCCTGGACAACATGGTGAAA 443 TAACAT _ A G	
		CCT ACAG ATGGTGAAA	
		GGA TGTT TACCACTTT	
		_____ CC G G	
GAM49 WASF3		TAAAATTCTGACCAAGTGGTGAAAAG 447 AACA CT A A I	
		TC AC GA TGGTGAAA	
		AG TG TT ACCACTTT	
		TTTA AC G C I	
GAM49 WASF3		TAAAATTCTGACCAAGTGGTGAAAAG 447 TAACA_ CT A A II	
		TC AC GA TGGTGAAAAG	
		AG TG TT ACCACTTTC	
		ATTTTA AC G C II	
GAM49 WDR1		AACATCAAAGCATGATGGTGAAA 434 A CTA_ GA I	
		CATC CA ATGGTGAA	
		GTAG GT TACCACTT	
		_ TTTC AC I	
GAM49 WDR1		AACATCAAAGCATGATGGTGAAA 434 TA CTA_ GA GI	
		ACATC CA ATGGTGAAA	
		TGTAG GT TACCACTTT	
		_ TTTC AC GI	
GAM50 ACP1		TAGA-TGTTGACCT-GGGCC 457 A CGA GA	
		TAGA TGTTGACCT GCC	
		ATCT ACAACTGGA CGG	
		_ CC_ II	
GAM50 PACSIN1		AGAATGTTGTTCTGGGGGCCGTGG 455 TA AC CGA_ A I	
		GAATGTTG CT GCCG GG	
		CTTACAAC GA CGGC CC	
		_ AA CCCC A C	
GAM50 SKI		TAGAATGTT-CCAGCAAGCAGAGG 458 GA T_ C I	
		TAGAATGTT CC CGAGC GAGG	

ATCTTACAA GG GTTCG CTCC
 ___ TC T I
 GAM50 TAZ AGATTGCGGAGCTGGAGCCGAGG 456 TA A T C C I
 GA TGT GA CT GAGCCGAGG
 || ||| || |||||
 CT ACG CT GA CTCGGCTCC
 ___ A C C C G
 GAM51 ACATN TATGATCAAATATACAGAAA 469 TATTAT G
 GATCAAG ATATGGAAA
 ||||| |||||
 CTAGTTT TATGTCTTT
 _____ A
 GAM51 ATRN TATGATCAAAGAGATGGA 468 TATTAT _ T AA
 GATCAAG GA ATGGA
 ||||| || |||||
 CTAGTTT CT TACCT
 _____ T C GG
 GAM51 CDKN2B TATAATGATCAAGCAACCCTGGAAAT 472 T _ A_ II
 TAT ATGATCAAG GAT TGGAAAT
 ||| ||||| ||| |||||
 ATA TACTAGTTC TTG ACCTTTA
 T G GG II
 GAM51 CETN1 TATTATTGAAGTAGAGATATGGAAAT 470 _ TCA _ II
 TATTAT GA AG GATATGGAAAT
 ||||| || || |||||
 ATAATA CT TC CTATACCTTTA
 A TGA T II
 GAM51 COL4A4 ATTATT-TAAAGTATATGGAAA 467 TATTATGATC _ T
 AAGG ATATGGAAA
 ||| |||||
 TTTC TATACCTTT
 AATAAA___ A T
 GAM51 DBT ATTCTTACCCAGGATATGGAGAAT 465 TATTATG A AATI
 ATC AGGATATGGA
 ||| |||||
 TGG TCCTATACCT
 AAGAA___ G CTTA
 GAM51 DDX6 TTTTGAAAAA--ATATGGAAAT 479 TATTA TC
 TGA AAGGATATGGAAA
 ||| |||||
 ACT TTTTATACCTTT
 A___ _
 GAM51 DSG1 ATTTTGCTCGAGCTATATGGAAA 464 TATTA A A G_ TI
 TG TC AG ATATGGAAA
 || ||| |||||
 AC AG TC TATACCTTT
 AAA___ G C GA TI
 GAM51 EDAR ATGACCTCAAGGATAGGTAAA 461 TATTATGA T _ T
 TCAAGGATA GG AAA
 ||||| || |||

AGTTCCTAT CC TTT
 GG_____ A T
 GAM51 EDN3 TATTCTAGGCAAGGATATGAAA 473 ATGAT AT
 TATT CAAGGATATGGAA
 ||| |||||
 ATAA GTTCCTATACTTT
 GATCC II
 GAM51 FOXF1 TTAT-ATAAAACATATGGAAAT 478 TATTATG C G
 AT AAG ATATGGAAAT
 || ||| |||||
 TA TTT TATACCTTTA
 TA_____ T G
 GAM51 HLF ATG-TCAAGAGGGATATGAAA 462 TATTATGATCAA T
 GGATATGGAAA
 |||||
 CCTATACCTTT
 GTTCTC_____ T
 GAM51 LILRB4 TATTTTGTTCCTG--TATGGAAAT 476 A A AAGGA
 TATT TG TC TATGGAAAT
 ||| || |||||
 ATAA AC AG ATACCTTTA
 A A GAC_
 GAM51 LRAT TATAATTAGAAATGATATGGAAA 474 TAT CAAG_____ TI
 TATGAT GATATGGAAA
 |||| |||||
 ATATTA CTATACCTTT
 _____ ATCTTTA II
 GAM51 MOCS2 ATGATCAAGGGTGTAGAAAT 463 TATTATGA ATA
 TCAAGG TGGAAA
 |||| |||||
 AGTTCC ATCTTT
 _____ CAC
 GAM51 PGAM1 TTATTAT-ACTGATATGGAAA 477 T ATCAAG
 ATTATG GATATGGAAA
 |||| |||||
 TAATAT CTATACCTTT
 _ GA_
 GAM51 PSD TAGTAAGTTTAAAG-TATGGAAAT 475 TATTATGATC A I
 AAGG TATGGAAAT
 ||| |||||
 TTTC ATACCTTTA
 ATCATTCAAA _ I
 GAM51 RP2 TATTATGATCAGGTAGATTGGGAA 471 A_ A AAATII
 TATTATGATCA GGAT TGG
 ||||| ||| |||
 ATAATACTAGT TCTA ACC
 CCA A CTTII
 GAM51 SLC12A2 ATTAAGATTGAG-ATATGGAA 466 TATTAT CAA A
 GAT GGATATGGAA
 || |||||

		CTA TCTATACCTT	
		AATT__ AC_ A	
GAM52	ALK	TGAGCCTCCCGCTCTCCGCGCCG 516 C G _ GCI	
		TG GCCT CC CTTTCCGCGCCG	
		AC CGGA GG GAGAGGCGCGGC	
		T G C III	
GAM52	BN51T	GCCTTCGGTCTCCGCGCCGG 495 TGCGCCTGCCC	
		TTTCCGCGCCGG	
		AGAGGCGCGGCC	
		AAGCC_____	
GAM52	BRF1	GCCT-CCCTTGCGGCGCGCCGGC 491 TGCGCCTG TC__	
		CCCTT CGCGCCGGC	
		GGGAA GCGCGGCCG	
		A_____ CGCC	
GAM52	BTEB1	GCCCCTGCCC---CGCGCCGGC 509 TG G TTTC	
		C CCTGCCC CGCGCCGG	
		G GGACGGG GCGCGGCC	
		_ G _	
GAM52	CYP2A6	CCTGCCCTTTCCCTGGCCCCG 482 TGCG G_ TT G GGC	
		CCT CCCT CC CGCC	
		GGA GGGA GG GCGG	
		G__ AA CC G GTI	
GAM52	EFNB2	TGCAGCCAGCCCTTTCCCCAGCC 513 _ T G_ GGCI	
		TGC GCC GCCCTTTCC C GCC	
		ACG CGG CGGGAAAGG G CGG	
		T T G T IIIC	
GAM52	GCK	GCCTGCCCTTTTGGCCAGG 494 TGCGCC CC G	
		TGCCCTTT GC CCGG	
		ACGGGAAA CG GGTC	
		_____ AC _	
GAM52	GPR48	TGCGGCCGCC--TCCGCGCCGGC 521 C CT	
		TGCG CTGCC TTCCGCGCCGGC	
		ACGC GGCGG AGGGCGCGGCCG	
		C _	
GAM52	GPX4	GCGCGTCGGCTTTCCGCGCC 503 T CCTGCC GG	
		GCG CTTTCCGCGCC	
		CGC GAAAGGCGCGG	
		G AGCC__ AI	
GAM52	GSR	CGCCAGCTCGGTCCCGCGCCGGC 487 TGCG T CCT_ I	
		CC GC TTCCGCGCCGGC	

		GG CG AGGGCGCGGCCG	
		____ T AGCC C	
GAM52	HMX1	GCGGCGGCC--TCCGCGCCGG 508 T_ CCT CTT	
		GCG GCC TCCGCGCCGG	
		CGC CGG AGGCGCGGCC	
		GC ____	
GAM52	IRS1	GCGTCTGGC-TCTGCGCGCCGGC 512 TG C CC C	
		CG CTG CTTT CGCGCCGGC	
		GC GAC GAGA GCGCGGCCG	
		__ A C_ C	
GAM52	JUND	CGCCTCCCCCG-CCGCGCCGGC 490 TGCG G TT	
		CCT CCCT CCGCGCCGGC	
		GGA GGGG GGCGCGGCCG	
		____ _ GC	
GAM52	KCNS3	GCGCCTGCC--GCCGCGGCGGC 511 TG CTTT C	
		CGCCTGCC CCGCG CGG	
		GCGGACGG GGCGC GCC	
		__ C__ C	
GAM52	LAMC1	GCCTGCACT--CCGCGCCG 493 CTGCCCTT	
		TGCGC TCCGCGCCG	
		ACGTG AGGCGCGGC	

GAM52	LTF	TGCGCCTGCCCT---GCGCC 519 TTCC G	
		TGCGCCTGCCCT GCGCC	
		ACGCGGACGGGA CGCGG	
		_____ I	
GAM52	MAFK	CGCGCTGTCCT---CGCGCCGGC 485 TG C C TTC	
		CGC TG CCT CGCGCCGG	
		GCG AC GGA GCGCGGCC	
		__ _ A ____	
GAM52	MAN2A2	GCGCCCGGCCT--CCGCGCCG 504 TG C TT G	
		CGCCTG CC TCCGCGCCG	
		GCGGGC GG AGGCGCGGC	
		__ C __ G	
GAM52	MAPK12	GCGCCTCGGGCCGGCTCCGCGCCG 497 TG ____ CT GCI	
		CGCCT GCC TTCCGCGCCG	
		GCGGA CGG GAGGCGCGGC	
		__ GCC CC G	
GAM52	MTCP1	CGCCTGCCCCAAACCGCGCGGGC 486 TGCG TT_ C I	
		CCTGCCCT CCGCGC GGC	

		GGACGGGG GGC	CGC		
		_____ TTT C C			
GAM52	MVK	CGCC-GCCCCT-CCGCGCCG	489	TGCGC	T
		CTGCCCTT CCGCGCCG			
		GGCGGGGA GGC			
		_____ -			
GAM52	NCKAP1	GCGCC--CCAATCCCGCGCCGGC	510	TGCGCCT	__
		GCCCT TTCCGCGCCGGC			
		CGGGG AGGGCGCGCCG			
		G_____ TT			
GAM52	NFRKB	GCGCCCGGCTCCCCTTCCGCGCC	498	TG	__ GGCI
		CGCCTG CCCTTCCGCGCC			
		GCGGGC GGGGAAGGCGCGG			
		__ CGA G			
GAM52	NFRKB	CGGCTCCCCTT-CCGCGCCCGGC	488	TGCGC G	-
		CT CCCTTCCGCGCC GGC			
		GA GGGGAAGGCGCGG CCG			
		C_____ G			
GAM52	OIP2	TGCGCCTGCGCCGCTCCTCTCCTGC	515	_ T GCG G II	
		TGCGCCTGC CC TTCC CC GC			
		ACGCGGACG GG GAGG GG CG			
		C C AGA A II			
GAM52	PAX8	GCGCCTGCCGCTGCCCTGGCCGGC	500	TG _ T GC I	
		CGCCTGCC CT TCC GCCGGC			
		GCGGACGG GA GGG CGGCCG			
		__ C C AC G			
GAM52	PCM1	GCCCGCACGACCCGCGCCGGC	496	T CT TTTCC	
		GCGC GCCC GCGCCGGC			
		CGTG TGGG CGCGGCCG			
		G C_ _____			
GAM52	PFKFB2	GCGCCTGCCCTGTAACGCGACCG	501	TG TTC_ _ CI	
		CGCCTGCCCT CGCG CCGG			
		GCGGACGGGA GCGC GGCT			
		__ CATT T II			
GAM52	POU3F1	GCGCCCGCGCCCTGCAGCGCGCCGGC	499	TG _ TC_ II	
		CGCCTGC CCTT CGCGCCGGC			
		GCGGGCG GGGG GCGCGGCCG			
		__ C CGTC CI			
GAM52	PPP2R2B	TGCGCCTGCC---TCCGCTGCC	518	CTT _ GG	
		TGCGCCTGCC TCCGC GCC			

ACGCGGACGG AGGCG CGG
 _____ A II
 GAM52 PXN GCCTGCCCTTCCCTGCCCC 492 TGCGCC _ G GG
 TGCCCTTTCC GC CC
 ||||| ||
 ACGGGAAGGG CG GG
 _____ A G GG
 GAM52 S100A10 TGAGCCTGCCC-TTCCTCTCGGG 520 C T GCGC C
 TG GCCTGCCCTT CC CGG
 || ||||| || ||
 AC CGGACGGGAA GG GCC
 T _ AGA_ C
 GAM52 SAS TGCGCCTGCACCGTCCCTCCCTGC 514 _ T GCG G II
 TGCGCCTGC CC TTCC CC GC
 ||||| || || || ||
 ACGCGGACG GG AGGG GG CG
 T C AGG A II
 GAM52 SDC1 GCGCCTGCCC--AGCGCGCCG 507 TG TTTC G
 CGCCTGCCC CGCGCCG
 ||||| |||||
 GCGGACGGG GCGCGGC
 _ TC_ G
 GAM52 SDC2 TGCGCCTGC---TCCCGCCGCCCGC 517 CCT _ G
 TGCGCCTGC TTCCGC GCC GC
 ||||| ||||| || ||
 ACGCGGACG AGGGCG CGG CG
 _ G G
 GAM52 SORCS2 GCGCCTG-CCGGTCCTCGCCG 506 TG CTT G G
 CGCCTGCC TCC CGCCG
 ||||| || |||||
 GCGGACGG AGG GCGGC
 _ CC_ A G
 GAM52 TESK1 CCCGCCCCCGCCGCGCCGGC 484 TGCGCCTG TT
 CCCT CCGCGCCGG
 ||| |||||
 GGGG GGCGCGGCC
 _____ GC
 GAM52 TIF1 CCTGCCCTTGCCGCCGCCGG 483 TGCGCCTG T _
 CCCTT CCGC GCCG
 |||| |||| ||||
 GGGAA GGCG CGGCC
 _____ C G
 GAM52 WDR1 GCGCCTGCCC--TGCGCGC 502 TG TTC CG
 CGCCTGCCCT CGCGC
 ||||| ||||
 GCGGACGGGA GCGCG
 _ C_ AI
 GAM52 WIG1 GCGCCGGCAGTCTCCGCGCCG 505 TG T CC GC
 CGCC GC TTTCCGCGCCG
 ||| || |||||

		GCGG CG AGAGGCGCGGC	
		___ C TC GI	
GAM53 AK3		AAGAC--AACCCCTCCCCT 525 GAAA TG G	
		GAC AGCCCCTCCCCT	
		CTG TTGGGGAGGGGA	
		___ G	
GAM53 CHIC2		CTGAGCCTCCGAGCTCCCCTGCC 528 GAAAGA CCC I	
		CTGAGC TCCCCTGCC	
		GGCTCG AGGGGACGG	
		GA___ G	
GAM53 MAB21L1		GAAAGACTGTCCTCCCCCTCTGC 529 AG _ _ CI	
		GAAAGACTG CC CCTCCC CTGC	
		CTTTCTGAC GG GGGGGG GACG	
		A_ A A II	
GAM53 MHC2TA		AGTCTGGCAGCCCCTCCTCGTGCC 526 GAAAGA ___ CC_ I	
		CTG AGCCCCTCC TGCC	
		GAC TCGGGGAGG ACGG	
		___ CG AGC G	
GAM53 RAB2L		GACCGAGTCCCCTCCCCGGC 530 GAAAGACT _ T	
		GAG CCCCTCCCC GC	
		CTC GGGGAGGGG CG	
		___ A C	
GAM53 RAD51L3		AGAC---GCCCCTCCCCTACC 527 GAAAGACTGA	
		GCCCCTCCCCTG	
		CGGGGAGGGGAT	
		G___	
GAM53 SOX15		AAAGACTGA-CTCCGCCCCTG 524 GA G C T C	
		AAGACTGA C CC CCCCTG	
		TTCTGACT G GG GGGGAC	
		___ _ A C A	
GAM54 APPBP2		TAAACTCAGGTTTCTAAATCA 538 TAAA___ A TGACGG	
		AGGTTTCTAAA CA	
		TCCAAAGATTT GT	
		ATTTGAG A IGGC	
GAM54 BAZ1A		TAAAAGGTT--TAAAACATTAAGG 544 TC GAC	
		TAAAAGGTT TAAAACAT GG	
		ATTTTCAA ATTTTGTA CC	
		___ ATT	
GAM54 DLEU2		TAAAAGGTTT--AAACAT 541 CTA GA	
		TAAAAGGTTT AAACAT	

ATTTTCCAAA TTTGTA
 — II
 GAM54 EGLN3 TAAAGGGATTTTTAAAACATGA 539 TA _ C CGG
 AAAGG TTT TAAAACATGA
 ||||| ||| |||||
 TTTCC AAA ATTTTGTACT
 A_ CT A III
 GAM54 GNB1 AAAATCTTGCTACAAACATGAC 534 TAAAAG_ TCTA GG
 GTT AAACATGAC
 ||| |||||
 CGA TTTGTACTG
 TTTAGAA TG_ AI
 GAM54 HLA-DOB TAAAAGGTTTTTAAAACAGTGA 540 CT_ _ CGGI
 TAAAAGGTTT AAAACA TGA
 ||||| ||||| |||
 ATTTTCCAAA TTTTGT ACT
 AAT C IIIG
 GAM54 MBL2 AAAAATTTCTTAAACATGAC 536 TAAA A
 AGGTTTCT AAACATGACG
 ||||| |||||
 TTAAAGA TTTGTACTGT
 — A
 GAM54 PPARBP TAAATGAGTTTAAAACATG 543 _ TC ACG
 TAAAA GGTT TAAAACATG
 ||||| ||| |||||
 ATTTT TCAA ATTTTGTAC
 AC _ III
 GAM54 ZNF22 AAATGTATCCTCAAAACATGATGG 535 TAAAAG TC C I
 GTT TAAAACATGA GG
 ||| ||||| |||
 TAG GTTTTGTACT CC
 TACA_ GA A A
 GAM54 ZNF22 AAAATGTATCTACAAACATGATGG 533 TAAAAG T _ C II
 GT TCTA AAACATGA GG
 || ||||| |||
 CA AGAT TTTGTACT CC
 TTTA_ T GT A AI
 GAM54 ZNF239 TAACTGGTTCCTAAAACAT 542 TAAAA GACG
 GGTTCCTAAAACAT
 |||||
 CCAAGGATTTTGTA
 ATTGA IIIG
 GAM54 ZNF6 AGGACTCATGAAACATGAC 537 TAAAAGGTT TA_ G
 TC AAACATGAC
 || |||||
 AG TTTGTACTG
 G_ TAC A
 GAM55 ANGPT1 ATACACATG-TTAAATTGC 549 TACCATAC ATG
 ACATG AAGTTG
 ||||| |||||

		TGTAC TTTAAC		
		_____ AA_		
GAM55	GALC	CATACAACATGATGAACATGCT	550	TACCAT _ GT
		ACA CATGATGAA TGCT		
		TGT GTACTACTT ACGA		
		_____ T GT		
GAM55	GALNS	CCATACACATACTGATCTTG	552	TACC A AG C
		ATACACATG TGA TTG		
		TATGTGTAT ACT AAC		
		_____ G AG A		
GAM55	GJB3	TACTATAC---TG-TGAAGTTGC	555	C ACA A
		TAC ATAC TG TGAAGTTGC		
		ATG TATG AC ACTTCAACG		
		A _____		
GAM55	HNRPA1	CCATACACATGA-GTATTTG	553	TACC TGAAG C
		ATACACATGA TTG		
		TATGTGTACT AAC		
		_____ CATA_ A		
GAM55	ITGA6	CCA-ACACATGATGTAAGT	551	TACCAT _
		ACACATGATG AAGTTG		
		TGTGTACTAC TTCAGT		
		T_____ A		
GAM55	LPIN2	TACCATACATATGCAAAGAAGT	554	C AT__ TGCT
		TACCATACA ATG GAAGT		
		ATGGTATGT TAC CTTCA		
		A GTTT IIIT		
GAM55	PRKG2	ACCATGCTTAT-ATGAAGTTGCT	548	TA ACACATG
		CCAT ATGAAGTTGCT		
		GGTA TACTTCAACGA		
		_____ CGAATA_		
GAM55	RET	ACAAT-CA-ATGATGAAGTT	547	TACCATA C
		CA ATGATGAAGTTG		
		GT TACTACTTCAAT		
		GTTA_____		
GAM56	CA3	GATCGTCGTAGTTGTGCTTGGC	558	ATG GGI
		GTCGTAGTTGTGT		
		CAGCATCAACACG		
		G_____ AAC		
GAM56	CA3	GATCGTCGTAGTTGTGCTTGGC	558	TCAGATG _
		GTCGTAGTTGTGT GGCT		

		CAGCATCAACACG CCGG	
		G_____ AA	
GAM56	LGI1	TCAGATGGT-G-A-TTGTCTTGCT 560	C A G GI
		TCAGATGGT GT GTT TGT	
		AGTCTACCA TA CAG ACG	
		C A A AI	
GAM56	LGI1	TCAGATGGT-G-A-TTGTCTTGCT 560	CGTA GTG
		TCAGATGGT GTTGT GCT	
		AGTCTACCA TAACA CGA	
		C____ GAA	
GAM56	SLC6A1	GATGGTCGTCG-GGGGTGG 559	AGTT_ TGI
		GATGGTCGT GTG	
		CTACCAGCA CAC	
		GCCCC CII	
GAM56	SLC6A1	GATGGTCGTCG-GGGGTGG 559	TCAGAT AGTT_ T
		GGTCGT GTG GG	
		CCAGCA CAC CC	
		_____ GCCCC _	
GAM57	DCC	GTTTATGGGTAATTGGTATGCTGC 566	ATC_____ IIIG
		GTTTATG GTATGCTG	
		CAAATAC CATACGAC	
		CCATTAAC GIII	
GAM57	DCC	GTTTATGGGTAATTGGTATGCTGC 566	TGACGTTTATGATC TI
		GTATGCTGC	
		CATACGACG	
		TACCCATTAAC____ TT	
GAM57	FHL1	TTTTTTTTCATATGCTGCT 572	TTTATGA II
		TCGTATGCTGC	
		AGTATACGACG	
		AAAAAAA AI	
GAM57	FRAT2	CGTTTATGACTGT-TTCTG 564	C ATGCTI
		CGTTTATGAT GT	
		GCAAATACTG CA	
		A AAGACI	
GAM57	FUS1	TGACTGGTATATGCCCTGCTATGCTGCT567	GAC T AT_ _ I
		GT TATG C GT ATGCTGC	
		CA ATAC G CG TACGACG	
		C_ T GG A A I	
GAM57	FUS1	TGACTGGTATATGCCCTGCTATGCTGCT567	_ T AT_ _ III
		TGAC GT TATG C GT ATGCTGCT	

		ACTG CA ATAC G CG TACGACGA	
		AC T GG A A III	
GAM57	GABRA5	TTTATGATC-TCTGTTTCT 571	GTA CTGCI
		TTTATGATC TG	
		II	
		AAATACTAG AC	
		AG_ AAAGA	
GAM57	IL21R	TGACGTTTATTGAGGGTCTGCT 568	GATCGTATG
		TGACGTTTAT CTGCT	
		III	
		ACTGCAAATA GACGA	
		ACTCCCA__	
GAM57	IL21R	TGACGTTTATTGAGGGTCTGCT 568 G	_ TC A I
		ACGTTTAT GA GT TGC	
		II II III	
		TGCAAATA CT CA ACG	
		_ A CC G I	
GAM57	MLLT4	GACGTTTATTAAC-TCTGC 565	GA__ GTATGI
		GACGTTTAT TC	
		II	
		CTGCAAATA AG	
		ATTG ACGIII	
GAM57	MLLT4	GACGTTTATTAAC-TCTGC 565 TG	GATCGTATG
		ACGTTTAT CTG	
		III	
		TGCAAATA GAC	
		_ ATTGA__	
GAM57	PTHLH	CGTTTATGA-CATGATGCTG 563	T _ II
		CGTTTATGA CGT ATGCT	
		III	
		GCAAATACT GTA TACGA	
		_ C CI	
GAM57	PTHLH	CGTTTATGA-CATGATGCTG 563 TGACGT	T _ C
		TTATGA CGT ATGCTG	
		III	
		AATACT GTA TACGAC	
		_____ _ C A	
GAM57	SLC4A10	TTTATGATCCAAGTATACT 570	_____ III
		TTTATGATC GTATGC	
		AAATACTAG CATATG	
		GTT AII	
GAM57	VENTX2	TGACGTTTAAAAGCACATGC 569	T T TGC
		TGACGTTTA GA CGTATGC	
		II	
		ACTGCAAAT TT GTGTACG	
		T C III	
GAM57	VENTX2	TGACGTTTAAAAGCACATGC 569	T T I
		GACGTTTA GA CGTATG	
		II	

CTGCAAAT TT GTGTAC
T C I

GAM58 BAK1 AGGTCTCAGTGGAGGACGGGATCA 576 TGAG AT____ A ACI
GTCTCAG GCG GATCA
||||| ||| |||||
CAGAGTC TGC CTAGT
____ ACCTCC C CGI

GAM58 CRY2 AGGTCTCAGCTGAAAG-TCA 580 _ A C ATCI
GGTCTCAG TG GAG
||||||| || |||
CCAGAGTC AC TTC
T G T AGII

GAM58 CRY2 AGGTCTCAGCTGAAAG-TCA 580 TGAG A C A A
GTCTCAG TG GAG TCA
||||||| || ||| |||
CAGAGTC AC TTC AGT
____ G T _ G

GAM58 EDG8 GAGGTCTCAGCT-C-ACATCA 584 AT_ AGATI
GAGGTCTCAG GCG
||||||| |||
CTCCAGAGTC TGT
GAG AGTII

GAM58 EDG8 GAGGTCTCAGCT-C-ACATCA 584 TG ATG AG A
AGGTCTCAG CG ATCA
||||||| || |||||
TCCAGAGTC GT TAGT
____ GA_ G_ G

GAM58 F13A1 TGAGGTCTCAACATGGGTGAT 587 _ CGA CAAC
TGAGGTCTCAG ATG GAT
||||||| ||| |||
ACTCCAGAGTT TAC CTA
G CCA IIIC

GAM58 F13A1 TGAGGTCTCAACATGGGTGAT 587 G _ CGAGAI
AGGTCTCAG ATG
||||||| |||
TCCAGAGTT TAC
_ G CCACTI

GAM58 FLRT2 AGGTCTCAGAGGATGTGTGAT 577 TGCGAGAI|||
AGGTCTCAGA
|||||||
TCCAGAGTCT
CCTACACACT

GAM58 FLRT2 AGGTCTCAGAGGATGTGTGAT 577 T_____ TCTCA_ GAGATCAAC
GAGG GATGC
||| |||||
CTCC CTACG
CAGAGT TACACA IIICAACTA

GAM58 HIVEP3 AGTTCTGGGTTG-GAGATCAAC 582 GG_ CAGA C I
TCT TG GAGATCAA
||| || |||||

		AGA AC CTCTAGTT		
		TCA CCCA _ I		
GAM58	IL1RAPL2	AGGTCTCAGATGCGTAGTTC	579	_ ATII
		AGGTCTCAGATGCG AG		
		TCCAGAGTCTACGC TC		
		A AAGI		
GAM58	IL1RAPL2	AGGTCTCAGATGCGTAGTTC	579 TGAG	_ A AA
		GTCTCAGATGCG AG TC		
		CAGAGTCTACGC TC AG		
		_____ A A GT		
GAM58	ISLR	GTCTCAGATGAG-GA-CAA	585	CGA CAI
		GTCTCAGATG GAT		
		CAGAGTCTAC CTG		
		TC_ TTI		
GAM58	MF12	GAGG-CTGAGATGCGAGGATCA	583 T C	_ I
		AGG CT AGATGCGAG ATC		
		TCC GA TCTACGCTC TAG		
		_ C C I		
GAM58	MF12	GAGG-CTGAGATGCGAGGATCA	583 TG T C	_ AC
		AGG CT AGATGCGAG ATCA		
		TCC GA TCTACGCTC TAGT		
		_____ C C CI		
GAM58	NAP1L3	AGGTCTCAGTT--GA-ATCAA	581 _	A CGA
		GGTCTCAG TG GATCA		
		CCAGAGTC AC TTAGT		
		T A _____		
GAM58	NAP1L3	AGGTCTCAGTT--GA-ATCAA	581 TGAG	A CGA
		GTCTCAG TG GATCA		
		CAGAGTC AC TTAGT		
		_____ A _____		
GAM58	RBP4	AGTTCTCAGATGAACTAGAT	578 G	C GAI
		AG TCTCAGATG GA		
		TC AGAGTCTAC TT		
		A T GATCT		
GAM58	RBP4	AGTTCTCAGATGAACTAGAT	578 TGAGG	CG____ CAAC
		TCTCAGATG AGAT		
		AGAGTCTAC TCTA		
		A_____ TTTGA AG		
GAM58	TFEB	TCTCAGATGAG-GATCCAC	586	CGA AAI
		TCTCAGATG GATC		

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AGAGTCTAC CTAG
TC_ GTG
GAM58 TFEB TCTCAGATGAG-GATCCAC 586 __ TC G GCGAGATCA
TGAGG TCA AT
||||| ||| ||
ACTCC GGT TG
CT TA G ACA|||CAA
GAM58 TPMT AGGTCTCAGAGAAGCAAGAATCA 575 GGT T__ TCI
CTCAGA GCGAGA
||||| |||||
GAGTCT CGTTCT
__ CTT TAG
GAM58 TPMT AGGTCTCAGAGAAGCAAGAATCA 575 TGAG T__ _ ACI
GTCTCAGA GCGAGA TCA
||||| ||||| |||
CAGAGTCT CGTTCT AGT
__ CTT T GAI
GAM59 ATP1A2 TCACAGGTTCAAGCAATTCTCC 601 A TC AG
TCA AGGTTT GCAATTCTCC
||| ||||| ||||| |||
AGT TCCAAG CGTTAAGAGG
G TT II
GAM59 ATP1A2 TCACAGGTTCAAGCAATTCTCC 601 CAA TC I
AGGTTT GCAATTCTC
||||| ||||| |||
TCCAAG CGTTAAGAG
GTG TT I
GAM59 AVPR2 CACAGGCTCTGGCCAATTCTCCA 596 AA C _ I
AGGTTTT GC AATTCTCC
||||| || ||||| |||
TCCGAGA CG TTAAGAGG
G_ C G I
GAM59 AVPR2 CACAGGCTCTGGCCAATTCTCCA 596 TCAA C _ GI
AGGTTTT GC AATTCTCCA
||||| || ||||| |||
TCCGAGA CG TTAAGAGGT
TG__ C G GI
GAM59 C5R1 TCCAAGGTTGAGCAATTCTCC 603 A TC AG
TC AAGGTTT GCAATTCTCC
|| ||||| ||||| |||
AG TTCCAAG CGTTAAGAGG
G CT II
GAM59 C5R1 TCCAAGGTTGAGCAATTCTCC 603 CA TC I
AAGGTTT GCAATTCTC
||||| ||||| |||
TTCCAAG CGTTAAGAG
GG CT I
GAM59 EGLN3 AGGTTGTGATAATTCTCCAG 593 TTCGC I
GGTT AATTCTCCA
||| ||||| |||

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		CCAA TTAAGAGGT		
		CACTA I		
GAM59	EGLN3	AGGTTGTGATAATTCTCCAG	593	TCAAAGGTTTTTCGC
		AATTCTCCA		
		TTAAGAGGT		
		ACACTA_____		
GAM59	FBXW1B	TCAAAGGTTGTCTGCATATTC	600	T _ _ TCCAG
		TCAAAGGTT TC GCA ATTC		
		AGTTTCCAA AG CGT TAAG		
		C A A IGA		
GAM59	FBXW1B	TCAAAGGTTGTCTGCATATTC	600	T _ ATT
		TCAAAGGTT TC GCA		
		AGTTTCCAA AG CGT		
		C A ATAAGI		
GAM59	FBXW7	CAAAGGTTTTTCAC-ATTCTGCAG	599 _	A C I
		AAAGGTTTTTCGCA TTCT CA		
		TTTCCAAAAGTGT AAGA GT		
		G _ C I		
GAM59	FBXW7	CAAAGGTTTTTCAC-ATTCTGCAG	599 TC	A C
		AAAGGTTTTTCGCA TTCT CAG		
		TTTCCAAAAGTGT AAGA GTC		
		_ _ C		
GAM59	GOCAP1	CATATGTATTTC-CAATTCTCC	595 AAAG _ G	I
		GT TTTC CAATTCTC		
		CA AAAG GTTAAGAG		
		TATA T _ I		
GAM59	GOCAP1	CATATGTATTTC-CAATTCTCC	595 TCAAAG _ G	AG
		GT TTTC CAATTCTCC		
		CA AAAG GTTAAGAGG		
		TATA_ T _ AI		
GAM59	IGFBP3	AAAGGTTTTTC-CTATTCTC	591	GCA I
		AAAGGTTTTTC ATTCT		
		TTTCCAAAAG TAAGA		
		GA_ G		
GAM59	IGFBP3	AAAGGTTTTTC-CTATTCTC	591 TCAA	GCA C
		AGGTTTTTC ATTCTC		
		TCCAAAAG TAAGAG		
		_ GA_ C		
GAM59	MEIS2	CAAAGAGACTTCTCCCAATTCTCCA	594 AA _ G	I
		AGG TTTTC CAATTCTCC		

		TCT AAGAG GTTAAGAGG		
		C_ G G I		
GAM59	MEIS2	CAAAGAGACTTCTCCCAATTCTCCA	594	TCAA _ G II
		AGG TTTTC CAATTCTCCAG		
		TCT AAGAG GTTAAGAGGTT		
		TTTC G G II		
GAM59	MYF6	CAACAGATTTTCGCAATTTTC	598	CAA T CI
		AGGTTT CGCAATT		
		TCTAAA GCGTTAA		
		TG_ _ AA		
GAM59	MYF6	CAACAGATTTTCGCAATTTTC	598	TCAA T C CA
		AGGTTT CGCAATT TC		
		TCTAAA GCGTTAA AG		
		TTG_ _ A CI		
GAM59	NKX3A	AAGATTTCCACGCAATTCTCCA	592	AGG TT I
		TT CGCAATTCTCC		
		AG GCGTTAAGAGG		
		TAA GT I		
GAM59	NKX3A	AAGATTTCCACGCAATTCTCCA	592	TCAAAGG TT
		TT CGCAATTCTCCAG		
		AG GCGTTAAGAGGTT		
		TAA___ GT		
GAM59	OPA3	TCATGGGTTCAAGCAATTCTCC	602	AA TC AG
		TCA GGTTT GCAATTCTCC		
		AGT CCAAG CGTTAAGAGG		
		AC TT II		
GAM59	OPA3	TCATGGGTTCAAGCAATTCTCC	602	CAAA TC I
		GGTTT GCAATTCTC		
		CCAAG CGTTAAGAG		
		GTAC TT I		
GAM59	SVIL	AAAGGTTGATTTCGCATAGATTCTCCAG	590	AAGGTT _ I
		TTCGCA ATTCTCCA		
		AAGCGT TAAGAGGT		
		ACT___ ATC I		
GAM59	SVIL	AAAGGTTGATTTCGCATAGATTCTCCAG	590	TCAA _ _ III
		AGGTT TTCGCA ATTCTCCAG		
		TCCAA AAGCGT TAAGAGGTC		
		___ CT ATC TCI		
GAM59	ZNF141	CAAAGGTTTGC-CACATTCT	597	_ ATTCII
		CAAAGGTTT TCGCA		

		GTTTCCAAA GGTGT			
		C AAGAI			
GAM59	ZNF141	CAAAGGTTTGC-CACATTCT	597 TC	_ A CCA	
		AAAGGTTT TCGCA TTCT			
		TTTCCAAA GGTGT AAGA			
		_ C _ AII			
GAM60	ABL1	TGACAC--CTGACCCCTGA	612 GT	GAA	
		TGACAC CTGACCCCTGA			
		ACTGTG GACTGGGGACT			
		_			
GAM60	CERD4	GACCAGCCTGTCC-CTGAGAAG	611 TGA C	AC	
		CA GTCTG CCCTGAGAAGG			
		GT CGGAC GGGACTCTTCT			
		TG_ _ A_			
GAM60	EPO	GACAGTTCCTCTGGCCCCTGAGA	609 TGACACG_	A AGGI	
		TCTG CCCCTGAGA			
		AGAC GGGGACTCT			
		TGTCAAGG C AIII			
GAM60	GAS7	TGACCGGTAAGACCCCTGAAAA	614 A TCT_	GG	
		TGAC CG GACCCCTGAGAA			
		ACTG GC CTGGGGACTTTT			
		_ CATT			
GAM60	GNLY	TGACACTTTATTCCCCTGAGAGGG	616 GTCTGA	A I	
		TGACAC CCCCTGAGA GG			
		ACTGTG GGGGACTCT CC			
		AAATAA C I			
GAM60	HPCAL1	CAGGTCTGACCCCAGCTAAGG	608 TGACAC	TGAG	
		GTCTGACCCC AAGG			
		CAGACTGGGG TTCC			
		_ TCGA			
GAM60	LTBP2	TGCCACA-CTGACCCCTGA	613 TGA T	GAA	
		CACG CTGACCCCTGA			
		GTGT GACTGGGGACT			
		ACG _			
GAM60	MAPK14	GACACTTCTCCACCCCTGAG	610 TG G G_	AAG	
		ACAC TCT ACCCCTGAG			
		TGTG AGA TGGGGACTC			
		_ A GG CII			
GAM60	PCDHB16	TGACAC--CTAACC-CTGAGAAG	615 GT	C	
		TGACAC CTGACCC TGAGAAG			

ACTGTG GATTGGG ACTCTTC

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GAM60 RCP      CAAGTCCTTGACCCCTGGAGCAGG 607 TGACAC  _  _ A I
                GTCT GACCCCTG AG AGG
                ||| ||||| |||
                CAGG CTGGGGAC TC TCC
                _ _ _ AA  C G A
GAM60 TCF1     ACAGGCCTGTGTCCTGAGAAG 606 TGACAC  ACC  G
                GTCTG CCTGAGAAG
                ||| |||||
                CGGAC GGA CTCTTC
                TC _ _ ACA  A
GAM61 BARX2    TTCCCTCAAAAGGGTTTTA 625 AA  _  ATGTA
                TTCC CAAA GGGTTTTA
                ||| ||| |||||
                AAGG GTTT CCCAAAAT
                GA T  ||GA
GAM61 C21orf2  TTCCAACAAAGCGCTTTACTG 627 G  A TAG
                TTCCAACAAAG GTTTTA TG
                ||||| ||||| ||
                AAGGTTGTTTC CGAAAT AC
                G  G ||
GAM61 COL4A4   TTCCAACAAATCTTTTAAATTTAG 629 GGG  TG_ I
                TTCCAACAAA TTTTAA TAG
                ||||| ||||| ||
                AAGGTTGTTT AAAATT ATC
                AG_ TAA I
GAM61 DMD      TCCACCAAGAAGGGTTTTTTTGTA 623 TT_ CA  AA I
                CCAA AAGGGTTTT TGTAG
                ||| ||||| ||||
                GGTT TTCCCAAAA ACATT
                GGT C_  AA I
GAM61 DNNT     TCCTACACGAAGGGTTTTTGATGT 622 TT A  _  A AGI
                CC ACA AAGGGTTTT ATGT
                || ||| ||||| ||||
                GG TGT TTCCCAAAA TACA
                _ A GC  C GII
GAM61 EGLN1    TTCCAACAATTTCTTTTAA 626 AGGG  TGTA
                TTCCAACAA TTTTAA
                ||||| |||||
                AAGGTTGTT AAAATT
                AAAG ||IG
GAM61 HTR2A    CCAAGCAGAATGGTTTTTAAT 621 TTCCAACAAAG  TA
                GGTTTTAATG
                |||||
                CCAAATTAT
                TTCGTCTTA_  TI
GAM61 SH3BP5   TTCTAGAAAATGGTTTTTAATG 628 TTCCAACAAAG  TAG
                GGTTTTAATG
                |||||
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		CCAAAATTAC			
		AAGATCTTTTA III			
GAM61	SPTBN4	TTCAAAGCCAAAGGG-TTTATTATAG 624 TTCCAA__ TAA II			
		CAAAGGGTTT TGTAG			
		GTTTCCCAA ATATC			
		AAGTTTCG TA_ II			
GAM61	TBXAS1	CAACAAAGGGTTTCAGTGTA 620 TTCCAA A			
		CAAAGGGTTTTA TGTA			
		GTTTCCCAAAGT ACAT			
		_____ C			
GAM61	ZNF189	AACAAAACAGGTTTTAATG 619 TTCCAACAAA TA			
		GGGTTTTAATG			
		TCCAAAATTAC			
		TTTG_____ CA			
GAM62	ADAM28	TAAACCAACCTCAAAT-CTTA 649 GT T CTTACA			
		TAAA CAACCTCAA TC			
		ATTT GTTGGAGTT AG			
		TG T AAT			
GAM62	ADAM28	TAAACCAACCTCAAAT-CTTA 649 _ GT T CTTI			
		AAA CAACCTCAA TC			
		TTT GTTGGAGTT AG			
		A TG T A			
GAM62	BACH2	AAAGTCAACCATCTATTCC 633 _ A II			
		AAAGTCAACC TC ATTC			
		TTTCAGTTGG AG TAAG			
		T A GI			
GAM62	BACH2	AAAGTCAACCATCTATTCC 633 TA _ A TAC			
		AAGTCAACC TC ATTCCT			
		TTTCAGTTGG AG TAAGGG			
		_____ T A			
GAM62	BNC	TAAAGTCAA-ATCAAATACTT 646 CC TTC AC			
		TAAAGTCAA TCAA CTT			
		ATTCAGTT AGTT GAA			
		T_ TAT II			
GAM62	BNC	TAAAGTCAA-ATCAAATACTT 646 _ CC TTCCTI			
		AAAGTCAA TCAA			
		TTTCAGTT AGTT			
		A T_ TATGAI			
GAM62	C18orf1	TAAAGTTTAAGCCTCAATTC 643 CAA__ CTTAC			
		TAAAGT CCTCAATTC			

		ATTTCA GGAGTTAAG			
		AATTC IIIAC			
GAM62	C18orf1	TAAAGTTTAAGCCTCAATTC	643	CAA__	III
		TAAAGT CCTCAATT			
		ATTTCA GGAGTTAA			
		AATTC GII			
GAM62	CDH1	AAAGTGAGACAAAATTCCTTA	636	TAA__ T	CCTC CA
		AG CAA AATTCCTTA			
		TC GTT TTAAGGAAT			
		TTCAC T ____ TI			
GAM62	CHC1L	AATGTGAACCTCAA-TAATTACA	638	AA_ C	TCC I
		GT AACCTCAAT TTAC			
		CA TTGGAGTTA AATG			
		TTA C TT_ I			
GAM62	CHC1L	AATGTGAACCTCAA-TAATTACA	638	TAAA C	TCC
		GT AACCTCAAT TTACA			
		CA TTGGAGTTA AATGT			
		TA__ C TT_			
GAM62	CRACC	AAAGTCAACGTTCTTCATTC	632		CTCAATTIII
		AAAGTCAAC			
		TTTCAGTTG			
		CAAGAAGTAA			
GAM62	CRACC	AAAGTCAACGTTCTTCATTC	632	TA ____ CA	CTTAC
		AAGTCAAC CT ATTC			
		TTTCAGTTG GA TAAG			
		____ CAA AG AIIIA			
GAM62	CYP26A1	TAAAGTCAACACAACACTCCTTA	644		CTCA_ CAI
		TAAAGTCAAC ATTCCTTA			
		ATTTTCAGTTG TGAGGAAT			
		TGTTG III			
GAM62	CYP26A1	TAAAGTCAACACAACACTCCTTA	644	A	CTCA_ I
		AAGTCAAC ATTCCTT			
		TTTCAGTTG TGAGGAA			
		_ TGTTG I			
GAM62	FGFR2	TATAGAGAACCTCAATCTCTT	648	AA TC	TC I
		AG AACCTCAAT CT			
		TC TTGGAGTTA GA			
		TA TC GA I			
GAM62	FGFR2	TATAGAGAACCTCAATCTCTT	648	TAA TC	TC ACA
		AG AACCTCAAT CTT			

		TC TTGGAGTTA GAA		
		ATA TC GA III		
GAM62	GRB14	TAAAGTCAATC-CAAGTCTTT 647	C T T CTTAC	
		TAAAGTCAA C CAA TC		
		I III II		
		ATTCAGTT G GTT AG		
		A _ C AAII		
GAM62	GRB14	TAAAGTCAATC-CAAGTCTTT 647 _	C T T CTI	
		AAAGTCAA C CAA TC		
		I III II		
		TTTCAGTT G GTT AG		
		A A _ C AAI		
GAM62	IPP	AACCTCCTATTAATTCCTTAC 639 _____	III G	
		AACCTC AATTCCTTA		
		TTGGAG TTAAGGAAT		
		GATAA GIII		
GAM62	IPP	AACCTCCTATTAATTCCTTAC 639 TAAAGTCAACCTC	A	
		AATTCCTTAC		
		TTAAGGAATG		
		ATAA_____ A		
GAM62	KCND2	AAGCTAAGCTTTATTCCTTACA 640	TC C CA I	
		AG AA CT ATTCCTTAC		
		TC TT GA TAAGGAATG		
		GA C AA I		
GAM62	KCND2	AAGCTAAGCTTTATTCCTTACA 640 TAAA TC C CA		
		G AA CT ATTCCTTACA		
		I		
		C TT GA TAAGGAATGT		
		____ GA C AA		
GAM62	MYBL1	TAAAGTCAAAAT-TATTCTTTAC 650	CCTCA C A	
		TAAAGTCAA ATTC TTAC		
		ATTCAGTT TAAG AATG		
		TTAA_ A I		
GAM62	NEBL	TAAAGTCAACATTTTTTCC 645	CTCAA TTAC	
		TAAAGTCAAC TTCC		
		ATTCAGTTG AAGG		
		TAAAA IIIA		
GAM62	NEBL	TAAAGTCAACATTTTTTCC 645	CTCAATTCII	
		TAAAGTCAAC		
		ATTCAGTTG		
		TAAAAAAGGI		
GAM62	PSEN1	AAAGTCA-CCTCAATTCTCTCAC 635	A _ I	
		AAGTCA CCTCAATTC CTTA		

		TTCAGT GGAGTTAAG GAGT			
		— A I			
GAM62	PSEN1	AAAGTCA-CCTCAATTCTCTCAC 635 TA A — A			
		AAGTCA CCTCAATTC CTTAC			
		TTCAGT GGAGTTAAG GAGTG			
		— — A G			
GAM62	SGCG	TCAACCTCAAATTCCCTTCA 651 — ACII			
		TCAACCTCAA TTCCTT			
		AGTTGGAGTT AAGGGA			
		T AGTI			
GAM62	SVIL	AAAATCACACTGCAATTCCTTA 634 A AC — I			
		AGTCA CT CAATTCCTT			
		TTAGT GA GTTAAGGAA			
		— GT C I			
GAM62	SVIL	AAAATCACACTGCAATTCCTTA 634 TA AC — CA			
		AAGTCA CT CAATTCCTTA			
		TTTAGT GA GTTAAGGAAT			
		— GT C AI			
GAM62	TAF1C	AGTCA-CATGCAATTCCTTTCA 641 ACCT ACI			
		GTCA CAATTCCTT			
		CAGT GTTAAGGAA			
		GTAC AGI			
GAM62	TAF1C	AGTCA-CATGCAATTCCTTTCA 641 TAAAGTCAACCT ACA			
		CAATTCCTT			
		GTTAAGGAA			
		GTGTAC — AGT			
GAM62	TMOD	AGTCAACCT-AAAACCTTA 642 C TT I			
		AGTCAACCT AA CCTT			
		TCAGTTGGA TT GGAA			
		— TT T			
GAM62	TMOD	AGTCAACCT-AAAACCTTA 642 TAAAGT C TT			
		CAACCT AA CCTTA			
		GTTGGA TT GGAAT			
		— — TT			
GAM62	ZNF200	AAAGTAAAC---AATTCCTTTCA 637 CAACCT AI			
		AAAGT CAATTCCTT			
		TTTCA GTTAAGGAA			
		TTT — AG			
GAM62	ZNF200	AAAGTAAAC---AATTCCTTTCA 637 TA CAACCT AC			
		AAGT CAATTCCTT			

		TTCA GTTAAGGAA		
		__ TTT__ AG		
GAM63	ADAT1	TGAGAACAA-GTCCAGGGCAG	670	_ GT C CAI
		GAGAACAAAG CA GGT		
		CTCTTGTTT GT CCG		
		A AG C TII		
GAM63	ATP2B2	AGCACACCCTCACTGGTCAGCTG	658	GA AGG _ I
		ACA TCAC GGTCAGCT		
		TGT AGTG CCAGTCGA		
		G_ GGG A I		
GAM63	CX3CR1	TGTGAACAAGGTCTGGACGG	668	TGA ACGIII
		GAACAAGGTC		
		CTTGTTCCAG		
		ACA ACCTGC		
GAM63	FY	GAGAACAAAGGTCTCTG-CAG	662	G ACG CI
		AGAACAAAGGTC GT		
		TCTTGTTCCAG CG		
		_ AGA TC		
GAM63	GLTSCR1	ACACAGGTCACGG--AGCTG	655	_ TC I
		ACA AGGTCACGG AGCT		
		TGT TCCAGTGCC TCGA		
		G _ C		
GAM63	H3F3B	TGAGAACAAAGTGCA--GTCAG	671	_ GTCA I
		GAGAACAAAG CGGTCA		
		CTCTTGTTT GTCAGT		
		A AC_ I		
GAM63	HUNK	TGAGGAAGACAGTCACGGTC	665	AACAA_ II
		TGAG GGTCACGGT		
		ACTC TCAGTGCCA		
		CTTCTG GI		
GAM63	IFITM2	TGGGATACA-GGTCACGGGCAG	666	_ GA A T I
		GA ACA GGTCACGG CA		
		CT TGT CCAGTGCC GT		
		CC A_ _ C I		
GAM63	IL1F8	GAGAACAAAGAT-A-GATCAGATG	663	CAC CI
		GAGAACAAAGGT GGTCAG		
		CTCTTGTTCTA CTAGTC		
		T_ TA		
GAM63	KIF3B	GAAGCAAGGTCACTGGTCA	660	_ _ III
		GAA CAAGGTCAC GGTC		

		CTT GTTCCAGTG CCAG		
		C A TII		
GAM63	KLK5	AACTAGAGAGACACGGTCAGC	654	AACAA__ T III
		GG CACGGTCAG		
		II IIIIIII		
		TC GTGCCAGTC		
		TTGATCTC T GII		
GAM63	LNK	GAGAACAAGTTTCCACTGCCAGCT	661	AG G__ G I
		AACAAG TCAC GTCAGC		
		IIIII III IIIII		
		TTGTTC GGTG CGGTCG		
		__ AAA A I		
GAM63	PNUTL1	TGAGAATAAATT-AGGGTCAGCTG	672	_ C GTCAC I
		GAGAA AAG GGTGTCAGCT		
		IIIII III IIIII		
		CTCTT TTT CCAGTCGA		
		A A AATC_ I		
GAM63	PODXL	AGAACAAGGGGTTCAAGGT	657	__ C III
		AGAACAAGG TCA GG		
		IIIIIII III II		
		TCTTGTTC AGT CC		
		CCA T AII		
GAM63	PSG11	AGAGCACGG-CT-GGTCAGCTG	659	_ A A CAC I
		GA CA GGT GGTGTCAGCT		
		II III IIIIIII		
		CT GT CCG CCAGTCGA		
		T C G A__ I		
GAM63	SCA1	TGAGAACAAAGTCTATGTGGCAGC	669	GA AC__ T I
		GAACAAGGTC GG CAG		
		IIIIIIII II III		
		CTTGTTTCAG CC GTC		
		__ ATACA _ I		
GAM63	SLC13A1	ACAAGGTCAGTAACAGCTG	656	CGGT II
		ACAAGGTCA CAGCT		
		IIIIIIII IIIII		
		TGTTCCAGT GTCGA		
		CATT CI		
GAM63	SORCS1	TGAGAACAAGTGGCCAAGGTC	667	__ C III
		TGAGAACAA GGTCA GGT		
		IIIIIIII IIIII III		
		ACTCTTGTT CCGGT CCA		
		GA T GII		
GAM63	STX1A	GAGGACAGGG-CA-GGTCAGCTG	664	A A T C I
		GAG ACA GG CA GGTGAGC		
		III III II IIIII		
		CTC TGT CC GT CCAGTCG		
		C C _ _ A		
GAM64	ACVR1	TGCTCCAGGCTG---TAGTCC	687	TT G CAT
		GC CCAGGCTGT AGTCC		
		II IIIIIII IIIII		

		CG GGTCCGACA TCAGG		
		— A —		
GAM64	ADORA1	CGCGCGGCAGCTCATAGTCCT 676 TTGCGCCA T_		
		GGC G TCATAGTCCTT		
		CCG C AGTATCAGGAG		
		CG_____ T G		
GAM64	AICDA	TTG-GCCAGGCTGGTCTCAAACCTCCT 692 C — TAG TII		
		TTG GCCAGGCTG TCA TCCT		
		AAC CGGTCCGAC AGT AGGA		
		— CAG TTG		
GAM64	ANKH	TTG-GCCAGGCTGGTCTCAAACCTCCT 692 C — TAG TII		
		TTG GCCAGGCTG TCA TCCT		
		AAC CGGTCCGAC AGT AGGA		
		— CAG TTG		
GAM64	ASL	TTGC-CCAGGCTGTGTCAAACCTCCT 690 G — TAG TI		
		TTGC CCAGGCT GTCA TCCT		
		AACG GGTCCGA CAGT AGGA		
		— CA TTG		
GAM64	AVP	CGCCAGGCTGTGCATGGGCC 677 TTGCGC A_ CT		
		CAGGCTGTGCAT GTC		
		GTCCGACAGTA CGG		
		_____ CC CG		
GAM64	B4GALT2	GCCAGGCTGTGGTCAGTCCT 680 TTGCGCCA CA_		
		GGCTGT TAGTCCT		
		CCGACA GTCAGGA		
		_____ CCA		
GAM64	CACNA1C	GGCGGCTCGCGCACCCAGGC 685 ACACG GG GT		
		GC CGCG CACCCAGG		
		CG GCGC GTGGGTCC		
		_____ A_ —		
GAM64	CD28	TGCGCCAGG-TCCCATAGTACT 688 TT CTG C		
		GCGCCAGG TCATAGT CTT		
		CGCGGTCC GGTATCA GAG		
		— AG_ T		
GAM64	CD68	TTG-GCCAGGCTGGTCTCAAACCTCCT 692 C — TAG TII		
		TTG GCCAGGCTG TCA TCCT		
		AAC CGGTCCGAC AGT AGGA		
		— CAG TTG		
GAM64	CRY2	GGCTGCTTGGGCACCCAGGC 686 ACACGGCG GC T		
		GC GG CACCCAGG		

		CG CC GTGGGTCC		
		_____ AA C		
GAM64	CYP4F3	TTG-GCCAGGCTGGTCTCAAACCTCCT 692	C	___ TAG TII
		TTG GCCAGGCTG TCA TCCT		
		AAC CGGTCCGAC AGT AGGA		
		_____ CAG TTG		
GAM64	EPHA8	CGG-GGTGGGCTCACCCAGGC 679	ACAC C C GG	
		GG GG GC TCACCCAGG		
		CC CC CG AGTGGGTCC		
		_____ A _____		
GAM64	FBXL7	TTG-GCCAAG--GTCATAGTCATT 696	C CT CTT	
		TTG GCCAGG GTCATAGTC		
		AAC CGGTTC CAGTATCAG		
		_____ TAA		
GAM64	GPR4	GCCAGGCTGCCTCAGTCATT 682	TTGCGCCA A CT	
		GGCTGTC TAGTC		
		CCGACGG GTCAG		
		_____ A TA		
GAM64	HCN2	CACGGCGGCG-GGAC-CCCAG 675	AC C TCA G	
		ACGGCGGCG GG CCCAG		
		TGCCGCCGC CC GGGTC		
		_____ TG_ G		
GAM64	HEM1	TGCTCGAGTCAG-CATAGTCCT 689	TT GCC GCT T	
		GC AG G CATAGTCCTT		
		CG TC C GTATCAGGAG		
		_____ AGC AGT _____		
GAM64	IL17R	TTG-GCCAGGCTGGCTCAAACCTCCT 694	C ___ TAG TI	
		TTG GCCAGGCTG TCA TCCT		
		AAC CGGTCCGAC AGT AGGA		
		_____ CG TTG		
GAM64	KIF3B	TTG-GCCAGGCTGGTCTCGAAGTCCT 693	C _ AT_ TII	
		TTG GCCAGGCTG TC AGTCCT		
		AAC CGGTCCGAC AG TCAGGA		
		_____ C AGCT		
GAM64	KNSL1	TTG-GCCAGGCTGGTCTCAAACCTCCT 692	C ___ TAG TII	
		TTG GCCAGGCTG TCA TCCT		
		AAC CGGTCCGAC AGT AGGA		
		_____ CAG TTG		
GAM64	LAMP2	TTG-GCCAGGCTGGTCTCAAACCTCCT 692	C ___ TAG TII	
		TTG GCCAGGCTG TCA TCCT		

		AAC CGGTCCGAC AGT AGGA		
		— CAG TTG III		
GAM64	MDFI	GCGCCAGGCTGGCTTAGCCC 683 TTGC TCA		
		GCCAGGCTG TAGTCCT		
		CGGTCCGAC ATCGGGG		
		— CGA		
GAM64	NPHP1	TTG-GCCAGGCTGGTCTCAAACCTCCT 692 C	— TAG TII	
		TTG GCCAGGCTG TCA TCCT		
		AAC CGGTCCGAC AGT AGGA		
		— CAG TTG III		
GAM64	PAICS	TTG-GCCAGGCTGGTCTCAAACCTCCT 692 C	— TAG TII	
		TTG GCCAGGCTG TCA TCCT		
		AAC CGGTCCGAC AGT AGGA		
		— CAG TTG III		
GAM64	POLH	TTG-GCCAGGCTGGTCTCAAACCTCCT 692 C	— TAG TII	
		TTG GCCAGGCTG TCA TCCT		
		AAC CGGTCCGAC AGT AGGA		
		— CAG TTG III		
GAM64	PRKY	TTG-GCCAGGCTGGTCTCAAACCTCCT 692 C	— TAG TII	
		TTG GCCAGGCTG TCA TCCT		
		AAC CGGTCCGAC AGT AGGA		
		— CAG TTG III		
GAM64	PTGIS	GGCGGCAGTGGGGGTCACCCAGGC 684 ACA C CGC I		
		CGG GG GGTACCCAGGC		
		GTC CC CCAGTGGGTCCG		
		C_ A C_ C		
GAM64	SWAP70	TTG-GCCAGGCTGCTCTTGAACCTCCT 695 C	CATAG_ TII	
		TTG GCCAGGCTGT TCCT		
		AAC CGGTCCGACG AGGA		
		— AGAACTTG III		
GAM64	TGFA	GCCAGGCTGTTCTA-TCCT 681 TTGCGCCA CA G		
		GGCTGT TA TCC		
		CCGACA AT AGG		
		— AG _		
GAM64	TPST2	CGCCAGGCTCACATCTCCCTT 678 TTGCGC GT AG		
		CAGGCT CAT TCCTT		
		GTCCGA GTA GGGAA		
		— GT GA		
GAM64	VHL	TTG-GCCAGGCTGGTCTCAAACCTCCT 692 C	— TAG TII	
		TTG GCCAGGCTG TCA TCCT		

		AAC CGGTCCGAC AGT AGGA		
		— CAG TTG III		
GAM64	XT3	TTG-GCCAGGCTGGCCTCAAACCTCCT 691 C	___ TAG TII	
		TTG GCCAGGCTG TCA TCCT		
		AAC CGGTCCGAC AGT AGGA		
		— CGG TTG III		
GAM65	ADAM19	ACAACCCAGGTCTCTTTCTG 700	CTTTI	
		CAGCTCAGGTCTCT		
		GTTGGGTCCAGAGA		
		AAGAI		
GAM65	ADAM19	ACAACCCAGGTCTCTTTCTG 700 TCAC	C C	
		AGCTCAGGTCTCT TTTG		
		TTGGGTCCAGAGA AGAC		
		— A C		
GAM65	DGKI	GCTCATGTC-CTCTTTGCC 716 G T I		
		GCTCA GTC CTCTTTGC		
		CGAGT CAG GAGAAACG		
		A _ G		
GAM65	DUSP6	CAGAGCTGAAATCTCTCTTTG 709 AC C I		
		AGCT AGGTCTCTCTTT		
		TCGA TTTAGAGAGAAA		
		TC C I		
GAM65	DUSP6	CAGAGCTGAAATCTCTCTTTG 709 TCAC C CC		
		AGCT AGGTCTCTCTTTG		
		TCGA TTTAGAGAGAAAC		
		TC _ C CI		
GAM65	EDAR	TCACAGCTCCAGAGCCCTCGTTG 717 _ GT T CCI		
		TCACAGCTC AG CTCTC TTG		
		AGTGTGAG TC GGGAG AAC		
		G TC C III		
GAM65	EDAR	TCACAGCTCCAGAGCCCTCGTTG 717 _ GT TTTI		
		ACAGCTC AG CTCTC		
		TGTCGAG TC GGGAG		
		G TC CAII		
GAM65	FMR2	CACAGCTCAAGTCTGGCTGTTT 707 AC CT TI		
		AGCTCAGGTCT CT		
		TCGAGTTCAGA GA		
		— CC CA		
GAM65	FMR2	CACAGCTCAAGTCTGGCTGTTT 707 TC CT TTGCC		
		ACAGCTCAGGTCT CT		

		TGTCGAGTTCAGA GA		
		___ CC CAAAA		
GAM65 HD		CACAGCTCAGTGACACTCTT 705	GT___	CTII
		CACAGCTCAG CTCT		
		GTGTCGAGTC GAGA		
		ACTGT AIII		
GAM65 HD		CACAGCTCAGTGACACTCTT 705 TC	GTCT_	TGC
		ACAGCTCAG CTCTT		
		TGTCGAGTC GAGAA		
		___ ACTGT TII		
GAM65 LTBP2		ACAGCTCAGCCCCCTCATTACC 702 TCAC	G	T
		AGCTCAG TCTCTC TTGCC		
		TCGAGTC GGGGAG AATGG		
		___ G T		
GAM65 LTBP2		ACAGCTCAGCCCCCTCATTACC 702	G	T I
		CAGCTCAG TCTCTC TTGC		
		GTCGAGTC GGGGAG AATG		
		G T I		
GAM65 MEF2C		ACAGCT-GCTCTCTCTTT 699	CAGG	I
		ACAGCT TCTCTCTT		
		TGTCGA AGAGAGAA		
		CG_ A		
GAM65 MEF2C		ACAGCT-GCTCTCTCTTT 699 TCAC	CAGG	G
		AGCT TCTCTCTTT		
		TCGA AGAGAGAAA		
		___ CG_ G		
GAM65 NCOA6		TCACAGCTCAAAATTGCTCTTTG 718	TCT_	CCI
		TCACAGCTCAGG CTCTTTG		
		AGTGTGAGTTT GAGAAAC		
		TAAC III		
GAM65 NCOA6		TCACAGCTCAAAATTGCTCTTTG 718 C	TCT_	I
		ACAGCTCAGG CTCTTT		
		TGTCGAGTTT GAGAAA		
		_ TAAC I		
GAM65 PDGFB		GCTCCGGTTTTCTCTTTGC 715	A C_	II
		GCTC GGT TCTCTTTG		
		CGAG CCA AGAGAAAC		
		G AA GI		
GAM65 PRNP		CATCTCAGGTCTACTCTATG 712 CAG	_	TTII
		CTCAGGTCT CTCT		

		GAGTCCAGA GAGA			
		GTA T TACI			
GAM65	PRNP	CATCTCAGGTCTACTCTATG	712	TCACAG	_ T C
		CTCAGGTCT CTCT TG			
		GAGTCCAGA GAGA AC			
		_____ T T A			
GAM65	RCN1	CACAGCTCAGAGTATCACCTTG	706	A	_ C T I
		CAGCTCAG GT TC CTTT			
		GTCGAGTC CA AG GGAA			
		_ T T T I			
GAM65	RCN1	CACAGCTCAGAGTATCACCTTG	706	TC	_ C T CC
		ACAGCTCAG GT TC CTTTG			
		TGTCGAGTC CA AG GGAAC			
		_ T T T AI			
GAM65	SERPINA5	CTCTGGACCTCTCTTTGCC	713	A _	II
		CTC GG TCTCTCTTTGC			
		GAG CC GGAGAGAAACG			
		A T GI			
GAM65	SGT	CAGGTCCGAGGTCTCTCTCTTCC	711	AG C	GI
		CT AGGTCTCTCTTT			
		GG TCCAGAGAGAGA			
		A_ C AG			
GAM65	SGT	CAGGTCCGAGGTCTCTCTCTTCC	711	TCACAG C	G I
		CT AGGTCTCTCTTT CC			
		GG TCCAGAGAGAGA GG			
		CA_ C A G			
GAM65	SLC22A3	CTCTTGCTCTCTTTAGCC	714	AG	CII
		CTC GTCTCTCTTTG			
		GAG CAGAGAGAAAT			
		AA CGG			
GAM65	SLC9A3R2	TCACATCTCTGGGTCTCTCT	719	G A_	TTGC
		TCACA CTC GGTCTCTCT			
		AGTGT GAG CCAGAGAGA			
		A AC IIIC			
GAM65	SLC9A3R2	TCACATCTCTGGGTCTCTCT	719	G A_	II
		TCACA CTC GGTCTCTC			
		AGTGT GAG CCAGAGAG			
		A AC AI			
GAM65	TBX6	CACACCT--GGTCTCTCTT	708	G CA	I
		CACA CT GGTCTCTCT			

		GTGT GA CCAGAGAGA		
		G _ A		
GAM65	TBX6	CACACCT--GGTCTCTCTT	708 TC G CA	G
		ACA CT GGTCTCTCTTT		
		TGT GA CCAGAGAGAAG		
		_ G _ I		
GAM65	TRPM1	CACAGCTCAGG-CTCTTTTCAGCC	710 _ T C T I	
		ACAGCTCAGG CTCT TT GC		
		TGTCGAGTCC GAGA AG CG		
		G _ A T I		
GAM65	TRPM1	CACAGCTCAGG-CTCTTTTCAGCC	710 TC T C T	
		ACAGCTCAGG CTCT TT GCC		
		TGTCGAGTCC GAGA AG CGG		
		_ _ A T		
GAM65	WBSCR5	AGCACAGTGGTCCCTCTTTGCC	703 GCTCA I	
		GGTCTCTCTTTGC		
		CCAGGGAGAAACG		
		TGTCA I		
GAM65	WBSCR5	AGCACAGTGGTCCCTCTTTGCC	703 TCACAGCTCA	
		GGTCTCTCTTTGCC		
		CCAGGGAGAAACGG		
		GTCA_____		
GAM65	XRCC3	TCA-ACCTCGGATC-CTCTTTGCC	720 CA CA TC I	
		CAGCT GG TCTCTTTGC		
		GTTGG CC GGAGAAACG		
		A_ AG TA I		
GAM65	XRCC3	TCA-ACCTCGGATC-CTCTTTGCC	720 TCA CA TC	
		CAGCT GG TCTCTTTGCC		
		GTTGG CC GGAGAAACGG		
		A_ AG TA		
GAM65	ZNF134	ACAGCTCA-GACCCTCTTGGC	701 _ T TGI	
		CAGCTCAGG CTCTCTT		
		GTCGAGTCT GGGAGAA		
		T _ CCI		
GAM65	ZNF134	ACAGCTCA-GACCCTCTTGGC	701 TCAC T T	
		AGCTCAGG CTCTCTT GC		
		TCGAGTCT GGGAGAA CG		
		_ _ C		
GAM65	ZNF174	CAGAGACTTAAGT-TCTCTTTGCC	704 ACA_ C C I	
		GCT AGGT TCTCTTTGC		

		TGA TTCA AGAGAAACG	
		TCTC A _ I	
GAM65	ZNF174	CAGAGACTTAAGT-TCTCTTTGCC 704 TCACA C C I	
		GCT AGGT TCTCTTTGCC	
		TGA TTCA AGAGAAACGG	
		TCTC_ A _ G	
GAM66	ADORA1	AGACAAG--CAGACTCCCCT 724 _ T TC I	
		GAC AGT GGA CTCCC	
		CTG TCG TCTGAGGGG	
		T T _ I	
GAM66	ADORA1	AGACAAG--CAGACTCCCCT 724 TGAGACTAGTT	
		CGGACTCCCCT	
		GTCTGAGGGGA	
		TGTTC_____	
GAM66	BARHL1	GAGACGGGGCTCCGCACTCCCCTTC 729 AGACTAG G I	
		TTCG ACTCCCCTT	
		AGGC TGAGGGGAA	
		TGCCCCG G I	
GAM66	BARHL1	GAGACGGGGCTCCGCACTCCCCTTC 729 TG TA_ _G II	
		AGAC GTTC G ACTCCCCTTC	
		TCTG CGAG C TGAGGGGAAG	
		_ CCC G G AI	
GAM66	CABC1	TGAGA--AGTG-GAACTCCCCTTC 736 CT TC	
		TGAGA AGT GGA CTCCCCTTC	
		ACTCT TCA CTTGAGGGGAAG	
		_ C_	
GAM66	CABC1	TGAGA--AGTG-GAACTCCCCTTC 736 _ CT TC	
		GAGA AGT GGA CTCCCCTT	
		CTCT TCA CTTGAGGGGAAG	
		A _ C_	
GAM66	CKTSF1B1	TGAGACTA--TCA-ACTCCCCTT 735 GT G	
		TGAGACTA TCG ACTCCCCTT	
		ACTCTGAT AGT TGAGGGGAAG	
		_ _	
GAM66	CKTSF1B1	TGAGACTA--TCA-ACTCCCCTT 735 _ GT G	
		GAGACTA TCG ACTCCCCTT	
		CTCTGAT AGT TGAGGGGAAG	
		A _ _	
GAM66	DNAJB1	AGACATTGTTCCTCACTCCCCTTC 723 GACTA G I	
		GTTC GACTCCCCTT	

		CAAG TTGAGGGGAA			
		GTAAA G I			
GAM66	DNAJB1	AGACATTTGTTCCAACCTCCCTTC	723	TGAGACTA G	I
		GTTC GACTCCCCTTC			
		CAAG TTGAGGGGAAG			
		TGTAAA__ G G			
GAM66	FOXD1	GAC-AGGGCGGACT-CCCTTC	728	T TT CTI	
		GAC AG CGGACTCCC			
		CTG TC GCCTGAGGG			
		_ CC AAG			
GAM66	FOXD1	GAC-AGGGCGGACT-CCCTTC	728	TGAGACT TT	C
		AG CGGACTCCC TT			
		TC GCCTGAGGG AG			
		_____ CC A			
GAM66	GLTSCR2	GAGACTAGTTC--TCTCCC	730	GGA I	
		GAGACTAGTTC CTCC			
		CTCTGATCAAG GAGG			
		A__ G			
GAM66	GLTSCR2	GAGACTAGTTC--TCTCCC	730	TG GGA CT	
		AGACTAGTTC CTCCC			
		TCTGATCAAG GAGGG			
		_____ A__ AI			
GAM66	HSPA8	GAGACTAGTTCTCTCTCCC	731	GGA II	
		GAGACTAGTTC CTCC			
		CTCTGATCAAG GAGG			
		AGA GI			
GAM66	HSPA8	GAGACTAGTTCTCTCTCCC	731	TG GGA CTT	
		AGACTAGTTC CTCCC			
		TCTGATCAAG GAGGG			
		_____ AGA AII			
GAM66	IKBKB	GAGAC-AG---GGACTCCCC	732	_ T TTC	
		AGAC AG GGACTCCC			
		TCTG TC CCTGAGGG			
		C _ _			
GAM66	IKBKB	GAGAC-AG---GGACTCCCC	732	TG T TTC	
		AGAC AG GGACTCCCC			
		TCTG TC CCTGAGGGG			
		_____ _ _			
GAM66	NESG1	TGATGATTAG---GGACTCCCC	733	_ C TTC	TT
		TGA GA TAG GGACTCCCC			

		ACT CT ATC CCTGAGGGG			
		A A _ _ _ _ II			
GAM66	NESG1	TGATGATTAG--GGACTCCCC	733	_ _ C TTC	I
		GA GA TAG GGACTCCC			
		II III IIIIIII			
		CT CT ATC CCTGAGGG			
		A A A _ _ _ I			
GAM66	NTSR1	GACTGGGGCTGGACTCCCC	726	A _ _ C	II
		GACT GTT GGACTCCC			
		IIII III IIIIIII			
		CTGA CGA CCTGAGGG			
		CCC _ _ GI			
GAM66	NTSR1	GACTGGGGCTGGACTCCCC	726	TGAGACTA C	TT
		GTT GGACTCCCC			
		III IIIIIII			
		CGA CCTGAGGGG			
		ACCC _ _ CT			
GAM66	NTSR1	GAATAGGCCTGACTCCCCT	727	C TT G	II
		GA TAG C GACTCCCC			
		II III I IIIIIII			
		CT ATC G CTGAGGGG			
		T CG A AI			
GAM66	NTSR1	GAATAGGCCTGACTCCCCT	727	TGAGAC TT G	T
		TAG C GACTCCCCT			
		III I IIIIIII			
		ATC G CTGAGGGGA			
		_ _ _ CG A C			
GAM66	RAB1A	GACTTCGCTCGGACTCCCC	725	A _	II
		GACT GTTCGGACTCCC			
		IIII IIIIIIIII			
		CTGA CGAGCCTGAGGG			
		AG GI			
GAM66	RAB1A	GACTTCGCTCGGACTCCCC	725	TGAGACTA	
		GTTTCGGACTCCCCT			
		IIIIIIIIII			
		CGAGCCTGAGGGGG			
		AAG _ _ _			
GAM66	WNT10B	TGAAACTA-TAGGGACTCCCC	734	GTTC	TT
		TGAGACTA GGACTCCCC			
		IIIIII IIIIIII			
		ACTTTGAT CCTGAGGGG			
		ATC _ _ II			
GAM66	WNT10B	TGAAACTA-TAGGGACTCCCC	734	_ GTTC	I
		GAGACTA GGACTCCC			
		IIIIII IIIIIII			
		CTTTGAT CCTGAGGG			
		A ATC _ _ I			
GAM67	ARHGEF7	TTGGGTCAGGG-GTGC-CCAG	747	TATT	CT T
		GGGTCAGGG TGC CCAG			
		IIIIII III IIII			

CCCAGTCCC ACG GGTC
 _____ C_ _
 GAM67 COL4A2 TGGG-CAGGGCTTGCCCTCCAG 744 TATTGGGT _ A
 CAGGGCTTGC TCCAG
 ||||| ||||
 GTCCCGAACG AGGTC
 C_____ GG C
 GAM67 DGCR2 TCAGGGCTTCAGGTCCAGA 742 TA TG _ TGCT
 T GGT CAGGGCT CCAG
 | || ||||| ||||
 A CCA GTCTCGG GGTC
 A_ GT AG _
 GAM67 GM2A TTAGGTCAGGGCTGCTTGCCOCAG 746 TATT _ AI
 GGGTCAGGGCT TGCTCCAG
 ||||| |||||
 TCCAGTCCCGA ACGGGGTC
 _____ CGA GG
 GAM67 PES1 GGGTCAGGGCTGGCTGGAGA 741 TATTGGGT T CC
 CAGGGCT GCT AG
 ||||| || ||
 GTCCCGA CGA TC
 _____ C CC
 GAM67 SLC2A8 TTGGAGTCACAGGCTTGCTCCA 745 TATT _ GA
 GGGTCA GGGCTTGCTCCA
 |||| |||||
 CTCAGT TCCGAACGAGGT
 C_ G AG
 GAM67 TAP2 ATTGGGTCAGGGTGTGGACTCTAG 739 TA CTT_ C AI
 TTGGGTCAGGG GCTC AG
 ||||| || ||
 AACCCAGTCCC TGAG TC
 _____ ACACC A CI
 GAM67 TRH TGGGTCAGGGCTCTGC-CCA 743 TATTGG _ T G
 GTCAGGGCT TGC CCA
 ||||| || ||
 CAGTCCCGA ACG GGT
 _____ G _ G
 GAM67 WBP2 GGGTCAGGGGCCCTTGTTCC 740 TATT AGGG C AG
 GGGTC CTTG TCC
 |||| ||| ||
 CCCGG GAAC AGG
 GTC_ _ A GC
 GAM68 ADARB1 GCTGGGGACAACCGTGGACACCT 774 _ C_ IIIA
 GCTGGGGAC CCG GCACC
 ||||| || ||||
 CGACCCCTG GGC TGTGG
 TT ACC A||
 GAM68 ARHGAP6 GCCCGCCGTGGCTCCCCGCGCAC 767 G _ GA_ CTI
 GCCCG CTG GG CCCGCGCAC
 |||| || || |||||

		CGGGC GGC CC GGGCGCGTG			
		_ A GAG III			
GAM68	ARHGAP6	GCCCGCCGTGGCTCCCCGCGCAC	767	C G _ GA_ I	
		CCG CTG GG CCCGCGCA			
		III III II IIIIIII			
		GGC GGC CC GGGCGCGT			
		_ _ A GAG I			
GAM68	B3GNT3	GCCCAGAGGCTGGGGACCC	764	___	GCGCACC
		GCCC GGCTGGGGACCC			
		III IIIIIIIII			
		CGGG CCGACCCCTGGG			
		TCT IIITCCA			
GAM68	B3GNT3	GCCCAGAGGCTGGGGACCC	764	___	III
		GCCC GGCTGGGGACC			
		III IIIIIIIII			
		CGGG CCGACCCCTGG			
		TCT GII			
GAM68	CSF3	CCCAGGTGGGGACCCTCAGGACC	753	C C G CAI	
		GG TGGGGACCC CG			
		II IIIIIII II			
		CC ACCCCTGGG GT			
		T _ A CCT			
GAM68	CSF3	CCCAGGTGGGGACCCTCAGGACC	753	GC C G C_ TI	
		CCGG TGGGGACCC CG ACC			
		III IIIIIII II III			
		GGTC ACCCCTGGG GT TGG			
		_ C A CC TI			
GAM68	DDAH2	CGGCTGGGGCCCCACCCCCC	762	GCCCGG A G A	
		CTGGGG CCC CGC CC			
		IIIII III III II			
		GACCCC GGG GTG GG			
		_____ _ _ G			
GAM68	DDAH2	CGGCTGGGGCCCCACCCCCC	762	A GCACI	
		GGCTGGGG CCCGC			
		IIIII IIIII			
		CCGACCCC GGGTG			
		G GGGGI			
GAM68	EIF2B1	GCCC--CAGGGGACCCGAGC	772	GGCT C AC	
		GCCC GGGGACCCG GC			
		III IIIIIII II			
		CGGG CCCCTGGGC CG			
		GT_ T II			
GAM68	EIF2B1	GCCC--CAGGGGACCCGAGC	772	GGCT CI	
		GCCC GGGGACCCG			
		III IIIIIII			
		CGGG CCCCTGGGC			
		GT_ TC			
GAM68	EP300	GCCCGGCTGCTGGA-CCGCG	768	G_ _ CII	
		GCCCGGCTG GGACC CG			
		IIIII IIIII II			

		CGGGCCGAC CCTGG GC			
		GA C III			
GAM68	EP300	GCCCCGGCTGCTGGA-CCGCG 768	G_	C	CACC
		GCCCCGGCTG GGACC GCG			
		CGGGCCGAC CCTGG CGC			
		GA _ IIIT			
GAM68	FANCG	GCCCA-CTGGGGACCCAGCTCA 770	G	C	ACCT
		GCCCCG CTGGGGACCCG GC			
		CGGGT GACCCCTGGGT CG			
		_ _ AGTI			
GAM68	FANCG	GCCCA-CTGGGGACCCAGCTCA 770	C G	_	GCI
		CC GCTGGGGACCC GC			
		GG TGACCCCTGGG CG			
		_ G T AGI			
GAM68	FZD1	CCCGGCTGGCGGCGCCGCGC 751	_ AC	II	
		CCCGGCTGG GG CCGCG			
		GGCCGACC CC GGCGC			
		G GC GI			
GAM68	FZD1	CCCGGCTGGCGGCGCCGCGC 751	GC	_ AC	ACC
		CCGGCTGG GG CCGCG			
		GGCCGACC CC GGCGC			
		_ G GC AII			
GAM68	HOXA3	CCCGGCTGGGCGCGGGGCACCT 756	GAC	___	I
		CCGGCTGGG CCGC GCACC			
		GGCCGACCC GGCG CGTGG			
		_ CCC I			
GAM68	HOXA3	CCCGGCTGGGCGCGGGGCACCT 756	GC	GAC	___ I
		CCGGCTGGG CCGC GCACCT			
		GGCCGACCC GGCG CGTGGA			
		_ _ CCC C			
GAM68	IL17R	CCCGGCTGGGGACGCAGCG 752	C_	II	
		CCCGGCTGGGGAC C GC			
		GGCCGACCCCTG G CG			
		C T CI			
GAM68	IL17R	CCCGGCTGGGGACGCAGCG 752	GC	C_	CACC
		CCGGCTGGGGAC C GCG			
		GGCCGACCCCTG G CGC			
		_ C T TIII			
GAM68	IRS1	CCCGGCTGGAGTCCGGCACA 754	A C	I	
		CCGGCTGGGG CC GCGC			

		GGCCGACCTC GG CGTG		
		A C I		
GAM68	IRS1	CCCGGCTGGAGTCCGGCACA 754 GC	A C	CC
		CCGGCTGGGG CC GCGCA		
		GGCCGACCTC GG CGTGT		
		— A C CI		
GAM68	ITPKB	GCCCAGCGTTGGGGACCCTCCCTCC 766 C —		GCGCACI
		CGGC TGGGGACCC		
		GTCG ACCCCTGGG		
		— CA AGGGAII		
GAM68	ITPKB	GCCCAGCGTTGGGGACCCTCCCTCC 766 —		GCGCA II
		GCCCGGC TGGGGACCC CCT		
		CGGGTCG ACCCCTGGG GGA		
		CA AG— GG		
GAM68	KCNK10	GCCCGGCT--GGA--GCGCACC 773	ACC	A
		GCCCGGCTGGGG CCGGC		
		CGGGCCGACCTC GCGTG		
		— G		
GAM68	KCNK10	GCCCGGCT--GGA--GCGCACC 773		GACCC
		GCCCGGCTGGG GCGCAC		
		CGGGCCGACCT CCGCTG		
		—		
GAM68	MN1	GCCGGAGTCTCCGCGCACC 775	AC_	II
		GCTGGGG CCGCGCAC		
		CGGCCTC GGCGCGTG		
		AGA GI		
GAM68	OAS3	GCTGGGGACTCCGC-CCCCT 776	_	GCA II
		GCTGGGGAC CCGC CC		
		CGACCCCTG GGCG GG		
		A GG_ AI		
GAM68	OTX1	GGCTGGGGA--CGCGCTCCT 781	CC	ACI
		GGCTGGGGAC GCGC		
		CCGACCCCTG CCGC		
		— AGG		
GAM68	OVOL1	CTGGGGACCTGCAGCCCCT 763	C _	A II
		CTGGGGACC GC GC CC		
		GACCCCTGG CG CG GG		
		A T G AI		
GAM68	OVOL1	CTGGGGACCTGCAGCCCCT 763	GCCCGG	G A GC A
		CTG GG CCC GC CC		

		GAC TC GGG CG GG		
		TG___ G G A_ _		
GAM68	PACE	CCGGCTGGG--CCAGCGCCCCT	758	GA C ACI
		CCGGCTGGG CC GCGC		
		GGCCGACCC GG CGCG		
		___ T GGG		
GAM68	PACE	CCGGCTGGG--CCAGCGCCCCT	758	GCCC GA C A
		GGCTGGG CC GCGC CC		
		CCGACCC GG CGCG GG		
		___ T G		
GAM68	PCOLN3	GGC-GGGGACCCGCACTCC	780	T ACI
		GGC GGGGACCCGCGC		
		CCG CCCCTGGGCGTG		
		___ AGG		
GAM68	PCOLN3	GGC-GGGGACCCGCACTCC	780	GCCCGGCTG A
		GGGACCCGCGC C		
		CCCTGGGCGTG G		
		___ A		
GAM68	PFKFB3	GGCTGGGGATGCCCG-GCAC	778	___ _ All
		GGCTGGGGA CCCG CGC		
		CCGACCCCT GGGC GTG		
		AC C		
GAM68	PFKFB3	GGCTGGGGATGCCCG-GCAC	778	___ T G A CGCGCACC
		GCCCGGC G GG CC		
		CGGGCCG T CC GG		
		CCCCTA _ G _ TCCAC		
GAM68	PRX	CGGCTGGGGCCTCCACAGCA	759	AC_ C
		CGGCTGGGG CCGCG		
		GCCGACCCC GGTGT		
		GGA CGTI		
GAM68	PRX	CGGCTGGGGCCTCCACAGCA	759	GCCCGG AC_ _ CC
		CTGGGG CCGC GCA		
		GACCCC GGTG CGT		
		___ GGA T CC		
GAM68	RPH3AL	GCCCTGGCTGGGGA---TGCACCT	765	_ CCC AI
		GCCC GGCTGGGGA GCGC		
		CGGG CCGACCCCT CGTG		
		A A_ GA		
GAM68	RPH3AL	GCCCTGGCTGGGGA---TGCACCT	765	_ CCCGC
		GCCC GGCTGGGGA GCACCT		

		CGGG CCGACCCCT CGTGGA			
		A A_____			
GAM68	SCNN1A	GCCTGGCTGGGGAGCCCGC 769 C _ GCACC			
		GCC GGCTGGGGA CCCGC			
		CGG CCGACCCCT GGGCG			
		A C IIITC			
GAM68	SCNN1A	GCCTGGCTGGGGAGCCCGC 769 C _ II			
		GCC GGCTGGGGA CCCG			
		CGG CCGACCCCT GGGC			
		A C GI			
GAM68	SET7	CGGCTGGGGACACTGCCAGCT 760 CC_ G CCI			
		GCTGGGGAC GC CA			
		CGACCCCTG CG GT			
		TGA G CII			
GAM68	SLC1A2	CGGCGCGCGACCCGCGCTCC 761 TGGG ACI			
		GGC GACCCGCGC			
		CCG CTGGGCGCG			
		CGCG AGI			
GAM68	SLC6A8	GCCCGGCTGG---CCCGCG 771 GGA			
		GCCCGGCTGG CCCGC			
		CGGGCCGACC GGGCG			

GAM68	SLC6A8	GCCCGGCTGG---CCCGCG 771 GGA CA			
		GCCCGGCTGG CCCGCG			
		CGGGCCGACC GGGCG			
		_____ II			
GAM68	SLC6A8	GGCTGGGGACCACACGCAC 779 _ AIII			
		GGCTGGGGACC CGCG			
		CGACCCCTGG GTGTG			
		T CGTG			
GAM68	SORL1	CCGGCTGGGCCGGGACCGCGCGCGCC 757 _ CC G _ A TII			
		GC GGCTGGG ACC CGCGC CC			
		CG CCGGCC TGG GCGCG GG			
		C AC _ C C CGI			
GAM68	SORL1	CCGGCTGGGCCGGGACCGCGCGCGCC 757 C G _ ACI			
		GGCTGGG ACC CGCGC			
		CCGGCCC TGG GCGCG			
		C _ C CGI			
GAM68	TCF7	GCTGGGGACCCGGGGCAGCCT 777 C_ _ III			
		GCTGGGGACCCG GCA CC			

		CGACCCCTGGGC CGT GG	
		CC C All	
GAM68	TEF	CCCGGACTCGG--CTCGCGCACCT 750 _ _ G GACC I	
		CCGG CT GG CGCGCACCT	
		GGCC GA CC GCGCGTGG	
		G T G GA_ I	
GAM68	TEF	CCCGGACTCGG--CTCGCGCACCT 750 GC _ G GACC	
		CCGG CT GG CGCGCACCT	
		GGCC GA CC GCGCGTGG	
		_ T G GA_	
GAM68	TNNC2	CCCTGGTGGGGACCCG-GCA 755 G C C C CC	
		CC GG TGGGGACCCG GCA	
		GG CC ACCCCTGGGC CGT	
		_ A _ _ CI	
GAM68	TNNC2	CCCTGGTGGGGACCCG-GCA 755 _ _ C C I	
		CC GG TGGGGACCCG GC	
		GG CC ACCCCTGGGC CG	
		G A _ _ I	
GAM69	B3GAT1	TCAGTAGGCTGGGGCCCTTTCC 788 _ A_ GCTII	
		TCAG GGCT GCCCTTTCC	
		AGTC CCGA CGGGAAAGG	
		AT CCC IIITC	
GAM69	COL4A4	TCAGGCGCCCAGCCCTTTCTCGC 789 _ _ _ TII	
		TCAGG GCT AGCCCTTTC CGC	
		AGTCC CGG TCGGGAAAG GCG	
		G G A III	
GAM69	CSRP1	AGGCCAGCCCTTTCCCCT 784 TCAG G G	
		G CTAGCCCTTTCC CT	
		C GGTCGGGAAAGG GA	
		_ G G	
GAM69	EGR3	GGGCTAGACGCCACCTTTCCGC 787 TC _ GC II	
		AGG GCTA CCTTTCCGCT	
		TCT CGGT GGAAAGGCGG	
		GA G _ GG	
GAM69	NRXN2	CAGGGCTAGCGGTGTCTGC 785 TC CCTT C	
		AGGGCTAGC TC GCT	
		TCCCGATCG AG CGG	
		_ CCAC A	
GAM69	PART1	CAGTGC-AGCCCTTTTCAGCT 786 TCAGG T C	
		GC AGCCCTTTC GCT	

		CG TCGGGAAAG CGA			
		TCA__ _ T			
GAM69	RFX2	TCAGCAC-AGCCCTTTTCAGCT	790	G T	C I
		TCAG GC AGCCCTTTC GCT			
		AGTC TG TCGGGAAAG CGA			
		G _ T I			
GAM69	TAGLN	TCAGGGCTAGCCCTCTCCGCT	791		I
		TCAGGGCTAGCCCTTTCCGCT			
		AGTCCCGATCGGGAGAGGCGA			
		I			
GAM70	ADRA1A	GAGGCTGA---GGCAGGCA	800	TG	TGA A
		AGGCTGA GGCAGGCA			
		TCCGACT CCGTCCGT			
		__ _ C			
GAM70	ATP7B	TGAGGCCAA-GAGGCAGGCA	813	TG T	AGC
		TGAGGC A GAGGCAGGCA			
		ACTCCG T CTCCGTCCGT			
		GT _			
GAM70	COL5A3	GAGGAGTGAGGAGGCAGGCA	798	TG C_ T	AGC
		AGG TGA GAGGCAGGCA			
		TCC ACT CTCCGTCCGT			
		_ TC C A			
GAM70	CYP1A2	TGAGGCAGGGGAGGCAGGCTAG	816	TGAT	AAGCG
		TGAGGC GAGGCAGGC			
		ACTCCG CTCCGTCCG			
		TCCC ATC			
GAM70	DCTN1	TGAGCCAGAGGAGGCAGGC	810	G _ T	AAGC
		TGAG CT GA GAGGCAGGC			
		ACTC GG CT CTCCGTCCG			
		_ T C G			
GAM70	DMPK	TGAGGCTGAGTGACCCAGTAGCAA	809	_ GG _	GCGI
		TGAGGCTGA TGA CAG GCAA			
		ACTCCGACT ACT GTC CGTT			
		C GG AT G			
GAM70	DYSF	GGCGGAGGAGGCAGGCCAG	807	TGAGGCT T	A C
		GA GAGGCAGGC AG			
		CT CTCCGTCCG TC			
		C _ _ C G A			
GAM70	FCRH1	TGAGCCTGA-GAGGCAGGC	811	G T	AAG
		TGAG CTGA GAGGCAGGC			

	ACTC GACT CTCCGTCCG	
	G _ III	
GAM70 FGF4	GAGGAGG-TGCGGGAGGCAAGCG 804 T_ C A A C	
	GAGG TG TG GG AGGCAAGCG	
	CTCC AC GC CC TCCGTTCGC	
	TC _ _ _ _	
GAM70 FGFR2	AGGCTCA-GAGCGCGCAGGCAAGC 797 TGAG GAT ____ GI	
	GCT GAG GCAGGCAAGC	
	CGA CTC CGTCCGTTCG	
	____ GT_ GCG AC	
GAM70 FLNB	AGGCTGATGAAGGGCTGG--AGCG 795 TGAG CA A__	
	GCTGATGAGG GGC AGCG	
	CGACTACTTC CCG TCGC	
	____ _ ACC	
GAM70 HSPA2	AGGCACATGGCGGCAGGCAAG 796 TGAG TG A_ CG	
	GC ATG GGCAGGCAAG	
	CG TAC CCGTCCGTTC	
	____ TG CG TC	
GAM70 HYAL4	GAGGCTGA--GGCAGGCA 800 TG TGA A	
	AGGCTGA GGCAGGCA	
	TCCGACT CCGTCCGT	
	____ _ C	
GAM70 MATN2	AGGCAGGATGAGGCAGAAGCAAG 794 TGAG T_ _ CGI	
	GC GATGAGGCAG GCAAG	
	CG CTACTCCGTC CGTTC	
	____ TC TT AAI	
GAM70 MGST3	TGAGGCTGAT--GCCAGGTAAG 817 AGG C C	
	TGAGGCTGATG CAGG AAG	
	ACTCCGACTAC GTCC TTC	
	G_ A I	
GAM70 MPP5	GCTGATGAGGGAAGGGAAGC 805 TGAGGCTG C_ C	
	ATGAGG AGG AAGC	
	TACTCC TCC TTCG	
	____ CT C	
GAM70 ODF2	TGAGG--ATGAGGCAGACA 812 CTG AG	
	TGAGG ATGAGGCAGGCA	
	ACTCC TACTCCGTCTGT	
	____ II	
GAM70 PCDH7	GAGGCAGAAGTGGCAGGCAA 801 TG T TGA C	
	AGGC GA GGCAGGCAAG	

		TCCG CT CCGTCCGTTT		
		___ T TCA I		
GAM70	PFKL	GCAGCTGAGGCAGGGCAAG	806	TGAGGCTGA _ C
		TGAGGCAGG CAAG		
		ACTCCGTCC GTTC		
		G_____ C C		
GAM70	PMCHL1	TGAGGCTG---AGGCAGGAAA	815	TGA CAAG
		TGAGGCTGA GGCAGG		
		ACTCCGACT CCGTCC		
		_____ TTTI		
GAM70	PRKCM	TGAGGCACACCAGGCAGGCAA	814	TG G GCG
		TGAGGC AT AGGCAGGCAA		
		ACTCCG TG TCCGTCCGTT		
		TG G III		
GAM70	SH3BP2	GAGGCTGA---GGCAGGAAA	802	TG TGA C
		AGGCTGA GGCAGG AAG		
		TCCGACT CCGTCC TTT		

GAM70	SLC2A8	TGATGGCTGATGACCCAGGGAA	808	_ GG CAAGCG
		TGA GGCTGATGA CAGG		
		ACT CCGACTACT GTCC		
		A GG CT		
GAM70	TRIM9	GAGGCCGAGCTGAGGCAGG	799	TG _ CAAGC
		AGGCTGA TGAGGCAGG		
		TCCGGCT ACTCCGTCC		
		_____ CG T G		
GAM70	VPREB3	GAGGCAGG-GAGGCAGGCAAG	803	TG TGAT C
		AGGC GAGGCAGGCAAG		
		TCCG CTCCGTCCGTTC		
		_____ TCC_ A		
GAM71	ANGPT1	GCATGTATA-TTATTTTAAG	826	TGGC GTGAGG
		ATGTATA TTAAGG		
		TACATAT AATTCT		
		_____ AATAA_		
GAM71	ATP8A2	TGGC---TAGAATGAGGTAA	833	ATG T G
		TGGC TA AGTGAGGTAA		
		ACCG AT TTA CTCCAATT		
		_____ C I		
GAM71	ATP8A2	TGGC---TAGAATGAGGTAA	833	_ ATG T
		GGC TA AGTGAGGTAA		

CCG AT TTA CTCCAAT
A _ C

GAM71 HAS2 GCATGGCTAGTGAGGTATATAGG 825 _ ATGTA TA_ AI
TGGC TAGTGAGGT AGG
|||| ||||||| |||
ACCG ATCACTCCA TCC
T _ TATA GG

GAM71 HAS2 GCATGGCTAGTGAGGTATATAGG 825 A TA TAAGI
TG TAGTGAGGT
|| |||||||
AC ATCACTCCA
_ CG TATAT

GAM71 HK2 GCTTGTAGA-TGAGGTTAAAGA 827 CA_ TA I
TGTA GTGAGGTTAAGG
|||| |||||||||
ACAT TACTCCAATTTCT
CGA C_ I

GAM71 HK2 GCTTGTAGA-TGAGGTTAAAGA 827 TGGCA TA
TGTA GTGAGGTTAAGGA
|||| |||||||||
ACAT TACTCCAATTTCT
A_ C_

GAM71 JAM3 GCTTTTATAAATGAGGTAA 824 ATG _ II
GC TATAG TGAGGTAA
|| |||| |||||||
CG ATATT ACTCCAAT
AAA T TI

GAM71 JAM3 GCTTTTATAAATGAGGTAA 824 TGGCA T G
TGTA AGTGAGGTTAAG
|||| |||||||||
ATAT TTA CTCCAATTT
AAA_ _ G

GAM71 LAMC2 GGCTAGGTATAGTGAGTGTTCTGGA 828 GCAT _ AA I
GTATAGTGAG GTT GG
||||||| ||| ||
CATATCACTC CAA CC
ATC_ A GA I

GAM71 LAMC2 GGCTAGGTATAGTGAGTGTTCTGGA 828 TG AT_ _ AA II
GC GTATAGTGAG GTT GGA
|| ||||||||| ||| |||
CG CATATCACTC CAA CCT
_ ATC A GA CI

GAM71 MEN1 GGCAAATTCTTTAGTGAGG-TAAG 829 GGCATGTA TI
TAGTGAGGT
|||||||
ATCACTCCA
TAAGAA_ TT

GAM71 MEN1 GGCAAATTCTTTAGTGAGG-TAAG 829 TG TGTA_ T AI
GCA TAGTGAGGT AAGG
||| ||||||| |||

		CGT ATCACTCCA TTCT		
		__ TTAAGAA _ II		
GAM71 MGAM		TGGCATGTAGGGAGGGTGGTTCAG 830	AT T	TTAA AI
		TGGCATGT AG GAGG GG		
		ACCGTACA TC CTCC CC		
		_ C CA_ AA		
GAM71 MGAM		TGGCATGTAGGGAGGGTGGTTCAG 830 G	AT T	TTAAI
		CATGT AG GAGG		
		GTACA TC CTCC		
		_ _ C CACCA		
GAM71 MPP5		CATGTATAGAGA-ATAAAGGA 823 _	T GTT	I
		ATGTATAG GAG AAGG		
		TACATATC CTT TTCC		
		G T AT_ I		
GAM71 MPP5		CATGTATAGAGA-ATAAAGGA 823 TGGCAT	T GTT	
		GTATAG GAG AAGG		
		CATATC CTT TTCC		
		_____ T AT_		
GAM71 MYH6		TGGCAAG---AGTGAGGTT 832	TGTAT	
		TGGCA AGTGAGGT		
		ACCGT TCACTCCA		
		TC__		
GAM71 MYH6		TGGCAAG---AGTGAGGTT 832	TGTAT	AA
		TGGCA AGTGAGGTT		
		ACCGT TCACTCCAA		
		TC__ II		
GAM71 NEDD4		ATGAATCCAGAGAGGTTAAG 820	TA__ T	III
		ATG TAG GAGGTAA		
		TAC GTC CTCCAATT		
		TTAG T CII		
GAM71 NEDD4		ATGAATCCAGAGAGGTTAAG 820 TGGCATGTA	T	G
		TAG GAGGTAAAG		
		GTC CTCCAATTC		
		TAG_____ T A		
GAM71 SLC17A4		CATTTGAAGTGAGGTTAGGG 822	CATGTAT	AI
		AGTGAGGTTA		
		TCACTCCAAT		
		AAACT__ CC		
GAM71 SLC17A4		CATTTGAAGTGAGGTTAGGG 822 TGGCATGTAT		A
		AGTGAGGTTA GG		

		TC	ACTCCAAT	CC		
		AACT	_____	C		
GAM71	SRD5A2	TG	ACTTATATAGTGAGTTT	831	A	GTII
		TGGC	TGTATAGTGAG			
		ACTG	ATATATCACTC			
		A	AAAI			
GAM71	SRD5A2	TG	ACTTATATAGTGAGTTT	831	A	GTTAAGG
		TGGC	TGTATAGTGAG			
		ACTG	ATATATCACTC			
		A	AAAI			
GAM71	STK6	TGGG	GAGATA-AGTG--GTTAAGGA	834	CAT T GA	
		TGG	GTA AGT GGTTAAGGA			
		ACC	TAT TCA CCAATTCCT			
		CTC	_ _			
GAM71	STK6	TGGG	GAGATA-AGTG--GTTAAGGA	834	_ CAT T GA	
		GG	GTA AGT GGTTAAGG			
		CC	TAT TCA CCAATTCC			
		A CTC	_ _			
GAM71	ZNF138	ATGT	TATAGTAAGTGTTGAG	821	_ AAI	
		ATGT	TATAGTGAG GTT			
		TAC	ATATCATTC CAA			
		A CTCI				
GAM71	ZNF138	ATGT	TATAGTAAGTGTTGAG	821	TGGCATGT _ A	
		ATAGT	GAG GTT AGG			
		TATCATTC	CAA TCT			
		_____	A C			
GAM72	GEMIN5	TGTT	GTTGATTGCTGGGCC	841	CT _ CCAG	
		TGT	GTTGAT GCTGGGCC			
		ACA	CAACTA CGACCCGG			
		AC	A IIIG			
GAM72	GEMIN5	TGTT	GTTGATTGCTGGGCC	841	CT _ II	
		TGT	GTTGAT GCTGGGC			
		ACA	CAACTA CGACCCG			
		AC	A GI			
GAM72	GPC6	TGTCT	GTTGGTG-TGAGCTCGAGG	842	A C CCC I	
		TGTCT	GTTG TG TGGGC AGG			
		ACAGACAAC	AC ACTCG TCC			
		C _	AGC I			
GAM72	GPC6	TGTCT	GTTGGTG-TGAGCTCGAGG	842	_ A C CCCAGI	
		GTCT	GTTG TG TGGGC			

		CAGACAAC AC ACTCG			
		A C _ AGCTCI			
GAM72	HYAL3	TGTTGATGCT-GGCCTCTGG	844 _	G CCAGI	
		GTTGATGCTGG CC			
		CAACTACGACC GG			
		A _ AGACI			
GAM72	HYAL3	TGTTGATGCT-GGCCTCTGG	844	TGTCTGTT	G CCA
		GATGCTGG CC	G		
		CTACGACC GG	C		
		_____ _ AGA			
GAM72	MEF2B	TGTCTGCCTTG-TGCTGGGCC	840	GA_	CCAG
		TGTCTGTT TGCTGGGCC			
		ACAGACGG ACGACCCGG			
		AAC IIIG			
GAM72	MEF2B	TGTCTGCCTTG-TGCTGGGCC	840	GA_	II
		TGTCTGTT TGCTGGGC			
		ACAGACGG ACGACCCG			
		AAC GI			
GAM72	NDUFV3	GTCTGTTGGAAGCTGGGCC	838	AT_	II
		GTCTGTTG GCTGGGCC			
		CAGACAAC CGACCCGG			
		CTT GI			
GAM72	NDUFV3	GTCTGTTGGAAGCTGGGCC	838	TG AT_	CAG
		TCTGTTG GCTGGGCC			
		AGACAAC CGACCCGGG			
		_____ CTT AII			
GAM72	OGG1	GTTTGTCTGGGGCTGGGCC	837 _	TTGAT	CAG
		TGTCTG GCTGGGCC			
		ACAGAC CGACCCGGG			
		AA CC_ TII			
GAM72	OGG1	GTTTGTCTGGGGCTGGGCC	837 _	TTGAT	II
		GTCTG GCTGGGCC			
		CAGAC CGACCCGG			
		CAAA CC_ GI			
GAM72	SFTPD	TCTTTT--TGTTAGGCCCCAGG	839	CTGTTGA C	I
		TG TGGGCCCCAG			
		AC ATCCGGGGTC			
		AGAAAA_ A I			
GAM72	TNFRSF7	TGCTGATGCT-GGCCTCTGG	843 _	G CCAGI	
		GTTGATGCTGG CC			

		CGACTACGACC GG			
		A _ AGACI			
GAM72	TNFRSF7	TGCTGATGCT-GGCCTCTGG	843	TGTCTGTT	G CCA
		GATGCTGG CC G			
		CTACGACC GG C			
		_____ _ AGA			
GAM73	AVPR1A	GGGTTTCTTCCTTCTCACC	848	G___	III
		GGGTTTCTT CTCAC			
		CCCAAAGAA GAGTG			
		GGAA GII			
GAM73	AVPR1A	GGGTTTCTTCCTTCTCACC	848	TGTGGGG	G CCC
		TTTCTT CTCACC			
		GAAGGA GAGTGG			
		AA_____ A CTC			
GAM73	C14orf1	TGTGG---TCTTGCTCACACACA	859	GGTT	CCCC
		TGTGG TCTTGCTCAC			
		ACACC AGAACGAGTG			
		_____ TGTG			
GAM73	C14orf1	TGTGG---TCTTGCTCACACACA	859	GGTT	CI
		TGTGG TCTTGCTCAC			
		ACACC AGAACGAGTG			
		_____ TG			
GAM73	ELMO1	TGTGGGGTTTGGTCTT-CTCA	854	___	G CCCCC
		TGTGGGGTT TCTT CTCA			
		ACACCCCAA AGAA GAGT			
		ACC _ IIIAC			
GAM73	ELMO1	TGTGGGGTTTGGTCTT-CTCA	854	___	G III
		TGTGGGGTT TCTT CTC			
		ACACCCCAA AGAA GAG			
		ACC _ TII			
GAM73	G2A	TGTCGTGTCCCTTGCTCACC	858	GGG TT	CCC
		TGT GT CTTGCTCACC			
		ACA CA GAACGAGTGG			
		GCA GG III			
GAM73	G2A	TGTCGTGTCCCTTGCTCACC	858	GTGGG TT	I
		GT CTTGCTCAC			
		CA GAACGAGTG			
		CAGCA GG I			
GAM73	GCK	TGGGGTTTCTTCCTGAGCC	853	G CACCII	
		TGGGGTTTCTT CT			

		ACCCCAAAGAA GA			
		G CTCGGI			
GAM73	GCK	TGGGGTTTCTTCCTGAGCC	853	TGTG	G CAC CC
		GGGTTTCTT CT CC			
		II II			
		CCCAAAGAA GA GG			
		_____ G CTC TC			
GAM73	HSF4	GGGGCTTC--GCTCACCCCC	847	_ TT	I
		GGGTTTC GCTCACCCCC			
		CCCGAAG CGAGTGGGG			
		C _ I			
GAM73	HSF4	GGGGCTTC--GCTCACCCCC	847	TGTGGG	TT
		GTTTC GCTCACCCCC			
		CGAAG CGAGTGGGG			
		_____ _			
GAM73	IL13RA1	GTGAGGGTTTCTT-ATCTCCCC	850	T T	C A CA
		G GGGGTTTCTTG TC CCCC			
		A TCCCAAAGAAT AG GGGG			
		_ C _ A AI			
GAM73	IL13RA1	GTGAGGGTTTCTT-ATCTCCCC	850	T_	_ A CI
		GGGGTTTCTTG CTC CC			
		II			
		TCCCAAAGAAT GAG GG			
		AC A _ II			
GAM73	MMP14	TGTGGCCTT-CAGGCTCACCCCCA	860	G G TT	I
		TGTG G TTTC GCTCACCCCCA			
		ACAC C GAAG CGAGTGGGGGT			
		_ G TC I			
GAM73	MMP14	TGTGGCCTT-CAGGCTCACCCCCA	860	_ G G TT	I
		GTG G TTTC GCTCACCCCC			
		CAC C GAAG CGAGTGGGGG			
		A _ G TC I			
GAM73	MYO1D	TGTGGG-TGACTCTGCTCACCC	855	GT_ T	CCA
		TGTGGG TTCT GCTCACCC			
		ACACCC GAGA CGAGTGGG			
		ACT _			
GAM73	MYO1D	TGTGGG-TGACTCTGCTCACCC	855	GT_ T	I
		GTGGG TTCT GCTCACC			
		CACCC GAGA CGAGTGG			
		ACT _ I			
GAM73	PCDHA11	GGGTTTCTT----CCCCCA	849	TGC A	
		GGGTTTCT TC CCCC			
		II			

CCCAAAGA AG GGGG

GAM73 PYCR1 TGTGGGGTGTCAACTTCACCCCCA 861 T TT _ I
TGTGGGGT TC GCT CACCCCCA
||||||| || ||| |||||||
ACACCCCCA AG TGA GTGGGGGT
C T_ A I

GAM73 PYCR1 TGTGGGGTGTCAACTTCACCCCCA 861 T TT _ I
GTGGGGT TC GCT CACCCCC
||||||| || ||| |||||||
CACCCCCA AG TGA GTGGGGG
C T_ A I

GAM73 RALBP1 TGTGGGGTTTGTGTT-TTCGACCCC 857 C GC _ CA
TGTGGGGTTT TT TC ACCCC
||||||| || || |||||
ACACCCCCAAA AA AG TGGGG
C A_ C II

GAM73 RALBP1 TGTGGGGTTTGTGTT-TTCGACCCC 857 C GC _ I
GTGGGGTTT TT TC ACCC
||||||| || || |||||
CACCCCCAAA AA AG TGGG
C A_ C I

GAM73 TIA1 GTGGGGTTTCTCGGCTGACC 851 _ CACII
GTGGGGTTTCTTG CT
||||||| ||
CACCCCCAAAGAGC GA
C CTGGI

GAM73 TIA1 GTGGGGTTTCTCGGCTGACC 851 TG _ C CCC
TGGGGTTTCTTG CT ACC
||||||| || |||
ACCCCCAAAGAGC GA TGG
C C TII

GAM73 TRPM6 TGGGATCTTCTTGCTCCTCCC 852 GG AC I
GG TTTCTTGCTC CC
|| ||||||| ||
CC GAAGAACGAG GG
TA GA I

GAM73 TRPM6 TGGGATCTTCTTGCTCCTCCC 852 TGT GG AC CA
GG TTTCTTGCTC CCC
|| ||||||| |||
CC GAAGAACGAG GGG
_ TA GA AA

GAM73 VASP TGTGGGGTTCATTGGTGCATCCCCA 856 C CT_ C II
TGTGGGGTTT TTG CA CCCCCA
||||||| || || |||||
ACACCCCCAAG AAC GT GGGGT
T CAC A II

GAM73 VASP TGTGGGGTTCATTGGTGCATCCCCA 856 G C CT_ _ CI
TGGGGTTT TTG CA CCCC
||||||| ||| || |||||

		ACCCCAAG AAC GT GGGG		
		— T CAC A II		
GAM74 ADORA1		AGTCCTCCGGCTCCCGCCG 864 TGGAAGT A		
		CTCCGGCTCC GTCGT		
		GAGGCCGAGG CGGCG		
		_____ G		
GAM74 AK1		GGAAG---CGGCTCCAG-CGT 869 TG TCTC T		
		GAAG CGGCTCCAG CG		
		CTTC GCCGAGGTC GC		
		— — —		
GAM74 CCBL1		TGGAAGTCTACCG--TCC-GTC 872 _ GC A GT		
		TGGAAGTCT CCG TCC GTC		
		ACCTTCAGA GGC AGG CAG		
		T _ _ II		
GAM74 DTR		TGGAAGTCTTTCCCTCTGCAGTC 871 _ GG C GTCI		
		TGGAAGTCT CC CT CAGTC		
		ACCTTCAGA GG GA GTCAG		
		AAG GA C IIIC		
GAM74 ERBB4		TGGAAGTCT-CAGATCCCGT 874 C CT AGTCGT		
		TGGAAGTCTC GG CC		
		ACCTTCAGAG CT GG		
		T AG CAIIIC		
GAM74 ITK		GGAAGTCTCCTAGCT-CAGT 867 TG _ C CGT		
		GAAGTCTCC GGCTC AGT		
		CTTCAGAGG TCGAG TCA		
		— A _ TII		
GAM74 MAN2C1		GGAAGTCTCTCCGGCGTCAg 865 TG _ TC TCGT		
		GAAGTC TCCGGC CAG		
		CTTCAG AGGCCG GTC		
		— AG CA CIII		
GAM74 OSCAR		TGGAAGTCTCGGGCTGCAGT 875 C C CGT		
		TGGAAGTCTC GGCT CAGT		
		ACCTTCAGAG CCGA GTCA		
		C C III		
GAM74 SLC2A1		TGGAAGTCTC---ATCCAG 873 CGGC TC		
		TGGAAGTCTC TCCAG		
		ACCTTCAGAG AGGTC		
		T _ _ II		
GAM74 SORBS1		GGAAGTCTCCTTCTACCCAG 868 TG GG _ TCGT		
		GAAGTCTCC CT CCAG		

		CTTCAGAGG GA GGTC		
		___ AA TG TIII		
GAM74	TNFRSF6B	GGAAGTCAACCGACTCCAGTCG	866	TG G T_ TC
		GAA TC CCGGCTCCAGTCG		
		CTT AG GGCTGAGGTCAGC		
		___ G TT TI		
GAM74	TNXB	GGAAGTCTCC--CT-CACTTGTC	870	TG GG CA__ GT
		GAAGTCTCC CTC GTC		
		CTTCAGAGG GAG CAG		
		___ ___ TGAA GI		
GAM75	ABCD1	CCTGAGGTCAGGGCCTTGAGA	878	TCGCCT AG
		GAGGTCGGG TTTGAGA		
		CTCCAGTCC GAACTCT		
		CG		
GAM75	ABCD1	CCTGAGGTCAGGGCCTTGAGA	878	AG I
		CTGAGGTCGGG TTTGAG		
		GACTCCAGTCC GAACTC		
		CG I		
GAM75	ALX4	CGCCTTGGCT-GGGAGTTTG	879	TC GA C AG
		GCCT GGT GGGAGTTTG		
		CGGA CCG CCCTCAAAC		
		___ A_ A CI		
GAM75	ALX4	CGCCTTGGCT-GGGAGTTTG	879	_ GA C I
		GCCT GGT GGGAGTTT		
		CGGA CCG CCCTCAAA		
		G A_ A I		
GAM75	AQP6	TCGCCTCAGGTCAGGAGTTTGAGA	902	G I
		TCGCCT AGGTCGGGAGTTTGAGA		
		AGCGGA TCCAGTCCTCAAACCTCT		
		G I		
GAM75	AQP6	TCGCCTCAGGTCAGGAGTTTGAGA	902	G I
		CGCCT AGGTCGGGAGTTTGAG		
		GCGGA TCCAGTCCTCAAACCTC		
		G I		
GAM75	ARSF	TCAGTTGAGGTCGGGAGTTTCGAGA	899	C I
		TCGC TGAGGTCGGGAGTTTGAGA		
		AGTG ACTCCAGCCCTCAAGCTCT		
		A I		
GAM75	ARSF	TCAGTTGAGGTCGGGAGTTTCGAGA	899	C I
		CGC TGAGGTCGGGAGTTTGAG		

		GTG ACTCCAGCCCTCAAGCTC			
		A I			
GAM75	ATP1B2	TCACCTGAGGTCGGGAGTTTCGAGA 895			I
		TCGCCTGAGGTCGGGAGTTTGAGA			
		AGTGGACTCCAGCCCTCAAGCTCT			
		I			
GAM75	ATP1B2	TCACCTGAGGTCGGGAGTTTCGAGA 895			I
		CGCCTGAGGTCGGGAGTTTGAG			
		GTGGACTCCAGCCCTCAAGCTC			
		I			
GAM75	ATP6V1A1	TCACCTGAGGTCTGGAGTTTCGAGA 897	G		I
		TCGCCTGAGGTC GGAGTTTGAGA			
		AGTGGACTCCAG CCTCAAGCTCT			
		A I			
GAM75	ATP6V1A1	TCACCTGAGGTCTGGAGTTTCGAGA 897	G		I
		CGCCTGAGGTC GGAGTTTGAG			
		GTGGACTCCAG CCTCAAGCTC			
		A I			
GAM75	AVPR1A	TCGGC-GAGGTCGGGAAGGTGAG 890	CC		TT A
		TCG TGAGGTCGGGAG TGAG			
		AGC GCTCCAGCCCTT ACTC			
		C_ CC I			
GAM75	AVPR1A	TCGGC-GAGGTCGGGAAGGTGAG 890	C_ CT		TT I
		GC GAGGTCGGGAG TGA			
		CG CTCCAGCCCTT ACT			
		AGC _ CC I			
GAM75	CACNG6	TCCCTTGGGCTCAG-AGTTTGAGA 901	G GA CG		I
		TC CCT GGT GGAGTTTGAGA			
		AG GGA CCG TCTCAAACCTCT			
		_ AC AG I			
GAM75	CACNG6	TCCCTTGGGCTCAG-AGTTTGAGA 901	CG GA CG		I
		CCT GGT GGAGTTTGAG			
		GGA CCG TCTCAAACCTC			
		AG AC AG I			
GAM75	CBFA2T2	TCACCTGAGGTCCGGGGTTTGAGA 894	_ A		I
		CGCCTGAGGTC GGG GTTTGAG			
		GTGGACTCCAG CCC CAAACTC			
		G _ I			
GAM75	CBFA2T2	TCACCTGAGGTCCGGGGTTTGAGA 894	_ A		I
		TCGCCTGAGGTC GGG GTTTGAGA			

		AGTGGACTCCAG CCC CAAACTCT	
		G _ I	
GAM75 CYP1A2		TCACTTGAGGTCAGGAGTTTGAGA 898 C	I
		TCGC TGAGGTCGGGAGTTTGAGA	
		AGTG ACTCCAGTCCTCAAACCTCT	
		A I	
GAM75 CYP1A2		TCACTTGAGGTCAGGAGTTTGAGA 898 C	I
		CGC TGAGGTCGGGAGTTTGAG	
		GTG ACTCCAGTCCTCAAACCTC	
		A I	
GAM75 DFFB		TCACCTGAGGTCAGGAGTTTCGAGA 892	I
		TCGCCTGAGGTCGGGAGTTTGAGA	
		AGTGGACTCCAGTCCTCAAGCTCT	
		I	
GAM75 DFFB		TCACCTGAGGTCAGGAGTTTCGAGA 892	I
		CGCCTGAGGTCGGGAGTTTGAG	
		GTGGACTCCAGTCCTCAAGCTC	
		I	
GAM75 DFFB		TCACCTGAGGTCAGGAGTTTGAGA 893	I
		TCGCCTGAGGTCGGGAGTTTGAGA	
		AGTGGACTCCAGTCCTCAAACCTCT	
		I	
GAM75 DFFB		TCACCTGAGGTCAGGAGTTTGAGA 893	I
		CGCCTGAGGTCGGGAGTTTGAG	
		GTGGACTCCAGTCCTCAAACCTC	
		I	
GAM75 DISC1		TCGCCTGAGGTCAGGAGTTTGAGA 904	I
		TCGCCTGAGGTCGGGAGTTTGAGA	
		AGCGGACTCCAGTCCTCAAACCTCT	
		I	
GAM75 DISC1		TCGCCTGAGGTCAGGAGTTTGAGA 904	I
		CGCCTGAGGTCGGGAGTTTGAG	
		GCGGACTCCAGTCCTCAAACCTC	
		I	
GAM75 FCAR		TCACCTGAGGTCGGGAGTTTCGAGA 895	I
		TCGCCTGAGGTCGGGAGTTTGAGA	
		AGTGGACTCCAGCCCTCAAGCTCT	
		I	
GAM75 FCAR		TCACCTGAGGTCGGGAGTTTCGAGA 895	I
		CGCCTGAGGTCGGGAGTTTGAG	

		GTGGACTCCAGCCCTCAAGCTC		
		I		
GAM75	FCAR	TCACCTGAGGTCAGGAGTTCGAGA 892		I
		TCGCCTGAGGTCGGGAGTTTGAGA		
		AGTGGACTCCAGTCCTCAAGCTCT		
		I		
GAM75	FCAR	TCACCTGAGGTCAGGAGTTCGAGA 892		I
		CGCCTGAGGTCGGGAGTTTGAG		
		GTGGACTCCAGTCCTCAAGCTC		
		I		
GAM75	HCS	GCTTGAGCTCAGGAGTTTGAGA 885 CC G		I
		TGAG TCGGGAGTTTGAG		
		ACTC AGTCCTCAAACCTC		
		GA G I		
GAM75	HCS	GCTTGAGCTCAGGAGTTTGAGA 885 TCGCC G		
		TGAG TCGGGAGTTTGAGA		
		ACTC AGTCCTCAAACCTCT		
		A G		
GAM75	HCS	TCACCCGACGTCGGGAGTTCAAGA 891 G TG I		
		TCGCCTGA GTCGGGAGTT AGA		
		AGTGGGCT CAGCCCTCAA TCT		
		G GT I		
GAM75	HCS	TCACCCGACGTCGGGAGTTCAAGA 891 G TG I		
		CGCCTGA GTCGGGAGTT AG		
		GTGGGCT CAGCCCTCAA TC		
		G GT I		
GAM75	LTB4R	TCACTTGATGTTAGCAGTTTGAGA 900 C G CG G I		
		TCGC TGA GT G AGTTTGAGA		
		AGTG ACT CA C TCAAACCTCT		
		A A AT G I		
GAM75	LTB4R	TCACTTGATGTTAGCAGTTTGAGA 900 C G CG G I		
		CGC TGA GT G AGTTTGAG		
		GTG ACT CA C TCAAACCTC		
		A A AT G I		
GAM75	MAK	TCACCTGAGGTCAGGAGTTTGAGA 893		I
		TCGCCTGAGGTCGGGAGTTTGAGA		
		AGTGGACTCCAGTCCTCAAACCTCT		
		I		
GAM75	MAK	TCACCTGAGGTCAGGAGTTTGAGA 893		I
		CGCCTGAGGTCGGGAGTTTGAG		

		GTGGACTCCAGTCCTCAAACCTC		
GAM75	MEFV	TCACCTGAGGTCAGGAGTTTGAGA 893		
		TCGCCTGAGGTCGGGAGTTTGAGA		
		AGTGGACTCCAGTCCTCAAACCTCT		
GAM75	MEFV	TCACCTGAGGTCAGGAGTTTGAGA 893		
		CGCCTGAGGTCGGGAGTTTGAG		
		GTGGACTCCAGTCCTCAAACCTC		
GAM75	MEFV	TCACCTGAGGTCAGGAGTTCGAGA 892		
		TCGCCTGAGGTCGGGAGTTTGAGA		
		AGTGGACTCCAGTCCTCAAGCTCT		
GAM75	MEFV	TCACCTGAGGTCAGGAGTTCGAGA 892		
		CGCCTGAGGTCGGGAGTTTGAG		
		GTGGACTCCAGTCCTCAAGCTC		
GAM75	MLANA	TCACCTGAGGTCAGGAGTTTGAGA 893		
		TCGCCTGAGGTCGGGAGTTTGAGA		
		AGTGGACTCCAGTCCTCAAACCTCT		
GAM75	MLANA	TCACCTGAGGTCAGGAGTTTGAGA 893		
		CGCCTGAGGTCGGGAGTTTGAG		
		GTGGACTCCAGTCCTCAAACCTC		
GAM75	MTRF1	CTGAGGTCGGAACCTTCCGAGA 880 TG	G__	
		AGGTCGGGA TTTGAG		
		TCCAGCCTT AGGCTC		
		__ GGA		
GAM75	NCOA6	TCACTTGAGGTCAGGAGTTTGAGA 898 C		
		TCGC TGAGGTCGGGAGTTTGAGA		
		AGTG ACTCCAGTCCTCAAACCTCT		
		A		
GAM75	NCOA6	TCACTTGAGGTCAGGAGTTTGAGA 898 C		
		CGC TGAGGTCGGGAGTTTGAG		
		GTG ACTCCAGTCCTCAAACCTC		
		A		
GAM75	NDRG3	TCACCTGAGGTCAGGAGTTTGAGA 893		
		TCGCCTGAGGTCGGGAGTTTGAGA		

		AGTGGACTCCAGTCCTCAAACCTCT		
		I		
GAM75	NDRG3	TCACCTGAGGTCAGGAGTTTGAGA 893	I	
		CGCCTGAGGTCGGGAGTTTGAG		
		GTGGACTCCAGTCCTCAAACCTC		
		I		
GAM75	NQO1	TCACCTGAGGTCAGGAGTTTGAGA 893	I	
		TCGCCTGAGGTCGGGAGTTTGAGA		
		AGTGGACTCCAGTCCTCAAACCTCT		
		I		
GAM75	NQO1	TCACCTGAGGTCAGGAGTTTGAGA 893	I	
		CGCCTGAGGTCGGGAGTTTGAG		
		GTGGACTCCAGTCCTCAAACCTC		
		I		
GAM75	NXF3	GCCTGGGGACGGGAGTTTGGAGA 883 C A T	AGI	
		CTG GG CGGGAGTTTG		
		GAC CC GCCCTCAAAC		
		_ C T CTC		
GAM75	NXF3	GCCTGGGGACGGGAGTTTGGAGA 883 TCGC A T	_ I	
		CTG GG CGGGAGTTTG AGA		
		GAC CC GCCCTCAAAC TCT		
		___ C T C T		
GAM75	ODF2	TCGC-TGATGGTTTCGGGAGTTT 886 C _ _	GAGA	
		TCGC TGA GG TCGGGAGTTT		
		AGCG ACT CC AGCCCTCAAA		
		_ A AA IIIA		
GAM75	ODF2	TCGC-TGATGGTTTCGGGAGTTT 886 CGC _ _	I	
		CTGA GG TCGGGAGTT		
		GACT CC AGCCCTCAA		
		___ A AA I		
GAM75	RGS9	TCGCTTGAGCCCAGGAGTTTGAG 889 C G	AI	
		TCGC TGAG TCGGGAGTTTGAG		
		AGCG ACTC GGTCTCAAACCTC		
		A G II		
GAM75	RGS9	TCGCTTGAGCCCAGGAGTTTGAG 889 C G	I	
		CGC TGAG TCGGGAGTTTGAG		
		GCG ACTC GGTCTCAAACCT		
		A G I		
GAM75	SAS	TCACCTGAGGTCAGGAGTTTCGAGA 892	I	
		TCGCCTGAGGTCGGGAGTTTGAGA		

		AGTGGACTCCAGTCCTCAAGCTCT	
GAM75	SAS	TCACCTGAGGTCAGGAGTTGAGA 892	
		CGCCTGAGGTCGGGAGTTTGAG	
		GTGGACTCCAGTCCTCAAGCTC	
GAM75	SCML2	TCACCTGAGGTCAGGAGTTTGAGA 893	
		TCGCCTGAGGTCGGGAGTTTGAGA	
		AGTGGACTCCAGTCCTCAAACCTCT	
GAM75	SCML2	TCACCTGAGGTCAGGAGTTTGAGA 893	
		CGCCTGAGGTCGGGAGTTTGAG	
		GTGGACTCCAGTCCTCAAACCTC	
GAM75	SIL	TCACCTGAGGTCGGGAGTTTGAGA 896	
		TCGCCTGAGGTCGGGAGTTTGAGA	
		AGTGGACTCCAGCCCTCAAACCTCT	
GAM75	SIL	TCACCTGAGGTCGGGAGTTTGAGA 896	
		CGCCTGAGGTCGGGAGTTTGAG	
		GTGGACTCCAGCCCTCAAACCTC	
GAM75	SPN	TCACCTGAGGTCAGGAGTTTGAGA 893	
		TCGCCTGAGGTCGGGAGTTTGAGA	
		AGTGGACTCCAGTCCTCAAACCTCT	
GAM75	SPN	TCACCTGAGGTCAGGAGTTTGAGA 893	
		CGCCTGAGGTCGGGAGTTTGAG	
		GTGGACTCCAGTCCTCAAACCTC	
GAM75	SULT2B1	TCACCTGAGGTCAGGAGTTTGAGA 893	
		TCGCCTGAGGTCGGGAGTTTGAGA	
		AGTGGACTCCAGTCCTCAAACCTCT	
GAM75	SULT2B1	TCACCTGAGGTCAGGAGTTTGAGA 893	
		CGCCTGAGGTCGGGAGTTTGAG	
		GTGGACTCCAGTCCTCAAACCTC	
GAM75	TAT	GCCTGAGGTCAGGAGTTTGAGA 884	
		CCTGAGGTCGGGAGTTTGAG	

		GGACTCCAGTCCTCAAAC			
		I			
GAM75	TAT	GCCTGAGGTCAGGAGTTTGAGA	884	TCGC	
		CTGAGGTCGGGAGTTTGAGA			
		GACTCCAGTCCTCAAAC			
GAM75	TES	CTGAGGTCAGGAGTTTGAGA	881		I
		TGAGGTCGGGAGTTTGAG			
		ACTCCAGTCCTCAAAC			
		I			
GAM75	TES	CTGAGGTCAGGAGTTTGAGA	881	TCGCCTGA	
		GGTCGGGAGTTTGAG			
		CCAGTCCTCAAAC			
GAM75	TNFRSF10B	TCACCTGAGGTCAGGAGTTTCGAGA	892		I
		CGCCTGAGGTCGGGAGTTTGAG			
		GTGGA			
		I			
GAM75	TNFRSF10B	TCACCTGAGGTCAGGAGTTTCGAGA	892		I
		TCGCCTGAGGTCGGGAGTTTGAGA			
		AGTGGA			
		I			
GAM75	TP53	TCGCCTGAGCCCAGGAGTTTGAGA	903	G	I
		TCGCCTGAG TCGGGAGTTTGAGA			
		AGCGGACTC GGTCTCAAAC			
		G			
		I			
GAM75	TP53	TCGCCTGAGCCCAGGAGTTTGAGA	903	G	I
		CGCCTGAG TCGGGAGTTTGAG			
		GCGGACTC GGTCTCAAAC			
		G			
		I			
GAM75	VHL	TCACCTGAGGTCAGGAGTTTGA	888		GA
		TCGCCTGAGGTCGGGAGTTTGA			
		AGTGGA			
		II			
GAM75	VHL	TCACCTGAGGTCAGGAGTTTGA	888		I
		CGCCTGAGGTCGGGAGTTTG			
		GTGGA			
		I			
GAM75	WARS	GCCTGAGGTCAGAGGA-TTTG	882	AGTTTII	
		GCCTGAGGTCGGG			

		CGGACTCCAGTCT			
		CCTAAAC			
GAM75	WARS	GCCTGAGGTCAGAGGA-TTTG	882	TCGC	_ AG AG
		CTGAGGTCGG G TTTG			
		I			
		GACTCCAGTC C AAAC			
		_____ T CT AA			
GAM75	ZNF133	TCACCTGAGGTCAGCAGTT	887	G	TGAG
		TCGCCTGAGGTCGG AGTT			
		AGTGGACTCCAGTC TCAA			
		G IIIA			
GAM75	ZNF133	TCACCTGAGGTCAGCAGTT	887	G	II
		TCGCCTGAGGTCGG AGT			
		AGTGGACTCCAGTC TCA			
		G AI			
GAM76	ADORA2A	TGTCACCTCTGGGC-CCAGC	917	TGA	C T CCT
		CACCTCTGG C CCAGC			
		I			
		GTGGAGACC G GGTGC			
		ACA C _ III			
GAM76	BSN	TGACCCC-CTAGC-TCCAGCCC	918	A C	T
		TGAC CCTCTGGC TCCAGCCC			
		ACTG GGGGATCG AGGTCGGG			
		_ _ I			
GAM76	CCNF	CACCCTTCGCCTCCAGCCC	910	TGACA	CTG
		CCT GCCTCCAGCCCT			
		GGA CGGAGGTCGGGG			
		_____ AG_			
GAM76	EN2	TGAGACCT--GGCCTCCATGCC	915	C CT	_ TG
		TGA ACCT GGCCTCCA GCCC			
		ACT TGGA CCGGAGGT CGGG			
		C _ A II			
GAM76	EPHA2	TGACACCCTCTGTCC-CCAGCCCTG	914	_ GC	I
		TGACACC TCTG CTCCAGCCCTG			
		ACTGTGG AGAC GGGGTCGGGAC			
		G A_ I			
GAM76	FGFR3	TGACACCTCTGGCCACCATGCACTG	916	T _ C	II
		TGACACCTCTGGCC CCA GC CTG			
		ACTGTGGAGACCGG GGT CG GAC			
		T A T II			
GAM76	GARP	ACACCT-TGGCCTCCAGGCCT	907	TGAC C	C
		ACCT TGGCCTCCAG CCT			

		TGGA ACCGGAGGTC GGA		
		_____ C		
GAM76	LNK	CACCACTGCACTCCAGCCC	908	TGACACCTCTG _ T
		GC CTCCAGCCC		
		CG GAGGTCGGG		
		GTGA_____ T C		
GAM76	PLXNA1	GACACCGCTGGCCTCCAGTCCCT	912	TG T _ GI
		ACACC CTGGCCTCCAG CCCT		
		TGTGG GACCGGAGGTC GGGA		
		_____ C A GI		
GAM76	POU2F2	CACCACTGGCCTCCTGCC	909	TGACACCT A
		CTGGCCTCC GCCCT		
		GACCGGAGG CGGGG		
		GT_____ A		
GAM76	RET	CCTCTTCCCCTCCAGCCCTG	911	TGACACCTCTGG
		CCTCCAGCCCT		
		GGAGGTCGGGA		
		AGG_____		
GAM76	XRCC3	GACACCCCAGGC-TCCAGCCCTG	913	TG T C
		ACACCTC GGC TCCAGCCCTG		
		TGTGGGG CCG AGGTCGGGAC		
		_____ T _		
GAM77	ABCB4	ATCATCCTGCATTCCTC-TCTT	921	_ GC G GG
		ATCATCCTG GT CCTC TCTT		
		TAGTAGGAC TA GGAG AGAA		
		G A_ _ II		
GAM77	ABCB4	ATCATCCTGCATTCCTC-TCTT	921	_ _ GC G I
		TCATCCTG GT CCTC TCT		
		AGTAGGAC TA GGAG AGA		
		T G A_ _ I		
GAM77	AQP6	TCCTGGTGCCTTGGCCGTTCTTG	935	C_ _ IIIC
		TCCTGGTGCC TCGT CTT		
		AGGACCACGG GGCA GAA		
		AACC A CIII		
GAM77	AQP6	TCCTGGTGCCTTGGCCGTTCTTG	936	CTC TTIIIC
		TCCTGGTGCC GTC		
		AGGACCACGG CGG		
		AAC CAAGGA		
GAM77	BCL7A	CCTGGTG-CCTGGTGCTTG	926	CTC _ II
		CCTGGTGCC GT CTTG		

		GGACCACGG CA GAAC		
		AC_ C CI		
GAM77 BLTR2		TCATCCTGG-G-CCTC-TCCTGG 932	T _ GTCTI	
		TCATCCTGG GCC CTC		
		III III		
		AGTAGGACC CGG GAG		
		_ A GACCI		
GAM77 BLTR2		TCATCCTGG-G-CCTC-TCCTGG 932 AT	T C G	
		CATCCTGG GCC TC TCTTG		
		III II		
		GTAGGACC CGG AG AGGAC		
		— — — —		
GAM77 CACNA1D		CCTGGTGCCCTGGTACATGG 927	C CTTGII	
		CCTGGTGCCCT GT		
		II		
		GGACCACGGGA CA		
		C TGTACC		
GAM77 COX6A1		CCTGGTGCCCGGGTAGTGG 929	TCGTCTTGII	
		CCTGGTGCCC		
		GGACCACGGG		
		CCCATCACCI		
GAM77 FKRP		TCGTCCTGGTGCTCTCCTCCTG 931 ATCA	C G G	
		TCCTGGTGC CTC TCTTG		
		III		
		AGGACCACG GAG AGGAC		
		GC_ A G G		
GAM77 FKRP		TCGTCCTGGTGCTCTCCTCCTG 931 CA	C G I	
		TCCTGGTGC CTC TCTT		
		III		
		AGGACCACG GAG AGGA		
		GC A G I		
GAM77 GAS		CCTGGTGCCCTCTCAGGTCT 925	_ TCIII	
		CCTGGTGCC CTCG		
		GGACCACGG GAGT		
		A CCAGA		
GAM77 IHPK2		TCCGTGTGTCCCTCTCGTCTTGG 933 ATCATCCTG G _	I	
		GT CC CTCGTCTTGG		
		II II		
		CA GG GAGCAGAACC		
		ACA_____ G A G		
GAM77 IHPK2		TCCGTGTGTCCCTCTCGTCTTGG 933 CCTG G _	I	
		GT CC CTCGTCTTGG		
		II II		
		CA GG GAGCAGAAC		
		ACA_ G A I		
GAM77 LEP		CATCCTGGTGGCCTGGCCTGGG 924	C C TGI	
		ATCCTGGTG CCT GTCT		
		III		

		TAGGACCAC GGA CGGA		
		C C CCI		
GAM77 LEP		CATCCTGGTGGCCTGGCCTGGG 924 ATCA C C T		
		TCCTGGTG CCT GTCT GG		
		AGGACCAC GGA CGGA CC		
		_____ C C C		
GAM77 MGAT4B		CCTGGTGCCTGTGTCTCTGG 928 CTC GII		
		CCTGGTGCC GTCTT		
		GGACCACGG CAGAG		
		ACA ACC		
GAM77 PRKCABP		ATGACCCTGGTG-CCT-GTCCTGG 922 ATC CTC		
		ATCCTGGTGCC GTCTTGG		
		TGGGACCACGG CAGGACC		
		TAC A_		
GAM77 PRKCABP		ATGACCCTGGTG-CCT-GTCCTGG 922 TC_ CTC I		
		ATCCTGGTGCC GTCTTG		
		TGGGACCACGG CAGGAC		
		TAC A_ I		
GAM77 SLA		TCCTGGTGCCCT-TTCTTG 937 CG I		
		TCCTGGTGCCCT TCTT		
		AGGACCACGGGA AGAA		
		A_ C		
GAM77 SLA		TCCTGGTGCCCT-TTCTTG 937 ATCATCCT CG		
		GGTGCCCT TCTT		
		CCACGGGA AGAA		
		_____ A_		
GAM77 SUV39H2		CATCCTGGTCCCATCATCATG 923 G TC_ TTI		
		ATCCTGGT CCC GTC		
		TAGGACCA GGG TAG		
		_ TAA TAI		
GAM77 SUV39H2		CATCCTGGTCCCATCATCATG 923 ATCA G TC_ T G		
		TCCTGGT CCC GTC TG		
		AGGACCA GGG TAG AC		
		_____ _ TAA T A		
GAM77 SYN3		TCAGCCT--TGGCCTCGTCTT 930 _ T _ TGC I		
		CA CCT GG CCTCGTCT		
		GT GGA CC GGAGCAGA		
		A C A _ I		
GAM77 SYN3		TCAGCCT--TGGCCTCGTCTT 930 AT T _ TGC G		
		CA CCT GG CCTCGTCTT		

		GT GGA CC GGAGCAGAA		
		__ C A __ G		
GAM77	ZNF146	TCCTGGTGCCTCTCAAGTCCTGG	934	CCT _ _ I
		GGTGCC CTC GTCTTG		
		CCACGG GAG CAGGAC		
		__ A TT I		
GAM78	ABCA1	AAACACAA--GTTGTGTTTTTC	940	_ TC G CC
		AAAC CAA GTTGTGTTT TC		
		TTTG GTT CAACACAAA AG		
		T __ A II		
GAM78	ABCA1	AAACACAA--GTTGTGTTTTTC	940	_ TC GI
		AAC CAA GTTGTGTTT		
		TTG GTT CAACACAAA		
		T __ AA		
GAM78	BBS4	AATCTAATATTTGTGTTTG	946	AAACCAATCG TCCC
		TTGTGTTTG		
		AACACAAAC		
		TTAGATTATA IIIC		
GAM78	CALM1	AAACCAATTTTAAATGTGTTTGT	944	CGT__ CCCC
		AAACCAAT TGTGTTTGT		
		TTTGTTA ACACAAACA		
		AAATTT IIIC		
GAM78	CFTR	AAACAATATAGTTGTGTTT	941	AAAC C__ GTCCC
		CAAT GTTGTGTTT		
		GTTA CAACACAAA		
		TTT_ TAT IIIC		
GAM78	ENAM	CAA-CGTTGTGTT--TCCCC	950	T G I
		CAA CGTTGTGTTT TCC		
		GTT GCAACACAAA GGG		
		_ G I		
GAM78	FOXG1B	CAATCGTTAATTTTGTCCCC	951	TG I
		AATCGTTG TTTGTCCC		
		TTAGCAAT AAACAGGG		
		TA I		
GAM78	FOXG1B	CAATCGTTAATTTTGTCCCC	951	AAACCAAT TG
		CGTTG TTTGTCCC		
		GCAAT AAACAGGG		
		_____ TA		
GAM78	KLHL1	AAAACAATCCTTTGTGTTTG	945	AAAC G_ TCCC
		CAATC TTGTGTTTG		

		GTTAG AACACAAAC		
		TTTT GA IIIC		
GAM78 KLHL1		AAAACAATCCTTTGTGTTTG 945 AAAC G_ II		
		CAATC TTGTGTTT		
		GTTAG AACACAAA		
		TTTT GA CI		
GAM78 LANCL1		AAACCAAACCTCTAATTGTGTTTGT 942 AACCAATC I		
		GTTGTGTTTG		
		TAACACAAAC		
		TTTGAGAT I		
GAM78 LANCL1		AAACCAAACCTCTAATTGTGTTTGT 942 _ _ CCCI		
		AAACCAA TC GTTGTGTTTGT		
		II		
		TTTGTT AG TAACACAAACA		
		TG AT IIIC		
GAM78 PBX2		ACCA---GTTCTGTTTGTCCCC 949 _ ATC G		
		CCA GTT TGTTTGTCCC		
		GGT CAA ACAAACAGGG		
		T _ G		
GAM78 PBX2		ACCA---GTTCTGTTTGTCCCC 949 AAACCAATC G		
		GTT TGTTTGTCCC		
		CAA ACAAACAGGG		
		GT_____ G		
GAM78 SCML1		AAACCAATCTACAGATTGTTTCTTGTCC943 _____ G_ CCII		
		AAACCAATC GTTGT TTTGTCC		
		TTTGTTAG TAACA GAACAGG		
		ATGTC AA IIIC		
GAM78 SCNN1A		ACCCTTGTTGTGTTTTGTCC 948 AAA AATC _ CC		
		CC GTTGTGTTT GTCC		
		GG CAACACAAA CAGG		
		_ AAC_ A AC		
GAM78 SCNN1A		ACCCTTGTTGTGTTTTGTCC 948 CCAATC _ I		
		GTTGTGTTT GTC		
		CAACACAAA CAG		
		GGAAC_ A I		
GAM78 TNS		ACCCATAGCTTGGTTGTTTGTCCC 947 AAA ATCG _ CI		
		CCA TTG TGTTTGTCCC		
		GGT AAC ACAAACAGGG		
		_ ATCG CA AG		
GAM78 TNS		ACCCATAGCTTGGTTGTTTGTCCC 947 CCAATCGTTG I		
		TGTTTGTCC		

		ACAAACAGG			
		TATCGAACCA I			
GAM79 ABR	GGGAGCCGGGGGAGGCCGAA	959	A_ _	CAIII	
	GGGA CGGGG AGGCC				
	CCCT GCCCC TCCGG				
	CG C CTTII				
GAM79 ABR	GGGAGCCGGGGGAGGCCGAA	959	T AAC	CAACCCT	
	GGG GGGGAGGCC				
	CTC CCCCTCCGG				
	C GGC CTTCIII				
GAM79 ADCY8	GGGAA---GGAGGCCCAGAACCT	961	ACG _	I	
	GGGA GGGAGGCCCA ACC				
	CCCT TCCTCCGGGT TGG				
	_ CT A				
GAM79 ADCY8	GGGAA---GGAGGCCCAGAACCT	961	TG ACG _	CT	
	GGA GGGAGGCCCA ACC				
	CCT TCCTCCGGGT TGG				
	_ _ CT AA				
GAM79 CDKN2D	TGGGAGCCGGG---CCCAACCCT	970	A_ GGAG		
	TGGGA CGG GCCCAACCCT				
	ACCCT GCC CGGGTTGGGA				
	CG _				
GAM79 CDKN2D	TGGGAGCCGGG---CCCAACCCT	970	_ A_ GGAG		
	GGGA CGG GCCCAACCC				
	CCCT GCC CGGGTTGGG				
	A CG _				
GAM79 CHRNA4	TGGGA-CGCAGAG-CCCAACCC	969	A G G T		
	TGGGA CG GGAG CCCAACCC				
	ACCCT GC TCTC GGGTTGGG				
	_ G _ I				
GAM79 CHRNA4	TGGGA-CGCAGAG-CCCAACCC	969	_ A G G I		
	GGGA CG GGAG CCCAACC				
	CCCT GC TCTC GGGTTGG				
	A _ G _ I				
GAM79 CTF1	TGGGTAAAGGGGGAGGCCAAA	964	AAC_	CAACCCT	
	TGGG GGGGAGGCC				
	ACCC CCCCTCCGG				
	ATTTC TTTIIT				
GAM79 CTF1	TGGGTAAAGGGGGAGGCCAAA	964	AAC_	CAIII	
	TGGG GGGGAGGCC				

		ACCC CCCCTCCGG				
		ATTTC TTTII				
GAM79	CTF1	GGGACAGGGCTGAGGCCCAA	960	A	___	III
		GGGA CGGGG AGGCCCA				
		CCCT GTCCC TCCGGGT				
		_ GAC TII				
GAM79	CTF1	GGGACAGGGCTGAGGCCCAA	960	TG A	___	CCCT
		GGA CGGGG AGGCCCAA				
		CCT GTCCC TCCGGGTT				
		___ _ GAC TIII				
GAM79	DGKG	GAA-GTGGAGGCCAGCCC	954	GAACGG		A I
		GGAGGCCCA CC				
		CCTCCGGGT GG				
		CTTCA_ C G				
GAM79	DPP6	GGAAAGGGAAACAAGGCCCAACCC	956	GAAC	___	I
		GGG GAGGCCCAACC				
		CCC TTCCGGGTTGG				
		___ TTTG I				
GAM79	DPP6	GGAAAGGGAAACAAGGCCCAACCC	956	T__	CG G	II
		GGGAA G GAGGCCCAACCCT				
		CCCTT T TTCCGGGTTGGGG				
		TTT _ G TI				
GAM79	FE65L2	TGGGTCCGGGGGAGGCCCA	965	AA	_	ACCC
		TGGG CGGGG AGGCCCA				
		ACCC GCCCC TCCGGGT				
		AG C IIIT				
GAM79	FE65L2	TGGGTCCGGGGGAGGCCCA	965	AA	_	II
		TGGG CGGGG AGGCCC				
		ACCC GCCCC TCCGGG				
		AG C TI				
GAM79	GTF2F1	GAGCGAGGAC-CCCAACCCT	955	AA_	GG	I
		CGGGGA CCCAACC				
		GCTCCT GGGTTGGG				
		CTC G_ I				
GAM79	GTF2F1	GAGCGAGGAC-CCCAACCCT	955	TGGGAA		GG
		CGGGGA CCCAACC				
		GCTCCT GGGTTGGG				
		_____ G_				
GAM79	IRS2	GGGAAGGTCCGGGGAGGCC	958	_____		IIIG
		GGGAA CGGGGAGGCC				

		CCCTT GCCCCTCCGG			
		CCAG GIII			
GAM79 IRS2		GGGAAGGTCCGGGGAGGCC	958 T__ AA		AACCCT
		GGG CGGGGAGGCC			
		TCC GCCCCTCCGGG			
		CCT AG CIIITC			
GAM79 MAP2K1		TGGGAA---GGAGGCCCAA	967 ACG		
		TGGGA GGGAGGCCA			
		ACCCT TCCTCCGGGT			

GAM79 MAP2K1		TGGGAA---GGAGGCCCAA	967 ACG		CC
		TGGGA GGGAGGCCAA			
		ACCCT TCCTCCGGGTT			
		_____ II			
GAM79 MYO15A		GGGAA--GGGAGGCCAGCCC	962 AC		ACI
		GGGA GGGGAGGCCA			
		CCCT TCCCTCCGGGT			
		_____ CGG			
GAM79 MYO15A		GGGAA--GGGAGGCCAGCCC	962 TG AC		A
		GGA GGGGAGGCCA CCC			
		CCT TCCCTCCGGGT GGG			
		_____ C			
GAM79 NCF4		TGGGA--GGGGAGGCCACGAGCCT	966 AC		CAAC_ I
		TGGGA GGGGAGGCC CCT			
		ACCCT CCCCTCCGG GGA			
		_____ TGCTC I			
GAM79 NCF4		TGGGA--GGGGAGGCCACGAGCCT	966 _ AC		CAACCCI
		GGGA GGGGAGGCC			
		CCCT CCCCTCCGG			
		A _ TGCTCGG			
GAM79 SLC1A4		GGGAA---GGAGGCCCATCTCT	963 ACG		ACI
		GGGA GGGAGGCCA			
		CCCT TCCTCCGGGT			
		_____ AGA			
GAM79 SLC1A4		GGGAA---GGAGGCCCATCTCT	963 TG ACG		ACCC
		GGA GGGAGGCCA			
		CCT TCCTCCGGGT			
		_____ AGAG			
GAM79 SMARCA5		GGGATGGACGGGGAGGCCTAGGCCT	957 _ A		CAA_ CI
		GGA CGGGGAGGCC CC			

		CCT GCCCCTCCGG GG		
		A _ ATCC II		
GAM79	SMARCA5	GGGATGGACGGGGAGGCCTAGGCCT 957 TG__ A CAAC II		
		GGA CGGGGAGGCC CCT		
		CCT GCCCCTCCGG GGA		
		CCTA _ ATCC CI		
GAM79	WHSC1	TGAGAA---GTAGGCCCAACCC 968 AC GG		
		TGGGA GG AGGCCCAACCC		
		ACTCT TC TCCGGGTTGGG		
		_ A_		
GAM79	WHSC1	TGAGAA---GTAGGCCCAACCC 968 _ AC GG		
		GGGA GG AGGCCCAACC		
		CTCT TC TCCGGGTTGG		
		A _ A_		
GAM80	ACCN1	TGATCGAA--TTTCAGAGA 992 AG GGT		
		TGATTGA ATTCAGAGA		
		ACTAGCT TAAAGTCTCT		
		_		
GAM80	ADH7	GATACATGATTTTCAGATGAGG 985 TGATTGAA _ TCA		
		GATTTTCAGA GAGG		
		CTAAAGTCT CTCC		
		TATGTA_ A CII		
GAM80	BCL11B	GAATGTAGGTTTCAGAGAG 986 TGAT A A GTC		
		TG AG TTTCAGAGAG		
		AC TC AAAGTCTCTC		
		TT_ A C GII		
GAM80	COMT	TTGCAG--TTCAGAGAGGT 995 TGATTGAAGAT		
		TTCAGAGAGGT		
		AAGTCTCTCCA		
		GTC_____		
GAM80	DAZ	AGCCTGAACGTG-CTGA-GTTAC 976 CTTATGTCTI		
		AGCCTGAACGTGT		
		TCGGA CTTGACG		
		ACTCAATGI		
GAM80	DAZ	AGCCTGAACGTG-CTGA-GTTAC 976 CA CTTATGTCAC		
		GCCTGAACGTGT		
		CGGA CTTGACG		
		_ ACTCAATGTI		
GAM80	DAZ	CAGACTGAACGTG-CTGA-GTTAC 982 C CTTATGTCAC		
		CAG CTGAACGTGT		

		GTC GACTTGCACG			
		T ACTCAATGII			
GAM80	DAZ	CAGACTGAACGTG-CTGA-GTTAC	982	C	CTTATGTCT
		CAG CTGAACGTGT			
		GTC GACTTGCACG			
		T ACTCAATGI			
GAM80	DCX	TGAATCACAATTTTCAGAGTAGGT	991	TTGAA	_ CAI
		TGA GATTTTCAGAG AGGT			
		ACT TTAAAGTCTC TCCA			
		TAGTG A			
GAM80	DPYSL3	GCCTGTTTGATGTGTCTTATG	987	AAC__	
		GCCTG GTGTCTTAT			
		CGGAC CACAGAATA			
		AAACTA CII			
GAM80	DPYSL3	GCCTGTTTGATGTGTCTTATG	987	CAGCCTGAAC	TCAC
		GTGTCTTATG			
		CACAGAATAC			
		GACAACTA_ TTII			
GAM80	GABRP	CTGTAACGTGTCTCATTGTTAC	983	CAGCCTG	_ CAC
		AACGTGTCTTAT GT			
		TTGCACAGAGTA CA			
		_____ A ATG			
GAM80	GABRP	CTGTAACGTGTCTCATTGTTAC	983	TG	_ CAI
		AACGTGTCTTAT GT			
		TTGCACAGAGTA CA			
		A_ A ATI			
GAM80	GPD2	ATTCATTATTTTCAGAGTGGT	978	TGATTGAAG	A C
		ATTTTCAGAG GGT			
		TAAAGTCTC CCA			
		AGTAA_ A A			
GAM80	GPR17	CAGCCTGAAATGTGTGGCCTGTGTC	980	C_ _ A	ACII
		CAGCCTGAA GTGT CTT TGTC			
		GTCGGAATT CACA GGA ACAG			
		TA CC C IIIC			
GAM80	HEM1	TGTTTGA-GATT-CAGAGAGG	993	A A T	TC
		TG TTGA GATT CAGAGAGG			
		AC AACT CTAA GTCTCTCC			
		A _ _ II			
GAM80	HSPD1	TGTAGTTAACAGAGAGGTCA	988	TGATTGAAGATTT	
		CAGAGAGGTCT			

		GTCTCTCCAG		
		CAATT_____		
GAM80	IL1RAPL2	GAAGATTTCTAGAGTTCA	984	TGATTGA T _ GGT
		AGA TTCAG AGA		
		TCT AAGTC TCT		
		AAAGA_ C G		
GAM80	LRP1	AGCCTTGCGCAAAGTGTCTTAT	973	GAAC_____
		AGCCT GTGTCTTA		
		TCGGA CACAGAAT		
		ACCGTTT A		
GAM80	LRP1	AGCCTTGCGCAAAGTGTCTTAT	973	CA GAAC_____ TCAC
		GCCT GTGTCTTATG		
		CGGA CACAGAATAT		
		_ ACCGTTT C		
GAM80	MCP	ATTGAAGATTTTAATAGA-GTCA	977	TGAT CAG_ G
		TGAAGATTT AGAG TCA		
		ACTTCTAAA TCTC AGT		
		_ ATTA _		
GAM80	MFAP3	TGACTGAAAAGTATCAGAGAGG	990	TT_ TCA
		TGATTGAAGA TCAGAGAGG		
		ACTGACTTTT AGTCTCTCC		
		CAT		
GAM80	PMX1	AGCAGGATAGGTGTCTTATG	974	CA CT AC_ TCA
		GC GA GTGTCTTATG		
		CG CT CACAGAATAC		
		_ TC ATC C		
GAM80	PMX1	AGCAGGATAGGTGTCTTATG	974	CT AC_
		AGC GA GTGTCTTAT		
		TCG CT CACAGAATA		
		TC ATC CI		
GAM80	PPP1CC	TGACTGAGAAAGATTTACGAGA	989	_____ GGTCAI
		TGATTGA AGATTTCA GAGA		
		ACTGACT TCTAAAGT CTCT		
		CTT G ACT		
GAM80	RECQL5	AGCCT--ACGGGCTGTCTTATGTCA	975	CA AAC_ CI
		GCCTG G TGTCTTATGTCA		
		CGGAT C ACAGAATACAGT		
		_ GCC G CI		
GAM80	RECQL5	AGCCT--ACGGGCTGTCTTATGTCA	975	G AAC_ I
		CCTG G TGTCTTATGTC		

		GGAT C ACAGAATACAG		
		_ GCC G I		
GAM80	SCN3A	TTGCAG-TGACAGAGAGGTCA	996	TGATTGAAGATTT
		CAGAGAGGTC		
		GTCTCTCCAG		
		GTCACT_____		
GAM80	SLC1A1	TTGTAGATTTTCAGATGTAGGTC	994	TGATTGA G_ A
		AGATTTTCAGA AGGTC		
		TCTAAAGTCT TCCAG		
		A_____ ACA C		
GAM80	USP9Y	CACCCTGCATGTGTCTTAT	981	G AAC GTCA
		CA CCTG GTGTCTTAT		
		GT GGAC CACAGAATA		
		G GTA IIC		
GAM80	USP9Y	CACCCTGCATGTGTCTTAT	981	G AAC II
		CA CCTG GTGTCTTA		
		GT GGAC CACAGAAT		
		G GTA AI		
GAM80	WBSCR1	ATTGAAGATGTAAG-TAGGTCA	979	TGAT TTCA _
		TGAAGAT GAG AGGTCA		
		ACTTCTA TTC TCCAGT		
		_____ CA_ A		
GAM81	ABCB6	CAGGATGAAATAAGCCAGG	1011	CAT II
		CAGGATGAAAT CTAG		
		GTCCTACTTTA GGTC		
		TTC CI		
GAM81	CCND1	AGGGGCAGGGGATAAGAATTCATC	999	AT_____ A TAGGI
		AGGGGCAGG GAA TCATC		
		TCCCCGTCC CTT AGTAG		
		CCTATT A IIIGG		
GAM81	CCND1	AGGGGCAGGGGATAAGAATTCATC	999	C_ GAA AI
		AGGGG AGGAT ATC		
		TCCCC TCTTA TAG		
		TAT AG_ II		
GAM81	DGAT2	AGGGGCAAAAAGTGAATCATCTA	1003	_ A GGI
		AGGGGCAGGA TGAA TCATCTA		
		TCCCCGTTTT ACTT AGTAGAT		
		TC _ III		
GAM81	DGAT2	AGGGGCAAAAAGTGAATCATCTA	1003	G _ A I
		GGGCAGGA TGAA TCATCT		

		CCCGTTTT ACTT AGTAGA		
		— TC — I		
GAM81	DUSP5	AGGGGCAGGGAGGAAAACA 1000	AT_	T TCTAG
		AGGGGCAGG GAAA CA		
		TCCCCGTCC CTTT GT		
		CTC T III GG		
GAM81	DUSP5	AGGGGCAGGGAGGAAAACA 1000	AT_	TCII
		AGGGGCAGG GAAA		
		TCCCCGTCC CTTT		
		CTC TGTI		
GAM81	ENTPD6	CAGGATGAAGTCACGTCCAGG 1010	A _	III
		CAGGATGAA TCA TCTAG		
		GTCCTACTT AGT AGGTC		
		C GC CII		
GAM81	EPB49	AGGGGCAGGTGAGGAAAGCAGCTGGG 1001	AT__	T T A II
		AGGGGCAGG GAAA CA CT GG		
		TCCCCGTCC CTTT GT GA CC		
		ACTC C C C II		
GAM81	EPB49	AGGGGCAGGTGAGGAAAGCAGCTGGG 1001 G	AT__	T T AGI
		GGCAGG GAAA CA CT		
		CCGTCC CTTT GT GA		
		— ACTC C C CII		
GAM81	FAAH	AGGGGCAGGA--ACCTCATCT 1005	TGAAA	AG
		AGGGGCAGGA TCATCT		
		TCCCCGTCCT AGTAGA		
		TGG__ II		
GAM81	FAAH	AGGGGCAGGA--ACCTCATCT 1005 _	TGAAA	I
		GGGGCAGGA TCATC		
		CCCCGTCCT AGTAG		
		T TGG__ I		
GAM81	GABRE	GGGGCAGGA--AAAAC-TCTAG 1016	T A	ATCI
		GGGGCAGGA GAA TC		
		CCCCGTCCT TTT AG		
		T G ATCI		
GAM81	GABRE	GGGGCAGGA--AAAAC-TCTAG 1016 AG	T	CA
		GGGCAGGA GAAAT TCTAG		
		CCCGTCCT TTTTG AGATC		
		— — —		
GAM81	ICA1	AGGGGCAGGAAAAAAGCAT 1004	T T	CTAG
		AGGGGCAGGA GAAA CAT		

		TCCCCGTCCT TTTT GTA		
		T C III G		
GAM81	ICA1	AGGGGCAGGAAAAAAGCAT 1004	T TCAII	
		AGGGGCAGGA GAAA		
		TCCCCGTCCT TTTT		
		T CGTAI		
GAM81	IGBP1	GCTGGTTCATATCATCTAGG 1012	AGGGGCAGGATGAA	
		ATCATCTAG		
		TAGTAGATC		
		CAAGTA_____		
GAM81	IGBP1	GCTGGTTCATATCATCTAGG 1012	CA ATGAA I	
		GG ATCATCTAG		
		CC TAGTAGATC		
		GA AAGTA I		
GAM81	KLHL3	AGGGGCAGG--GAATTCACCTA 1006	AT A G	
		AGGGGCAGG GAA TCATCTA		
		TCCCCGTCC CTT AGTGGAT		
		_ A I		
GAM81	KLHL3	AGGGGCAGG--GAATTCACCTA 1006_	AT A I	
		GGGGCAGG GAA TCATCT		
		CCCCGTCC CTT AGTGGA		
		T _ A I		
GAM81	LCP1	AGGCGGAGGGGGGAAATCATCTGAGG 1002	_ C AT_ _ II	
		AGG GG AGG GAAATCATCT AGG		
		TCC CC TCC CTTTAGTAGA TCC		
		G _ CCC C II		
GAM81	LCP1	AGGCGGAGGGGGGAAATCATCTGAGG 1002	_ CA AT AGI	
		GGGG GG GAAATCATCT		
		CCTC CC CTTTAGTAGA		
		G CC _ CTC		
GAM81	MKI67	GGACTGGATGAAATGATCTTGG 1015	A C AGI	
		GGC GGATGAAAT ATCT		
		CTG CCTACTTTA TAGA		
		A C ACI		
GAM81	MKI67	GGACTGGATGAAATGATCTTGG 1015	AGGGGCA C A	
		GGATGAAAT ATCT GG		
		CCTACTTTA TAGA CC		
		TGA_____ C A		
GAM81	MX2	CAGGATGGAGAAATCATCT 1008	_____	
		CAGGAT GAAATCATC		

		GTCCTA CTTTAGTAG			
		CCT AII			
GAM81	PKIA	CAGGAAGAATCATCATCTAGG	1009	T _	III
		CAGGA GAA ATCATCTAG			
		III			
		GTCCT CTT TAGTAGATC			
		T AG CII			
GAM81	PKIA	CAGGAAGAATCATCATCTAGG	1009	AGGGGCA	TGAA
		GGA ATCATCTAGG			
		III			
		TCT TAGTAGATCC			
		_____ TAG_			
GAM81	SNX1	GGCAGGATG-CATCA-CTAGG	1014	AA	CTAI
		GGCAGGATG ATCAT			
		III			
		CCGTCCTAC TAGTG			
		G_ ATCC			
GAM81	SNX1	GGCAGGATG-CATCA-CTAGG	1014	AGGGGC	AA T
		AGGATG ATCA CTAG			
		III			
		TCCTAC TAGT GATC			
		_____ G_ _			
GAM81	TSGA10	GGCTGGTT-AAATCATCTA	1013	A ATG	I
		GGC GG AAATCATCT			
		III II			
		CCG CC TTTAGTAGA			
		A AA_ T			
GAM81	TSGA10	GGCTGGTT-AAATCATCTA	1013	AGGGGCA	ATG
		GG AAATCATCTA			
		II			
		CC TTTAGTAGAT			
		A_____ AA_			
GAM81	VIPR1	AGAGTCAGGATGAAAGTATGTAG	1007	G	TC C GI
		AGGG CAGGATGAAA AT TAG			
		II			
		TCTC GTCCTACTTT TA ATC			
		A CA C II			
GAM81	VIPR1	AGAGTCAGGATGAAAGTATGTAG	1007	_	TCATCTAI
		GGG CAGGATGAAA			
		III			
		CTC GTCCTACTTT			
		A CATACAII			
GAM82	APLP2	GTCAGTGCCTTTGGAGAAAG	1024	_____ ATG	ATAAC
		TGTC TTTGGAGAAAG			
		III			
		ACGG AAACCTCTTTC			
		AGTC _____ AIIIA			
GAM82	CPO	ATGTTCTCTGGAGAAAGATA	1019	TGTCATG	AC
		TTTGGAGAAAGATA			

		AGACCTCTTTCTAT		
		AG_____AT		
GAM82	DAPP1	ATGTT-GGATAAAGATAAC	1020	TGTCATGTT G
		TGGA AAAGATAA		
		ACCT TTTCTATT		
		_____A		
GAM82	GUCY1A3	TGTCATGTAAACAGGAGAAAGAT	1028	T_____AACAI
		TGTCATGTT GGAGAAAGAT		
		ACAGTACAA CCTCTTTCTA		
		TTTGT IIIAC		
GAM82	MCM2	CAGGCTTGGAGAAACA-AACA	1023	TGTCAT GAT
		GTTTGGAGAAA AAC		
		CGAACCTCTTT TTG		
		_____GT_		
GAM82	MS4A1	TGTCAAATTTGGAGAAACAAAA	1033	T GATAACA
		TGTCA GTTTGGAGAAA		
		ACAGT TAAACCTCTTT		
		T GTTTTII		
GAM82	MS4A2	TGTCAGCCCTGTAGAAAGATAA	1034	T GG_ CA
		TGTCA GTTT AGAAAGATAA		
		ACAGT CGGG TCTTTCTATT		
		_ ACA II		
GAM82	NRIP1	TGTCATGTTAGGATGAACAT	1031	T _ AGATAAC
		TGTCATGTT GGA GAA		
		ACAGTACAA CCT CTT		
		T A GTAIIIA		
GAM82	PCDH8	TGTTTCAGGTGAAAGATAA	1036	TGTCATGTTT A C
		GG GAAAGATAA		
		CC CTTTCTATT		
		GT_____A T		
GAM82	PIK3CG	TGCCATGCT-GGAGAAAGCTA	1032	T ATAAC
		TGTCATGTT GGAGAAAG		
		ACGGTACGA CCTCTTTC		
		_ GATII		
GAM82	PPP1R12B	TGTCATGTTAGGAAAGAATTAACA	1035	T A _ I
		TGTCATGTT GG GAAAGA TAACA		
		ACAGTACAA TC CTTTCT ATTGT		
		_ _ TA I		
GAM82	RNTRE	TCAGGTTTTGGAGAAAAACATAAC	1026	TGTCATG ACAI
		TTTGGAGAAAGATA		

		AAACCTCTTTTGT		
		TCCA_____ATTG		
GAM82	SLN	CATCTTTGGAGAACACATAA	1022	TGTCATG AG_ C
		TTTGGAGAA ATAA		
		AAACCTCTT TATT		
		G_____GTG A		
GAM82	SMT3H1	TCATTTTACCTGAACAAAGATAACA	1025	TGTCA TT G II
		TG TGGA AAAGATAACA		
		AT ACTT TTTCTATTGT		
		TAAA_ GG G TA		
GAM82	TDG	TGTCATGTTAGGAAAAACAT	1030	T G AAC
		TGTCATGTT GGAGAAA AT		
		ACAGTACAA CCTTTT TA		
		T G III		
GAM82	TUFT1	CAAGTTTGAAGGAGAAAGA	1021	TGTCA TTT TAAC
		TG GGAGAAAGA		
		AC CCTCTTTCT		
		CAA_ TT_ CTCI		
GAM82	UC28	TCAAGATTG-AGAAAGATCAACA	1027	TGTCATGTTTG _
		GAGAAAGAT AACA		
		CTCTTTCTA TTGT		
		TTCTAA_____G		
GAM82	WHSC1	TGTCATGTT---ACAATGAT	1029	TG___GAAAGATAA
		TGTCATGTT GA		
		ACAGTACAA CT		
		TGTTA AIIIACAAT		
GAM83	ATP1A2	GATTGCAAGGTCTGAAGGGGA	1049	T III
		GATT CAAGGTCTGGGG		
		CTAA GTTCCAGACTTC		
		C CCC		
GAM83	BLAME	TCAAAGTGCAGGGTCTGGGG	1056	T A AGT
		TCAGATT CA GGTCTGGGG		
		AGTTTGA GT CCAGACCCC		
		C C III		
GAM83	BLAME	TCAAAGTGCAGGGTCTGGGG	1056	T A I
		CAGATT CA GGTCTGGG		
		GTTTGA GT CCAGACCC		
		C C I		
GAM83	BYSL	ACTGCCCTGATCTGGGTCTTCAGC	1039	___A G TCTI
		ACTGT GT CTGGGTCTT AGC		

		TGACG TA GACCCAGAA TCG	
		GGAC _ G IIIT	
GAM83 CCR9		CAGCTCTCAGTGTCTGGGGA 1043 A AG I	
		AG TTTCA GTCTGGGG	
		II IIII IIIIII	
		TC AGAGT CAGACCCC	
		G CA I	
GAM83 CCR9		CAGCTCTCAGTGTCTGGGGA 1043 TC A AG T	
		AG TTTCA GTCTGGGGAG	
		II IIII IIIIII	
		TC AGAGT CAGACCCCTT	
		_ G CA I	
GAM83 CIT		CTGTGAGCTGGCGCTTGAGCTC 1046 AC TA _ T	
		TGTG CTGG G CTTGAGCTCT	
		III IIII IIIIII	
		ACAC GACC C GAACTCGAGG	
		_ TC G _	
GAM83 DDB2		GATTGAGAGGCCTCTGGGGAG 1048 TCA _ III	
		GATT AGGT CTGGGGA	
		III IIII IIIIII	
		CTAA TCCG GACCCCT	
		CTC GA CII	
GAM83 DDB2		GATTGAGAGGCCTCTGGGGAG 1048 TCAGATTTC A _ TA	
		AGGT CTGGGGAG	
		III IIIIII	
		TCCG GACCCCTC	
		ACTC _ GA TT	
GAM83 DPH2L2		ATTTGCCAAGGTCTGGAGA 1041 ATT _ III	
		TCAAGGTCTGGGG	
		IIIIIIIIII	
		GGTTCCAGACCTC	
		TAAAC TII	
GAM83 DPH2L2		ATTTGCCAAGGTCTGGAGA 1041 TCAGATT GT	
		TCAAGGTCTGGGGA	
		IIIIIIIIII	
		GGTTCCAGACCTCT	
		C _ AT	
GAM83 EN1		GATTTAAA----TGGGGAGTA 1051 ATTTCAAGGTC	
		TGGGGAGT	
		IIIIII	
		ACCCCTCA	
		CTAAATTT _	
GAM83 EPB49		GATGTCAGGGTCTGGGCAG 1050 T A GAI	
		GAT TCA GGTCTGGG	
		III III IIIIII	
		CTA AGT CCAGACCC	
		C C GTCI	
GAM83 EPB49		GATGTCAGGGTCTGGGCAG 1050 TCAGATT A G T	
		TCA GGTCTGGG AG	
		III IIIIII II	

AGT CCAGACCC TC
 C_____ C G C
 GAM83 GLTSCR1 TCAGATTTCAAAGTCGAGGG 1057 T AGT
 TCAGATTTCAAGGTC GGGG
 |||||
 AGTCTAAAGTTTCAG TCCC
 C III
 GAM83 GLTSCR1 TCAGATTTCAAAGTCGAGGG 1057 T I
 CAGATTTCAAGGTC GGG
 |||||
 GTCTAAAGTTTCAG TCC
 C I
 GAM83 GPR61 TCAGAATGGCAAGAGCTGCTGGGGAGTA1055 TTT_ _ _ III
 TCAGA CAAG GT CTGGGGAGTA
 |||| ||| || |||||
 AGTCT GTTC CG GACCCCTCAT
 TACC T AC III
 GAM83 GPR61 TCAGAATGGCAAGAGCTGCTGGGGAGTA1055 CAGATTT _ _ I
 CAAG GT CTGGGGAGT
 |||| || |||||
 GTTC CG GACCCCTCA
 TACC_ T AC I
 GAM83 IVD TCAGATTTTC-AGGATTAGGGA 1058 A TC GT
 TCAGATTTCA GG TGGGGA
 ||||| || |||||
 AGTCTAAAGT CC ATCCCT
 _ TA II
 GAM83 IVD TCAGATTTTC-AGGATTAGGGA 1058_ A TC I
 CAGATTTCA GG TGGGG
 ||||| || |||||
 GTCTAAAGT CC ATCCC
 A _ TA I
 GAM83 LOXL1 CAGCATTTCAAGGCCAAGGG 1042 _ T_ II
 CAG ATTTCAAGGTC GGG
 ||| ||||| |||
 GTC TAAAGTTCCGG CCC
 G TT II
 GAM83 LOXL1 CAGCATTTCAAGGCCAAGGG 1042 TCAG T_ AGT
 ATTTCAAGGTC GGGG
 ||||| |||
 TAAAGTTCCGG CCCC
 TCG_ TT III
 GAM83 MX1 CAGATTTTCAGGGAGT-GGGAGT 1044_ A TC AGI
 AGATTTCA GG TGGGG
 ||||| || |||||
 TCTAAAGT CC ACCCT
 G C TC CII
 GAM83 MX1 CAGATTTTCAGGGAGT-GGGAGT 1044 TC A TCTG A
 AGATTTCA GG GGGAGT
 ||||| || |||||

		TCTAAAGT CC CCCTCA	
		___ C TCA_ G	
GAM83	NCOA6	TGTGGACTG---CTTGAGCTC 1059	ACTG T GGT
		TG ACTG CTTGAGCT	
		AC TGAC GAACTCGA	
		___ C ___	
GAM83	P2RY2	GTGTCATTGACCTTGAGCTCT 1053	ACTGTGTACTG GT
		G CTTGAGCTCT	
		C GAACTCGAGA	
		AGTAA___ TG	
GAM83	PPP1R8	TGTGTACTG---TTGAGATCT 1060	ACTG GGT C
		TGTACTG TTGAG T	
		ACATGAC AACTC A	
		___ T	
GAM83	RELN	GTGTACACTCGGTCTTGAG 1052	ACTGTG G CTC
		TACT GGTCTTGAG	
		GTGA CCAGAACTC	
		AT___ G TTC	
GAM83	TMSB4Y	CTCTGTACTGGGAAGTGTGCT 1045	ACTG TC A CT
		TGTACTGGG TTG GCT	
		ACATGACCC GAC CGA	
		AG___ TT A AI	
GAM83	TRPM2	CTGTGCCCTG--TCTTGAGCTCT 1047	AC A GG
		TGTGT CT GTCTTGAGCTCT	
		ACACG GG CAGAACTCGAGA	
		___ _ A_	
GAM83	WNT8B	TCAGGATCCCTAGGTCTGGGAGAG 1054	_ TT A _ TAI
		TCAG AT C AGGTCTGGG GAG	
		AGTC TA G TCCAGACCC CTC	
		C GG A T	
GAM83	WNT8B	TCAGGATCCCTAGGTCTGGGAGAG 1054	A TT A AI
		GAT C AGGTCTGGGG	
		CTA G TCCAGACCCT	
		C GG A CI	
GAM83	ZNF147	AGATTTCCAGAACAATGGGGAGTA 1040	GA AG TC_ I
		TTTCA G TGGGGAGT	
		AAGGT T ACCCCTCA	
		A_ CT GTT I	
GAM83	ZNF147	AGATTTCCAGAACAATGGGGAGTA 1040	TCAG A TC_ I
		ATTTC AGG TGGGGAGTA	

		TAAAG TCT ACCCCTCAT		
		_____ G TGTT C		
GAM84	BCL2	TATAAGTGATAA-GAAAGTCTAAAA 1075 AG _ CT I		
		AAGT ATA GAGAGTCTAAA		
		TTCA TAT CTTTCAGATTT		
		TA C T_ I		
GAM84	BCL2	TATAAGTGATAA-GAAAGTCTAAAA 1075 TAG _ CT I		
		AAGT ATA GAGAGTCTAAAA		
		TTCA TAT CTTTCAGATTTT		
		ATA C T_ I		
GAM84	CCNT2	AGAAATATACTGAGATGTGCAA 1067 _ CTAI		
		AAGTATACTGAGA GT		
		TTTATATGACTCT CA		
		A CGTII		
GAM84	CCNT2	AGAAATATACTGAGATGTGCAA 1067 TA _ C AI		
		GAAGTATACTGAGA GT TAAA		
		CTTTATATGACTCT CA GTTT		
		_____ A C GI		
GAM84	CML66	AAGTATACTTGCTAGTACTA 1064 _ AG CTIII		
		AAGTATACT G AGT		
		TTCATATGA C TCA		
		A GA TGATI		
GAM84	CPO	TAGAAGTATAAATGAG-GTTTAA 1076 C_ A C AA		
		TAGAAGTATA TGAG GT TAA		
		ATCTTCATAT ACTC CA ATT		
		TT _ A II		
GAM84	CPO	TAGAAGTATAAATGAG-GTTTAA 1076 C_ A CTAI		
		AGAAGTATA TGAG GT		
		TCTTCATAT ACTC CA		
		TT _ AATI		
GAM84	CUL3	TAAAAGCATATTTGCAAGTCTAAAA 1077 C_ AG II		
		TAGAAGTATA TG AGTCTAAAA		
		ATTTTCGTAT AC TCAGATTTT		
		AA GT II		
GAM84	CUL3	TAAAAGCATATTTGCAAGTCTAAAA 1077 A C_ AG I		
		GAAGTATA TG AGTCTAAA		
		TTTCGTAT AC TCAGATTT		
		_ AA GT I		
GAM84	CYP1B1	GAAGTATACCAGA-AGGCAAAA 1074 GA TCTAAI		
		AAGTATACT GAG		

		TTCATATGG TTC		
		TC CGTTTI		
GAM84	CYP1B1	GAAGTATACCAGA-AGGCCAAAA	1074 TAGA	GA TCTAAAA
		AGTATACT GAG		
		TTCATATGG TTC		
		____ TC CGTTTTTC		
GAM84	DBY	AGAAATGTACA-AGAGTCTAAA	1070 _ A T I	
		GAAGT TAC GAGAGTCTAA		
		CTTTA ATG TTCTCAGATT		
		T C _ I		
GAM84	DBY	AGAAATGTACA-AGAGTCTAAA	1070 TA A T A	
		GAAGT TAC GAGAGTCTAAA		
		CTTTA ATG TTCTCAGATTT		
		_ C _ G		
GAM84	FANCC	AACTATCAGGGAGAGTCTACAA	1063 AGTATACT	AI
		GAGAGTCTA		
		CTCTCAGAT		
		ATAGTCC_ GT		
GAM84	FANCC	AACTATCAGGGAGAGTCTACAA	1063 TAGAAGTATACT	AAA
		GAGAGTCTA		
		CTCTCAGAT		
		ATAGTCC_____ GTT		
GAM84	GRM6	AGAATGTATACTGA---TCTTAAA	1066 _ GAG AAI	
		AGAA GTATACTGA TCT		
		TCTT CATATGACT AGA		
		A _ ATT		
GAM84	GRM6	AGAATGTATACTGA---TCTTAAA	1066 TA _ GAG AAAA	
		GAA GTATACTGA TCT		
		CTT CATATGACT AGA		
		_ A _ ATTT		
GAM84	GSBS	AAGTGTAAT-AGAGTCTAAA	1065 A__ TACTG	I
		GTA AGAGTCTAA		
		CAT TCTCAGATT		
		TTCA TA__ I		
GAM84	GSBS	AAGTGTAAT-AGAGTCTAAA	1065 TAGAA TACTG	
		GTA AGAGTCTAAA		
		CAT TCTCAGATTT		
		A__ TA__		
GAM84	POU3F1	AGTATACTGCGA-TTTAAA	1073 A GTCTAAI	
		AGTATACTG GA		

		TCATATGAC CT			
		G AAATTTI			
GAM84	RIG	AGATATCTACTGAGAGCCT	1068	A A	II
		AGA GT TACTGAGAGTC			
		TCT TA ATGACTCTCGG			
		A G AI			
GAM84	RIG	AGATATCTACTGAGAGCCT	1068	TA A A	AAA
		GA GT TACTGAGAGTCT			
		CT TA ATGACTCTCGGA			
		__ A G GII			
GAM84	SCA1	AGTATACTGAAACAATAAA	1072		GTCTAAII
		AGTATACTGAGA			
		TCATATGACTTT			
		GTTATTTI			
GAM84	SLBP	AGTATTCTAAAGAGTCTAA	1071	A _	II
		AGTAT CTGA GAGTCTA			
		TCATA GATT CTCAGAT			
		A T TI			
GAM84	SLBP	AGTATTCTAAAGAGTCTAA	1071	TAGAAGTATA _	A
		CTGA GAGTCTAA			
		GATT CTCAGATT			
		AA_____ T G			
GAM84	SLC30A3	AGCAG-ATGCTGAGAGTCT	1069	AGA TA__	I
		AGTA CTGAGAGTC			
		TCGT GACTCTCAG			
		__ CTAC A			
GAM84	SLC30A3	AGCAG-ATGCTGAGAGTCT	1069	TAGA T A	AA
		AG AT CTGAGAGTCT			
		TC TA GACTCTCAGA			
		CG__ _ C CI			
GAM85	APXL	AAGCTCTGCCAAACAAAATACTCT	1080	A A_ G	I
		GCT GCTAAA AAAATACTC			
		CGA CGGTTT TTTTATGAG			
		_ GA G I			
GAM85	APXL	AAGCTCTGCCAAACAAAATACTCT	1080	TA A_ G	I
		AGCT GCTAAA AAAATACTCT			
		TCGA CGGTTT TTTTATGAGA			
		_ GA G C			
GAM85	ATP11B	TAATCAAGCTAATACTAAAAATACTCT	1088	_ AA	I
		AAGCTA GCTA GAAAATACTC			

		TTCGAT TGAT TTTTATGAG		
		TA _ I		
GAM85	ATP11B	TAATCAAGCTAATACTAAAAAATACTCT1088_____	AA	III
		TAAGCTA GCTA GAAAATACTCT		
		GTTTCGAT TGAT TTTTATGAGA		
		ATTA TA _ III		
GAM85	C1D	CTGGCTTA-GAAAATACTC 1084 TAAGCTAGCTAA		
		AGAAAATACT		
		TCTTTTATGA		
		GAA_____		
GAM85	C1D	CTGGCTTA-GAAAATACTC 1084 A AA I		
		CT GCT AGAAAATACT		
		GA CGA TCTTTTATGA		
		C A_ G		
GAM85	CD34	AAG-TAGAGAAAGAAAATAC 1082 TA C CT TC		
		AG TAG AAAGAAAATAC		
		TC ATC TTTCTTTTATG		
		_ _ TC TI		
GAM85	CPD	CTTGCTAAAGAAAATCTTCT 1085 TA A CI		
		GCTAAAGAAAAT CT		
		CGATTCTTTTA GA		
		AA _ AG		
GAM85	CPD	CTTGCTAAAGAAAATCTTCT 1085 TAAGCTAG AC		
		CTAAAGAAAAT TC		
		GATTCTTTTA AG		
		GA		
GAM85	DCK	AAACTAG--AAAGAAAATA 1081 CT I		
		AAGCTAG AAAGAAAAT		
		TTTGATC TTTCTTTTA		
		_ T		
GAM85	DCK	AAACTAG--AAAGAAAATA 1081 TA CT CT		
		AGCTAG AAAGAAAATA		
		TTTGATC TTTCTTTTAT		
		_ _ AI		
GAM85	INSM1	AGCTAACAATTAAGAAAATA 1083 TA_ III		
		AGCTAGC AAGAAAAT		
		TCGATTG TTCTTTTA		
		TTAA TII		
GAM85	INSM1	AGCTAACAATTAAGAAAATA 1083 TAAG TA_ CTC		
		CTAGC AAGAAAATA		

		GATTG TTCTTTTAT			
		____ TTAA TAI			
GAM85 INSM1		GCTATACTAAAGAAA--ACTCT 1086 _ _		ACTCI	
		CTA GCTAAAGAAAAT			
		GAT TGATTTCTTTTG			
		C A AG			
GAM85 INSM1		GCTATACTAAAGAAA--ACTCT 1086 TAAGCTA		AT	
		GCTAAAGAAA ACTC			
		TGATTTCTTT TGAG			
		TA_____			
GAM85 M17S2		TAGCCAAAGAAAAATACTC 1093		_ II	
		TAGCTAAAGAAAA TACT			
		ATCGGTTTCTTTT ATGA			
		T GI			
GAM85 PCK1		TAGCTAAAGTGAAAAAACACT 1091		_____ C	
		TAGCTAAAG AAAATACT			
		ATCGATTTC TTTTGTGA			
		ACTT C			
GAM85 PLSCR1		TAG-TAAAGAAAATTATCT 1094 C		ACTCI	
		TAG TAAAGAAAAT			
		ATC ATTTCTTTTA			
		_ ATAGA			
GAM85 RALBP1		TAAGTTAAC-AAAGAAAATTAATCT 1089		C T ACTCTI	
		TAAG TAGC AAAGAAAAT			
		ATTG ATTG TTTCTTTTA			
		A _ ATTAGA			
GAM85 RALBP1		TAAGTTAAC-AAAGAAAATTAATCT 1089		C T ACTCI	
		AAG TAGC AAAGAAAAT			
		TTC ATTG TTTCTTTTA			
		A _ ATTAG			
GAM85 TACC1		TAA-CTGGCTGGAAAGAAAAT 1087 TA		A _ ACTC	
		AGCT GCT AAAGAAAAT			
		TTGA CGA TTTCTTTTA			
		A_ C CC T			
GAM85 TACC1		TAA-CTGGCTGGAAAGAAAAT 1087 TA		A _ II	
		AGCT GCT AAAGAAAA			
		TTGA CGA TTTCTTTT			
		A_ C CC AI			
GAM85 TMEM1		TAAGC-A-CTAAAGAAAAT 1090		TA ACT	
		TAAGC GCTAAAGAAAAT			

		ATTCG TGATTTCTTTTA			
		— III			
GAM85	TMEM1	TAAGC-A-CTAAAGAAAAT 1090 TA I			
		TAAGC GCTAAAGAAAA			
		ATTCG TGATTTCTTTT			
		— A			
GAM85	ZNF214	TAGGTAAAGAAAAATACACT 1092 C _ TCII			
		TAG TAAAGAAAA TAC			
		ATC ATTTCTTTT ATG			
		C T TGAI			
GAM86	BBOX1	TATGGTCATTGGAATCTTATT 1102 GT AAATTTGA			
		TATGGTCAT GAATC			
		ATACCAGTA CTTAG			
		AC AATAAIII			
GAM86	CDH6	ATGGTCATG-AAAGCAAAGTT 1098 TA T T TTTG			
		TGGTCATG GAA CAAA			
		ACCAGTAC TTT GTTT			
		— _ C CAAT			
GAM86	FGF13	TGGTAAATGTCACTGACAAATTTGA 1105 TATG_ G AT II			
		GTCAT TGA CAAATTTGA			
		CAGTG ACT GTTTAACT			
		CATTTA _ _ TG			
GAM86	FIGF	TGATCATACGAATCAAATT 1109 TATG G			
		GTCATGTGAATCAAATTT			
		TAGTATGCTTAGTTTAAG			
		— A			
GAM86	GJA1	CATGAGAAAGGTTCAAATTTGA 1100 TAT CATGTGAA			
		GGT TCAAATTTGA			
		CCA AGTTTAACT			
		TTT _			
GAM86	HMGB3	TATGATC--GTGA-TCAAATTT 1103 AT A G			
		TATGGTC GTGA TCAAATTT			
		ATACTAG CACT AGTTTAAA			
		— _ I			
GAM86	ICMT	TATGGTAAATGAGAATCAAAT 1101 C_ T TTGA			
		TATGGT ATG GAATCAAAT			
		ATACCA TAC CTTAGTTTA			
		TTT T IIIA			
GAM86	KCNJ6	TGGTCATGTAAAAATTAAAT 1106 TATG TCAAATTTG			
		GTCATGTGAA			

		CAGTACATTT		
		____ TTAATTTAT		
GAM86	MAPK4	TGGTCATGTGAGTTAATTCTG	1110 TATG	ATCAAATTTGA
		GTCATGTGA		
		CAGTACACT		
		____ CAATTAAGACA		
GAM86	RB1	ATGGGCA-GTCAATCAAATT	1097 TA T T G	TG
		TGG CA GT AATCAAATT		
		ACC GT CA TTAGTTTAA		
		__ C _ G CI		
GAM86	SLC6A6	TGGTCCTATGTGAATCTAAT	1104 TATG __	AAATTTG
		GTC ATGTGAATC		
		CAG TACACTTAG		
		____ GA ATTACAI		
GAM86	TACC1	ATGGTT-TGAGT-TCAAATTTG	1099 TA CATG A_	
		TGGT TGA TCAAATTTG		
		ACCA ACT AGTTTAAAC		
		__ A__ CA		
GAM86	TPM4	TGGTCATGT-ATTCATAATTTG	1108 TATG AA _ A	
		GTCATGTG TCA AATTTG		
		CAGTACAT AGT TTAAAC		
		____ A_ A G		
GAM86	TPX1	TGCTCTT-TGAAATCAAATTTG	1107 TATGGTCA T	A
		TG GAATCAAATTTG		
		AC TTTAGTTTAAAC		
		GAGAA__ _ A		
GAM87	ACCN2	ATGGTGTGAGAGAGTGGGGCTG-AGG	1113 TA AAT__ T	
		TGGTGTGAGA GGCTG AGG		
		ACCACACTCT CCGAC TCC		
		__ CTCACC _ AI		
GAM87	CALB2	GGTGTGTGCA--GGCTGTAGG	1117 TATG AGAAAT	
		GTGTG GGCTGTAG		
		CACAC CCGACATC		
		____ GT__		
GAM87	CARD10	GGTGTGAGAACAGACTCCAGG	1115 TATGGT AT G	
		GTGAGAA GGCT TAGG		
		CACTCTT CTGA GTCC		
		____ GT G		
GAM87	GNAT2	GGTGAGAGAGCAGGCTGTAGG	1114 TATGGTGT AAT	
		GAGA GGCTGTAGG		

		CTCT CCGACATCC	
		CT_____ CGT	
GAM87	KIAA0857	TGGCTGTGGGAAGAAATGGCTG	1121 TATG T_ TAGG
		GTG GAGAAATGGCTG	
		CAC TTCTTTACCGAC	
		CGA_ CC TGII	
GAM87	MBL2	TATGTGTGTGAGAATTTG-TGAAG	1118 _ ATGGCTGTAGGI
		TATG GTGTGAGAA	
		ATAC CACTCTT	
		A AAACACTTCIII	
GAM87	METTL1	TGAGAAATGGCAGAATAGG	1120 TA GTG AT _ AG
		TGGT AGAA GGC TGT	
		ACCG TCTT CCG ACA	
		_ _ AT T CA	
GAM87	PSCDBP	TATAGATGTGAGAAACAGCTG	1119 TAT_ TAGG
		GGTGTGAGAAATGGCTG	
		CTACACTCTTTGTCGAC	
		ATAT IIIG	
GAM87	RAB1A	TGCTGTGAGAAAAGGATGGAGG	1123 TATGG T C T
		TGTGAGAAA GG TG AGG	
		ACACTCTTT CC AC TCC	
		G_ T T C	
GAM87	ROBO1	GGTGTGAGAGCT-GCTG-AGG	1116 TATGGT AATG T
		GTGAGA GCTG AG	
		CACTCT CGAC TC	
		_ CGA_ _	
GAM87	YWHAG	TGATGTTACATATGGCTGTA	1122 TATG GAGAA
		GTGT ATGGCTGTAG	
		TACA TACCGACATT	
		_ ATGTA	
GAM88	ACTR1B	TGGGCTGCAC--CCCCTTGC	1139 G CT AT
		TGGG TGTA CCCCTTGC	
		ACCC ACGT GGGGGAACG	
		G _ II	
GAM88	AP2S1	AAGTGGGGTGAAGTCTCCTC	1127 TCACAAGT TACTG_
		GGGGTG CCTC	
		CCCCAC GGAG	
		_ TTCAGA	
GAM88	BCL11B	CACAATT---TGTACTGCCT	1130 TCACAA TG GG
		G G TGTACTGCCT	

		T T ACATGACGGA		
		_____ GT AA		
GAM88	BTG2	AAGTGGGGTGAAGATTCCTC	1126 TCACAAGT	TACTG_
		GGGGTG CCTC		
		CCCCAC GGAG		
		_____ TTCTAA		
GAM88	CARD15	CACAAATGAAATGGAAGTGCCTCT	1129 TC	GG T_ I
		ACAAGTG GTG ACTGCCTCT		
		TGTTTAC TAC TGACGGAGA		
		_____ TT CT A		
GAM88	CD8A	TGGGCTTTAGCCTCCCCCTT	1137 TG	GTA_ GCATA
		GGGT CTCCCCCTT		
		CCCG GAGGGGGAA		
		A_ AAATCG IIITA		
GAM88	CYP8B1	TCACAGG-GGGGTGTACTG	1134 A T	CCT
		TCACA G GGGGTGTACTG		
		AGTGT C CCCCACATGAC		
		_ C		
GAM88	EDG8	TCACATTGTGGGGTGTCTGCTGC	1133 A_ A_ CTCT	
		TCACA GTGGGGTGT CTGC		
		AGTGT CACCCACACA GACG		
		AA GC IIIT		
GAM88	GHRHR	TGGGGATGTGG-CCCCCTTGC	1136 _ ACT	ATA
		TGGGG TGT CCCCCTTGC		
		ACCCC ACA GGGGGAACG		
		T CC_		
GAM88	KCNJ5	TGGGGT---TCCCCCTTG	1138 GTAC	CA
		TGGGGT TCCCCCTTG		
		ACCCCA AGGGGGAAC		
		_____ II		
GAM88	KLHL3	TGGGGATGTCAAGAC-CCCCCTTGC	1135 _ AC_	ATATI
		TGGGG TGT TCCCCCTTGC		
		ACCCC ACA GGGGGAACG		
		T GTTCT IIITA		
GAM88	PCTK1	ACAAGTGGGCAGGTGAACATGGCTC	1128 TCAC	_ T _ C TII
		AAGTGGG GTG AC TG CTC		
		TTCACCC CAC TG AC GAG		
		_____ GTC T T C TCI		
GAM88	PPP1R12B	GGTGTACTCCCCAGAGCAT	1132 TGGGGT	CTT A
		GTACTCCCC GCAT		

		CATGAGGGG CGTA	
		_____ TCT A	
GAM88	SLC17A5	GGTGTACTCGCCACCTGGCA 1131 TGGGGT _ _ T TA	
		GTACTC CC CCT GCA	
		CATGAG GG GGA CGT	
		_____ C T C CT	
GAM89	ADRB3	CACTGCTTGAGAGCAGTAATAAGG 1149 ACA GT___ C I	
		GCT GC AGTAATAAG	
		CGA CG TCATTATTC	
		A__ ACTCT _ I	
GAM89	AGRN	CAGAGCTGTGCCCAGCAGTAA 1150 AC _ ATAI	
		AGCTGTGCC AGTA	
		TCGACACGG TCGT	
		C_ G CATI	
GAM89	AGRN	CAGAGCTGTGCCCAGCAGTAA 1150 TCAC _ A GGA	
		AGCTGTGCC AGTA TAA	
		TCGACACGG TCGT ATT	
		TC___ G C GII	
GAM89	AKAP13	TCACAGCTGGGCGGGGAGTAAG 1158 T C___ TAAGGA	
		TCACAGCTG GC AGTAA	
		AGTGTGAC CG TCATT	
		C CCCC CIIAG	
GAM89	AKAP13	TCACAGCTGGGCGGGGAGTAAG 1158 T C___ TAAI	
		CACAGCTG GC AGTAA	
		GTGTGAC CG TCATT	
		C CCCC IIIA	
GAM89	AKAP2	AAACATAACTGTGA-AAATGTG 1142 CA C C C A	
		AAC TAACTGTGA AG TGTG	
		TTG ATTGACACT TT ACAC	
		_ T T _ A	
GAM89	CCND1	ACAGCTGTGC--TTTATCAGGA 1145 _____ TAATAAGI	
		ACAGCTGTGC CAG	
		TGTCGACACG GTC	
		AAATA CTIIIGAA	
GAM89	CCND1	ACAGCTGTGC--TTTATCAGGA 1145 TCAC CAG ATA	
		AGCTGTGC TA AGG	
		TCGACACG AT TCC	
		_____ AA_ AG_	
GAM89	EPHA3	TCAAAGCCAGTGAGCCAGTAAT 1156 C ___T AAGGA	
		TCA AGCT G GCCAGTAAT	

		AGT TCGG C CGGTCATTA		
		T TCA T IIIAG		
GAM89	EPHA3	TCAAAGCCAGTGAGCCAGTAAT 1156 C ____T III		
		TCA AGCT G GCCAGTAA		
		AGT TCGG C CGGTCATT		
		T TCA T AII		
GAM89	FMOD	GCTTTTCCTGTAATAAGGA 1154 GTG A II		
		GCT CC GTAATAAGG		
		CGA GG CATTATTCC		
		AAA A TI		
GAM89	GALNT2	CAATACTAGCGTGTGACAGCTG 1146 AC AC_ TGA		
		CAA CTA TGTGACAGCTG		
		GTT GAT ACACTGTGCGAC		
		AT CGC III		
GAM89	GRINL1A	AACCTATCATCTGTGACAGC 1143 CAAA A__ TG TG		
		CCTA CTGTGACAGC		
		GGAT GACACTGTGCG		
		____ AGTA TTII		
GAM89	HDAC4	CACAGCTGTGC--GGAA-AAGG 1153 CAGTAATAI		
		CACAGCTGTGC		
		GTGTCGACACG		
		CCTTTTCCI		
GAM89	HDAC4	CACAGCTGTGC--GGAA-AAGG 1153 TC CAGTAAT		
		ACAGCTGTGC AAGG		
		TGTCGACACG TTCC		
		____ CCTT____		
GAM89	HOXC6	CACATCAATTGTGCCAGTGATAA 1148 A C AATAI		
		CAG TGTGCCAGT		
		GTT ACACGGTCA		
		A A CTATI		
GAM89	HOXC6	CACATCAATTGTGCCAGTGATAA 1148 TCA_ C A GAI		
		CAG TGTGCCAGT ATAAG		
		GTT ACACGGTCA TATTT		
		TGTA A C III		
GAM89	MIPEP	TCACAGCTGTAGCATTTATAA 1157 C GTA GGA		
		TCACAGCTGTG CA ATAA		
		AGTGTGACAT GT TATT		
		C AAA III		
GAM89	MIPEP	TCACAGCTGTAGCATTTATAA 1157 C GTAATAI		
		CACAGCTGTG CA		

		GTGTCGACAT GT			
		C AAATATI			
GAM89	NDUFA6	ACAGCTGTGCACCTAAGCAGG	1144	C____	ATAAGI
		CAGCTGTGC AGTA			
		GTCGACACG TCGT			
		TGGAT CIIIGA			
GAM89	NDUFA6	ACAGCTGTGCACCTAAGCAGG	1144	TCAC	CAGTAATA A
		AGCTGTGC AGG			
		TCGACACG TCC			
		____ TGGATTCTG C			
GAM89	NPAT	CAAACCTAACTGTAGTACAG	1147	__	CTGTG
		CAAACCTAACTGTG ACAG			
		GTTTGGATTGACAT TGTC			
		CA IIIAG			
GAM89	SCN8A	CACAGCTGTTCTGCATTGATAA	1151	TC	GCCA ATAAGGA
		ACAGCTGT GTA			
		TGTCGACA CGT			
		__ AGA_ AACTATT			
GAM89	SLC11A3	CACAGCTGTG---GTAAAAA	1152	CCA	TI
		CACAGCTGTG GTAA			
		GTGTCGACAC CATT			
		__ TT			
GAM89	SLC11A3	CACAGCTGTG---GTAAAAA	1152	TC	CCA TAAG
		ACAGCTGTG GTAA			
		TGTCGACAC CATT			
		__ __ TTTG			
GAM89	TEX15	TCAAAGGCCTGTGCCAG--ATAA	1155	C __	TAATAAGGA
		TCA AG CTGTGCCAG			
		AGT TC GACACGGTC			
		T CG TATTIIIAG			
GAM89	TEX15	TCAAAGGCCTGTGCCAG--ATAA	1155	TCACAG	TAAI
		CTGTGCCAG			
		GACACGGTC			
		TTCCG_ TATT			
GAM90	COG8	TCTCCATT-GGGGTCCAGCCCG	1165	TGTCA	G
		CCATTGGGG TTCCGGCTCG			
		GGTAACCCC AGGTCGGGC			
		A____ _			
GAM90	CRLF1	TGGCCCCAGTTTGGGTTCGGC	1167	T_ A	TTGG TCG
		GTC CCA GGGTTCGGC			

		CGG GGT CCCAAGCCG			
		AC _ CAAA III			
GAM90	DPEP1	GTCACAAGGCTTGGGGGTT	1162	TG CA__	CGGCTC
		TCAC TTGGGGGTT			
		AGTG AACCCCAA			
		_ TTCCG CIIIGC			
GAM90	EGLN2	TCACCTCGTGGGGGTTCCGC	1164	TGTC AT_	G C
		ACC TGGGGGTTC GCT			
		TGG ACCCCCAAG CGG			
		___ AGC G C			
GAM90	GLP1R	TGTCACCATGGCTTGGGGGCTTC	1166	___	G GGCTCG
		TGTCACCAT TGGGG TTC			
		ACAGTGGTA ACCCC AAG			
		CCGA G IIIGCT			
GAM90	PVR	TCATCCATTGGGG--TCGGGTC	1163	TGTCA GT	C
		CCATTGGGG TCGG TC			
		GGTAACCCC AGCC AG			
		TA__ _ C			
GAM90	TDRD1	ACCCCTGGGGGTTTCAGTTC	1161	TGTCACCAT	C
		TGGGGGTTCGG TC			
		ACCCCAAGTC AG			
		G_____ A			
GAM91	CPNE3	TGGC-GTACTTTATGTGTC	1170	C AA	GCG
		TGGC GTA TTATGTGTC			
		ACCG CAT AATACACAG			
		_ GA III			
GAM91	CPNE3	TGGC-GTACTTTATGTGTC	1170	C AA	I
		TGGC GTA TTATGTGT			
		ACCG CAT AATACACA			
		_ GA G			
GAM92	ADCY6	GAGACTTGGGAGGG--CAGG	1180		GCCAI
		GAGATTTGGGAGGG			
		CTCTGAACCCTCCC			
		GTCCI			
GAM92	ADCY6	GAGACTTGGGAGGG--CAGG	1180	TG	GC G
		AGATTTGGGAGGG CAGG			
		TCTGAACCCTCCC GTCC			
		_ _ A			
GAM92	ALOX15	TGGGACTTGGGAGGG--CAGGG	1190	A	GC G
		TG GATTTGGGAGGG CAGGG			

		AC CTGAACCCTCCC GTCCC		
		C _ I		
GAM92	ALOX15	TGGGACTTGGGAGGG--CAGGG	1190 _ A	GC I
		G GATTTGGGAGGG CAGG		
		C CTGAACCCTCCC GTCC		
		A C _ I		
GAM92	BCL3	AGCTCTGGGAGGGGACATGG	1175 AGA	C GI
		TTTGGGAGGGG CA		
		AGACCCTCCCC GT		
		G _ T AC		
GAM92	BCL3	AGCTCTGGGAGGGGACATGG	1175 TGAGA	C G
		TTTGGGAGGGG CA GGG		
		AGACCCTCCCC GT CCT		
		G _ T A		
GAM92	CD74	GACATGGGGGAGGGGCTGGGGGC	1182 AGATTT	CA I
		GGGAGGGGC GGGG		
		CCCTCCCCG CCCC		
		TGTACC AC I		
GAM92	CD74	GACATGGGGGAGGGGCTGGGGGC	1182 TGAGATTT	CA I
		GGGAGGGGC GGGGC		
		CCCTCCCCG CCCC		
		TGTACC _ AC A		
GAM92	COX15	TGAGATTT-GGAGGGGACA	1187	GA CAGGG
		TGAGATTTGG GGGGC		
		ACTCTAAACC CCCTG		
		TC TIIIC		
GAM92	COX15	TGAGATTT-GGAGGGGACA	1187	GA CI
		TGAGATTTGG GGGGC		
		ACTCTAAACC CCCTG		
		TC TI		
GAM92	CRAT	AGATTTGGG-GGGACCAGGG	1174 _ A	I
		GATTTGGG GGGGCCAGG		
		CTAAACCC CCCTGGTCC		
		T _ I		
GAM92	CRAT	AGATTTGGG-GGGACCAGGG	1174 TGAG	A
		ATTTGGG GGGGCCAGGGG		
		TAAACCC CCCTGGTCCCT		
		_ _		
GAM92	DRPLA	GATCGGGGAGGGG-CAGGGG	1185 _ T	C I
		ATT GGGAGGGGC AGGG		

		TAG CCCTCCCCG TCCC	
		C C _ I	
GAM92 DRPLA		GATCGGGGAGGGG-CAGGGG 1185 TGAGATT	C
		GGGAGGGGC AGGGG	
		CCCTCCCCG TCCCC	
		GC_____	
GAM92 F2RL3		AGATTGTG-GTTGCCAGGGGC 1178_ _ AGGG	I
		GATTG GG GCCAGGGG	
		CTAAAC CC CGGTCCCC	
		T A AA_ I	
GAM92 F2RL3		AGATTGTG-GTTGCCAGGGGC 1178 TGAG _ AGGG	
		ATTG GG GCCAGGGGC	
		TAAAC CC CGGTCCCCG	
		_____ A AA_	
GAM92 FUT4		TGAGATTGGAAGCTG-CACGGGC 1192	GG C G I
		TGAGATTGGGAG GC A GGGC	
		ACTCTAAACCTTC CG T CCCG	
		GA _ G I	
GAM92 FUT4		TGAGATTGGAAGCTG-CACGGGC 1192_	GG CA GI
		GAGATTGGGAG GC GGG	
		CTCTAAACCTTC CG CCC	
		A GA TG II	
GAM92 HOXB5		GATT--GGAGGGGCCAGGG 1184 GATTG	I
		GGAGGGGCCAGG	
		CCTCCCCGGTCC	
		CTAA_ C	
GAM92 HOXB5		GATT--GGAGGGGCCAGGG 1184 TGAGATTG	
		GGAGGGGCCAGGG	
		CCTCCCCGGTCCC	
		A_____	
GAM92 LDLR		GAGATTGGTGGATGAGGCAGGGCCAGGGG1179_____ A TT A	CIIC
		TG GAT GGG GGGGCCAGGGG	
		AC CTA TCC TCCCGGTCCCC	
		TCTAACC _ C_ G CIIC	
GAM92 LDLR		GAGATTGGTGGATGAGGCAGGGCCAGGGG1179 A_ TT A	I
		GAT GGG GGGGCCAGGG	
		CTA TCC TCCCGGTCCC	
		AC C_ G I	
GAM92 MUC5B		TGACATCAGGGAGGGGCAAGG 1189 G T C GC	
		TGA ATT GGGAGGGGC AGGG	

		ACT TAG CCCTCCCCG TTCC		
		G T _ II		
GAM92	MUC5B	TGACATCAGGGAGGGGCAAGG	1189	G T C I
		GA ATT GGGAGGGGC AG		
		II III IIIIIII II		
		CT TAG CCCTCCCCG TC		
		G T T I		
GAM92	MYO1C	TTGGGAGGGTCCAGTGGGC	1194	G _ II
		TTGGGAGGG CCAG GGG		
		IIIIII III III		
		AACCCTCCC GGTC CCC		
		A A GI		
GAM92	PACSIN1	GAGAGT--GG-GGGGCCAGGGG	1181	T ATT AG
		GAG TGGG GGGCCAGGGG		
		III III IIIIIII		
		CTC ACCC CCCGGTCCCC		
		T _ _		
GAM92	PACSIN1	GAGAGT-GGGAGGGG--AGGGGC	1183	_ TT CC
		AGA TGGGAGGGG AGGGG		
		III IIIIIII IIII		
		TCT ACCCTCCCC TCCCC		
		C C_ _		
GAM92	PACSIN1	GAGAGT-GGGAGGGG--AGGGGC	1183	T ATT CC
		GAG TGGGAGGGG AGGGG		
		III IIIIIII IIII		
		CTC ACCCTCCCC TCCCC		
		T _ _		
GAM92	PACSIN1	GAGAGT--GG-GGGGCCAGGGG	1181	AGATTTG A
		GG GGGGCCAGGG		
		II IIIIIII		
		CC CCCCGGTCCC		
		CTCTCA_ _		
GAM92	PKIA	TGACATT-GTGAGGGGCCAG	1188	GA _ G I
		GAT TTG GAGGGGCCA		
		III III IIIIIII		
		CTG AAC CTCCCCGGT		
		A_ T A I		
GAM92	PKIA	TGACATT-GTGAGGGGCCAG	1188	TGA _ G GGG
		GAT TTG GAGGGGCCAG		
		III III IIIIIII		
		CTG AAC CTCCCCGGTC		
		A_ T A III		
GAM92	PPP2R5D	AGAGTATGGAGGG-CCAGGG	1173	_ TTTG G I
		GA GGAGGG CCAGG		
		II IIIII IIII		
		CT CCTCCC GGTCC		
		T CATA _ I		
GAM92	PPP2R5D	AGAGTATGGAGGG-CCAGGG	1173	TGAGATTTG G G
		GGAGGG CCAGGG		
		IIII IIIII		

		CCTCCC GGTCCC			
		TCATA_____G			
GAM92	PPP5C	TGGGATT--GGAGGGGCCCTGGG	1191	A TG	AG C
		TG GATT GGAGGGGCC GGG			
		AC CTAA CCTCCCCGG CCC			
		C _____ GA I			
GAM92	PPP5C	TGGGATT--GGAGGGGCCCTGGG	1191_A	TG	AG I
		G GATT GGAGGGGCC GG			
		C CTAA CCTCCCCGG CC			
		A C _____ GA I			
GAM92	SYNGR1	AGATG-GGGAGGGG-CGGGGGC	1177_	TT	CA I
		GAT GGGAGGGGC GGGG			
		CTA CCCTCCCCG CCCC			
		T C_ C_ I			
GAM92	SYNGR1	AGATG-GGGAGGGG-CGGGGGC	1177	TGAGATTT	CA
		GGGAGGGGC GGGG			
		CCCTCCCCG CCCC			
		TAC_____C_			
GAM92	TFAP2A	TGAGGCGTGGGAGGGGC--GGGGC	1193	ATT	CA
		TGAG TGGGAGGGGC GGGGC			
		ACTC ACCCTCCCCG CCCC			
		CGC _____			
GAM92	TFAP2A	TGAGGCGTGGGAGGGGC--GGGGC	1193_	ATT	CA I
		GAG TGGGAGGGGC GGGG			
		CTC ACCCTCCCCG CCCC			
		A CGC _____ I			
GAM92	WARS	TTTGGGAGGGGGCATGGGC	1195	C _	GII
		TTTGGGAGGGG CA GGG			
		AAACCCTCCCC GT CCC			
		C A GII			
GAM92	WDR1	TGAGAGCCGCGGCGGGGCCAGGGGC	1186	T _ A	II
		TGAGA TTG GG GGGGCCAGGGGC			
		ACTCT GGC CC CCCC GTCCCCG			
		C G G II			
GAM92	WDR1	TGAGAGCCGCGGCGGGGCCAGGGGC	1186_	ATT	GA
		GAG TGG GGGGCCAGGGG			
		CTC GCC CCCC GTCCCC			
		T GGC G_ I			
GAM92	ZNF179	AGATTTGGGAAGGGTCATGGG	1176	C _	GI
		GATTTGGGAGGGG CA GG			

		CTAAACCCTTCCC GT CC		
		A A II		
GAM92	ZNF179	AGATTTGGAAGGGTCATGGG 1176 TGAG C _ C		
		ATTTGGGAGGGG CA GGGG		
		TAAACCCTTCCC GT CCCT		
		_____ A A T		
GAM93	AOC3	GAGCAACTCCTAC-TCCCAATA 1201 TG G AA		
		AG AACTCCTAC CTCAATAG		
		TC TTGAGGATG GGGTTATT		
		__ G A_		
GAM93	CAPN10	TGAGGAACTCCTCCTCCTC 1203 ACAA AATA		
		TGAGGAACTCCT CTC		
		ACTCCTTGAGGA GAG		
		GGAG IIIG		
GAM93	DLK1	TGAGGAACTCCAAGAA-TCTAGAG 1205 TACAACTCAATAGI		
		TGAGGAACTCC		
		ACTCCTTGAGG		
		TTCTTAGATCTCII		
GAM93	GCMB	GAATCTCC--CAACTCAATA 1200 TGAGGAA TA		
		CTCC CAACTCAAT		
		GAGG GTTGAGTTA		
		_____ _		
GAM93	IL10	AGGAACTCCT-GACCTCAA 1199 TGAG ACAA T		
		GAACTCCT CTCAA		
		CTTGAGGA GAGTT		
		_____ CTG_ C		
GAM93	LMO2	TGTGGAACCTCCT-CCCCTCAA 1204 TGA ACAA TA		
		GGAACCTCCT CTCAA		
		CCTTGAGGA GAGTT		
		ACA GGG_ II		
GAM93	MEN1	AGAAACTCCTACAAGTCAA 1198 TGAG C		
		GAACTCCTACAA TCAATA		
		TTTGAGGATGTT AGTTGT		
		_____ C		
GAM93	TBX3	GGAACCTCCTAC-CCCCAGTAG 1202 TGAGGA AA A		
		ACTCCTAC CTCA TA		
		TGAGGATG GGGT AT		
		_____ G_ C		
GAM94	AKAP2	ATGAAGCACATGGTTTCCT 1211 C T GTTC		
		ATG AGTAT TGGTTTCCT		

		TAC TCGTG ACCAAAGGA			
		T T IIC			
GAM94	AKAP2	ATGAAGCACATGGTTTCCT	1211	C T II	
		ATG AGTAT TGGTTTCC			
		TAC TCGTG ACCAAAGG			
		T T AI			
GAM94	ATP2B2	CAGTATTTGGTTTCCGATTGTT	1214	TGTIII	
		CAGTATTTGGTTTCC			
		GTCATAAACCAAAGG			
		CTAACA			
GAM94	ATP2B2	CAGTATTTGGTTTCCGATTGTT	1214	ATGCAG	___ CC
		TATTTGGTTTCC TGTT			
		ATAAACCAAAGG ACAA			
		CTA CG			
GAM94	C21orf33	ATGTGGTATTTCTGGTTTCCTGATC	1210	CA	___ T CII
		ATG GTATT TGGTTTCCTG TC			
		TAC CATAA ACCAAAGGAC AG			
		AC AG T III			
GAM94	C21orf33	ATGTGGTATTTCTGGTTTCCTGATC	1210	GCA	___ TI
		GTATT TGGTTTCCTG			
		CATAA ACCAAAGGAC			
		C___ AG TI			
GAM94	GALNT7	TGCAATATTTGGTTTTCT	1219		___ II
		TGCAGTATTTGGTTT CC			
		ACGTTATAAACCAAA GG			
		A AI			
GAM94	GALNT7	TGCAATATTTGGTTTTCT	1219	AT	___ TTC
		GCAGTATTTGGTTT CCTG			
		CGTTATAAACCAAA GGAT			
		A III			
GAM94	HIP12	CAGTATTTGGTAGCCT-TTCC	1216		TT GTTCI
		AGTATTTGGT CCT			
		TCATAAACCA GGA			
		G TC AAGII			
GAM94	HIP12	CAGTATTTGGTAGCCT-TTCC	1216	ATGCAG	TT G
		TATTTGGT CCT TTC			
		ATAAACCA GGA AAG			
		TC			
GAM94	HNF3B	CATTATTTTTTTCTGTT	1215	ATGCAG	GG C
		TATTT TTTCTGTT			

		ATAAA AAAGGACAA			
		_____ AA A			
GAM94	HNF3B	CATTATTTTTTTTCCTGTT	1215	CAG GG	II
		TATTT TTTCTGT			
		ATAAA AAAGGACA			
		GTA AA AI			
GAM94	IGHMBP2	GCAGTCTT--GTTTCCTGTT	1217	ATTG	I
		GCAGT GTTTCCTG			
		CGTCA CAAAGGAC			
		GAA__ A			
GAM94	IGHMBP2	GCAGTCTT--GTTTCCTGTT	1217	ATGC ATTG	
		AGT GTTTCCTGTT			
		TCA CAAAGGACAA			
		_____ GAA__			
GAM94	KCND2	ATGCATTATGATGGTTTCCT	1208	G T_ GTTC	
		ATGCA TAT TGGTTTCCT			
		TACGT ATA ACCAAAGGA			
		A CT IIIC			
GAM94	KCND2	ATGCATTATGATGGTTTCCT	1208	G T_ II	
		ATGCA TAT TGGTTTCC			
		TACGT ATA ACCAAAGG			
		A CT AI			
GAM94	PHKA2	ATGCAGTATT---TTTCCT	1212	GGT	
		ATGCAGTATTT TTCC			
		TACGTCATAAA AAGG			

GAM94	PHKA2	ATGCAGTATT---TTTCCT	1212	GGT GT	
		ATGCAGTATTT TTCCT			
		TACGTCATAAA AAGGA			
		_____ II			
GAM94	RABIF	ATGAAATACTATGGTTTCCTATTC	1209	C _ CI	
		ATG AGTATT TGGTTTCCTGTT			
		TAC TTATGA ACCAAAGGATAAG			
		T T II			
GAM94	RABIF	ATGAAATACTATGGTTTCCTATTC	1209	TGC _ I	
		AGTATT TGGTTTCCTGTT			
		TTATGA ACCAAAGGATAA			
		CT_ T I			
GAM94	SDPR	GCATTCTTTG-TTTCCTGTT	1218	ATGCAGTATTTG C	
		GTTTCCTGTT			

		CAAAGGACAA			
		TAAGAAA_____A			
GAM94	SDPR	GCATTCTTTG-TTTCCTGTT	1218	CA G__ I	
		GTATTT GTTTCCTGT			
		CGTAAG CAAAGGACA			
		__ AAA I			
GAM94	TGIF	CAGTATGTGGGCATCCTGTTCC	1213	A T TT_ I	
		GTAT TGG TCCTGTTT			
		CATA ACC AGGACAAG			
		_ C CGT I			
GAM94	TGIF	CAGTATGTGGGCATCCTGTTCC	1213	ATGCAGTATTT T	
		GGT TCCTGTTCC			
		CCG AGGACAAGG			
		ATACAC_____T			
GAM95	ARNT2	GATCCAAAACCTATTTTTGTGC	1222	__ __ IIIG	
		GATC AACCT TTTTGTG			
		CTAG TTGGA AAAACAC			
		GTT TA GIII			
GAM95	CCND1	TGAAACAG--CAACCTTTTTG	1225	C AT TG	
		TGA ACGG CAACCTTTTTG			
		ACT TGTC GTTGGAAAAAC			
		T _ II			
GAM95	CCND1	TGAAACAG--CAACCTTTTTG	1225	_ C AT I	
		GA ACGG CAACCTTTTT			
		CT TGTC GTTGGAAAAA			
		A T _ I			
GAM95	NCOA4	TGACCAGGTT-AATTTTTTTGTGC	1226	A ATCAACC I	
		TGAC CGG TTTTGTGC			
		ACTG GTC AAAAACACG			
		_ CAATTAA I			
GAM95	NCOA4	TGACCAGGTT-AATTTTTTTGTGC	1226	_ A ATCAACC I	
		GAC CGG TTTTGTG			
		CTG GTC AAAAACAC			
		A _ CAATTAA I			
GAM95	PTEN	TGACACAGCTACACAACCTTTTT	1224	AT__ GTGCI	
		TGACACGG CAACCTTTTT			
		ACTGTGTC GTTGGAAAAA			
		GATGT IIICG			
GAM95	PTEN	TGACACAGCTACACAACCTTTTT	1224	GAC AT__ I	
		ACGG CAACCTTTTT			

		TGTC GTTGGAAAA			
		___ GATGT I			
GAM95	RFPL1	TGACAAGTGA-CAACCTTTTCATGC 1223	CG_ T	TG I	
		TGACA GA CAACCTTTT TGC			
		ACTGT CT GTTGGAAAA ACG			
		TCA _ GT I			
GAM95	RFPL1	TGACAAGTGA-CAACCTTTTCATGC 1223	CG_ T	TG I	
		GACA GA CAACCTTTT TG			
		CTGT CT GTTGGAAAA AC			
		TCA _ GT I			
GAM95	RFPL2	TGACAAGTGA-CAACCTTTTCATGC 1223	CG_ T	TG I	
		TGACA GA CAACCTTTT TGC			
		ACTGT CT GTTGGAAAA ACG			
		TCA _ GT I			
GAM95	RFPL2	TGACAAGTGA-CAACCTTTTCATGC 1223	CG_ T	TG I	
		GACA GA CAACCTTTT TG			
		CTGT CT GTTGGAAAA AC			
		TCA _ GT I			
GAM95	RFPL3	TGACAAGTGA-CAACCTTTTCATGC 1223	CG_ T	TG I	
		TGACA GA CAACCTTTT TGC			
		ACTGT CT GTTGGAAAA ACG			
		TCA _ GT I			
GAM95	RFPL3	TGACAAGTGA-CAACCTTTTCATGC 1223	CG_ T	TG I	
		GACA GA CAACCTTTT TG			
		CTGT CT GTTGGAAAA AC			
		TCA _ GT I			
GAM96	ADCY3	GTCCTGCCCCACCAAGCCC 1245	TCAGA TG	CA	
		GTCC CACCAAGCCC			
		CGGG GTGGTTCGGG			
		___ _ AC			
GAM96	AQP6	GGGTCTTGGTGTCTGGGGAACAGGA 1240	GGT ___	CC I	
		CTTGGT GGGG CAGG			
		GAACCA CCCC GTCC			
		___ CAG TT I			
GAM96	AQP6	GGGTCTTGGTGTCTGGGGAACAGGA 1240	TG ___	CC ATI	
		GGTCTTGGT GGGG CAGGA			
		CCAGAACCA CCCC GTCCT			
		___ CAG TT GII			
GAM96	AXUD1	AGTC-TGCACCAAAGCCCAG 1231	TCAGAGTCC	C	
		TGCACCAAG CCA			

		ACGTGGTTT GGGT				
		_____ C				
GAM96	B4GALT2	CAGACTTACTGATCCAAGCCCCA	1233	TC	GTC_ CA	GI
		AGA CTG CCAAGCCCCA				
		TCT GAC GGTTCGGGGT				
		_ GAAT TA GI				
GAM96	BTNL3	TGGGTCTGTGGTGTGGGGCCC	1252	_ _	AGGAAT	
		TGGGTCT TGGT GGGGCCC				
		ACCCAGA ACCA CCCCGGG				
		C CA TAA				
GAM96	BTNL3	TGGGTCTGTGGTGTGGGGCCC	1252	_ _		
		TGGGTCT TGGT GGGGCC				
		ACCCAGA ACCA CCCC GG				
		C CA G				
GAM96	C1QB	TCAGCAG-CATTACCAAGCCC	1248	_	CCTG	CAG
		TCAG AGT CACCAAGCCC				
		AGTC TCG GTGGTTCGGG				
		G TAA_				
GAM96	CCND2	TGGGACTCCTTGGGGGCCCAGGA	1257	T GG	AT	
		TGGG CTT TGGGGGCCCAGGA				
		ACCC GAG ACCCCGGGTCCT				
		T GA				
GAM96	CCND2	TGGGACTCCTTGGGGGCCCAGGA	1257	T GG	I	
		GGG CTT TGGGGGCCCAGG				
		CCC GAG ACCCCGGGTCC				
		T GA I				
GAM96	CD79B	TGGCTCTTC-TGGGGGCCCAG	1256	G GG	GAA	
		TGG TCTT TGGGGGCCCAG				
		ACC AGAA ACCCCGGGTC				
		G G_				
GAM96	CD79B	TGGCTCTTC-TGGGGGCCCAG	1256_	G GG	I	
		GG TCTT TGGGGGCCCA				
		CC AGAA ACCCCGGGT				
		A G G_ I				
GAM96	CHRM1	GGGTCTCTCTGGGCTGCCCAGGAA	1242	GG GG	_ I	
		TCTT TGGG GCCCAGGA				
		AGAG ACCC CGGGTCCT				
		_ AG GA I				
GAM96	CHRM1	GGGTCTCTCTGGGCTGCCCAGGAA	1242	TG GG	_ TI	
		GGTCTT TGGG GCCCAGGAA				

		CCAGAG ACCC CGGGTCCTT			
		___ AG GA CI			
GAM96	CORO2B	GGGTCTTGGTCGTGGGCCCA	1241	__	III
		GGGTCTTGGT G GGGCCC			
		I			
		CCCAGAACCA C CCCGGG			
		G A TII			
GAM96	CORO2B	GGGTCTTGGTCGTGGGCCCA	1241 TG	__	GGAA
		GGTCTTGGT G GGGCCA			
		I			
		CCAGAACCA C CCCGGGT			
		___ G A AIII			
GAM96	F2RL3	TGGGCCT-GGTGGGGCCACAG	1255	T	_ GAA
		TGGGTCT GGTGGGGCC CAG			
		ACCCGGA CCACCCCGG GTC			
		_ T III			
GAM96	F2RL3	TGGGCCT-GGTGGGGCCACAG	1255	T	_ I
		GGGTCT GGTGGGGCC CA			
		CCCGGA CCACCCCGG GT			
		_ T I			
GAM96	FLOT2	AGTGCAACATCCAAGCCCCAG	1230	TCAGAGTCCT	_
		GCA CCAAGCCCCAG			
		TGT GGTTCGGGGTC			
		GT_____ A			
GAM96	GJB3	GAGCTCCAGCTC-AAGCCCCAG	1236	TCAGAG	T AC
		TCC GC CAAGCCCCAG			
		AGG CG GTTCGGGGTC			
		G_____ T A_			
GAM96	H4F2	TCAGAGTCCGACA-CAAGCCCC	1251	T C	AG
		TCAGAGTCC GCAC AAGCCCC			
		AGTCTCAGG TGTG TTCGGGG			
		C _ II			
GAM96	HIRA	CAGAGCTCCAGC-CCTAGCTCC	1232	TC	_ T A A C AG
		AGAG TCC GC CC AGC CC			
		TCTC AGG CG GG TCG GG			
		___ G T _ A A CI			
GAM96	HOXC5	GTCT--GTGGGGGCCCGGGA	1246	TG	A I
		GTCT GTGGGGCCC GG			
		CAGA CACCCCGGG CC			
		___ C T			
GAM96	HOXC5	GTCT--GTGGGGGCCCGGGA	1246	TGGGTCTTG	A
		GTGGGGCCC GGA			

			CACCCCGGG CCT			
		A	_____	C		
GAM96	NKX3A	TGGGTCTTGCTCGTTGCCCAGG	1254	G_ GG	AAT	
		TGGGTCTTG TG GCCCAGG				
		ACCCAGAAC GC CGGGTCC				
		GA AA III				
GAM96	NKX3A	TGGGTCTTGCTCGTTGCCCAGG	1254 G	G_ GG	I	
		GGTCTTG TG GCCCAG				
		CCAGAAC GC CGGGTC				
		GA AA I				
GAM96	PRDM4	CAGAGTCCTCTACTCCAGCCC	1234 TC	__ A A	CAG	
		AGAGTCCT GC CCA GCCC				
		TCTCAGGA TG GGT CGGG				
		GA A _ TII				
GAM96	RBP4	TCAGAGTCTGGAATCTTAAGCCCCAG	1250	C CACC__	II	
		TCAGAGTC TG AAGCCCCAG				
		AGTCTCAG AC TTCGGGGTC				
		_ CTTAGAA II				
GAM96	RFX2	GGTCT-GGTGGGGGCCCTGG	1244 T	AGI		
		GGTCT GGTGGGGCCC				
		CCAGA CCACCCCGGG				
		_ ACC				
GAM96	RFX2	GGTCT-GGTGGGGGCCCTGG	1244 TGGGTC	A A		
		TTGGTGGGGCCC GG				
		GACCACCCCGGG CC				
		A _____ A A				
GAM96	SERPINE1	GGGTCTTGGTATGTTGCCCAGG	1239 GG	GG__	I	
		TCTTGGTG GCCCAG				
		AGAACCAT CGGGTC				
		ACAA I				
GAM96	SERPINE1	GGGTCTTGGTATGTTGCCCAGG	1239 TG	GG__	AAT	
		GGTCTTGGTG GCCCAGG				
		CCAGAACCAT CGGGTCC				
		ACAA GII				
GAM96	SYNGR1	GGGTCTAGAGTGGGGGCCCAGGA	1238 GG T_ _ I			
		TCT GGTGGGG CCCAGG				
		AGA TCACCCC GGGTCC				
		_ TC C I				
GAM96	SYNGR1	GGGTCTAGAGTGGGGGCCCAGGA	1238 TG T_ _ ATI			
		GGTCT GGTGGGG CCCAGGA				

		CCAGA TCACCCC GGGTCCT			
		___ TC C AII			
GAM96	SYNGR1	GGGTCTT---GGGCCAAGG 1243	GGTG	CA	
		GGGTCTT GGGCC			
		CCCAGAA CCCGG			
		___ TT			
GAM96	SYNGR1	GGGTCTT---GGGCCAAGG 1243	TG	GGTG	C
		GGTCTT GGGCC AGG			
		CCAGAA CCCGG TCC			
		___ ___ T			
GAM96	TCTA	TGGGTCTTGCTCTGTTGCCCAGG 1253	G__ GG	AAT	I
		TGGGTCTTG TG GCCCAGG			
		ACCCAGAAC AC CGGGTCC			
		GAG AA IIIT			
GAM96	TCTA	TGGGTCTTGCTCTGTTGCCCAGG 1253	GG	G__ GG	I
		GTCTTG TG GCCCAG			
		CAGAAC AC CGGGTC			
		___ GAG AA I			
GAM96	TLR4	TCAGAGTCC--CAGCCAGGCGCGAG 1249	GCA	A	CCCAGI
		TCAGAGTCCT CCA GC			
		AGTCTCAGGG GGT CG			
		TC_ C CGCTCI			
GAM96	TNFRSF10B	AGCGTCCTGCACAGAAGGCCCAG 1229	TCAGA	C_ C	I
		GTCCTGCAC AAG CCCAG			
		CAGGACGTG TTC GGGTC			
		G___ TC C G			
GAM96	VENTX2	TCAGGAGTC-TGCACCAAG 1247	_ C	CCCC	
		TCAG AGTC TGCACCAAG			
		AGTC TCAG ACGTGGTTC			
		C _ IIIG			
GAM96	WNT14	TGGG-CT-GGTCTGAGCCCAGGAA 1258	CT G	T	
		TGGGT TGGT GGGCCCAGGAA			
		ACCCG ACCA CTCGGGTCCTT			
		___ G I			
GAM96	WNT14	TGGG-CT-GGTCTGAGCCCAGGAA 1258	_ CT G	I	
		GGGT TGGT GGGCCCAGGA			
		CCCG ACCA CTCGGGTCCT			
		A _ G I			
GAM96	WNT3A	GAGTCCTGCTCCA---CCCAG 1237	TCAGAG	A	AGC
		TCCTGC CCA CCC			

		AGGACG GGT GGG		
		_____ A _____		
GAM96	ZNF134	CAGGG-CCTGT-CCAAGCCCC	1235 TC A T CA	A
		AG G CCTG CCAAGCCCC		
		TC C GGAC GGTTCTGGGG		
		__ C _ A _ A		
GAM97	CLCN6	AAAGCTGCAATGTTAAGAAT	1265 TAAA CTG	
		AGCTGT GTTAAGAAT		
		TCGACG CAATTCTTA		
		_____ TTA		
GAM97	DAG1	AAAAGCTGTTAGGCCAAAAAAT	1263 TA CT T I	
		AAAGCTGT GGT AAGAAT		
		TTTCGACA CCG TTTTTA		
		__ AT T T		
GAM97	EXTL2	TAAACAGAGGCCTAGTTAAGAAT	1268 TAAA_ CT	II
		AG GTCTGGTTAAGAAT		
		TC CGGATCAATTCTTA		
		ATTTG TC	II	
GAM97	GYPA	TAAATTCTGTAGCTCTGGTTAAGAA	1271 TAAA_____ TG	TIII
		AGC TCTGGTTAAGAA		
		TCG AGACCAATTCTT		
		ATTTAAGACA _	IIIT	
GAM97	IL5RA	TAAAAGCTGTCT-GTTGTGAAT	1274 GTTAA I	
		TAAAAGCTGTCTG GAAT		
		ATTTTCGACAGAC CTTA		
		AACA_ I		
GAM97	MCL1	TACAAGCTGTC---TTAAGAAT	1275 TAA GGT	
		AAGCTGTCT TAAGAAT		
		TTTCGACAGA ATTCTTA		
		ATG _____		
GAM97	MFAP3	AAAGGTGATGGGTTAAGAA	1264 TAAA C TCT T	
		AG TG GGTTAAGAA		
		TC AC CCAATTCTT		
		_____ C TAC C		
GAM97	MKLN1	TAAAACTTGTGATGGTTAAGA	1269 _ C_ ATI	
		TAAAAGCT GT TGGTTAAGA		
		ATTTTGA CA ACCAATTCT		
		A CT III		
GAM97	NR3C2	TAAAAGCTGCTTTTG-TAAG	1270 T GGT_ AAT	
		TAAAAGCTG CT TAAG		

		ATTTTCGAC GA ATTC	
		_ AAAC III	
GAM97	PHB	AAGGCTGT---GTTAAGAAT 1266 TAAAA CTG	
		GCTGT GTTAAGAA	
		CGACA CAATTCTT	
		C_____	
GAM97	RAI14	AAAAGTTGA--GGTTAAGAA 1262 TA C TCT	
		AAAG TG GGTTAAGAA	
		TTTC AC CCAATTCTT	
		__ A T__	
GAM97	SIRT2	AAGAACTG-CTGGTTAAGA 1261 TAAA T A	
		AGCTG CTGGTTAAGA	
		TTGAC GACCAATTCT	
		TC__ _ C	
GAM97	TACC1	AAGCTGTCTTTGTTTAAAAAT 1267 TAAAAG GG__ I	
		CTGTCT TTAAGAAT	
		GACAGA AATTTTTA	
		_____ AACAA T	
GAM97	Z39IG	TAAAAGCTGTCTGGCCCTGAAGAA 1272 AA TII	
		TAAAAGCTGTCTGGTT GAA	
		ATTTTCGACAGACCGG CTT	
		GA CTT	
GAM97	ZNF179	TAAAGGCTGTCTGGCTTAGCTCAGAAT1273 A A AATIIIA	
		TAAA GCTGTCTGGTT AG	
		ATTT CGACAGACCGA TC	
		C A GAGTCTT	
GAM98	ABCC3	TGGTGTAGTCCATGATAGTGTT 1286 GC C_ TTI	
		GTGTAGTC TG AGT	
		CACATCAG AC TCA	
		GT TA CII	
GAM98	APPBP2	TTGGCATGTGTTCACTGCAGTTTT 1288 TATTG AG I	
		GTGT TCGCTGCAGTTTT	
		TACA AGTGACGTCAAAA	
		CCG__ CA G	
GAM98	APPBP2	TTGGCATGTGTTCACTGCAGTTTT 1288 TG AG I	
		GTGT TCGCTGCAGTTTT	
		TACA AGTGACGTCAAA	
		CG CA I	
GAM98	CAPN1	TTGGGG--GTCGCTGCAGT 1290 TGTA I	
		TTGG GTCGCTGCAG	

		AACC CAGCGACGTC	
		CC__ A	
GAM98 CAPN1		TTGGGG--GTCGCTGCAGT 1290 TATTGGTGTA	
		GTCGCTGCAGTT	
		CAGCGACGTCAG	
		CCCC_____	
GAM98 CASP6		TTTGTGTAACC-CTGCAGTTT 1291 TATTG GT G	
		GTGTA C CTGCAGTTT	
		CACAT G GACGTCAAA	
		A__ TG_	
GAM98 CASP6		TTTGTGTAACC-CTGCAGTTT 1291 TG_ GT G I	
		GTGTA C CTGCAGTT	
		CACAT G GACGTCAA	
		AAA TG_ I	
GAM98 CYFIP2		GTGGTCATGGCTGCAGTTT 1282 A __ III	
		GT GTC GCTGCAGTT	
		CA CAG CGACGTCAA	
		C TAC AII	
GAM98 FLNB		TGCTGTAGTCGCCTGGCAG 1285 G __ III	
		TG TG TAGTCGCT GCA	
		AC ACATCAGCGG CGT	
		G AC CII	
GAM98 FLNB		TGCTGTAGTCGCCTGGCAG 1285 TATTGG __ TTT	
		TGTAGTCGCT GCAG	
		ACATCAGCGG CGTC	
		_____ AC TCA	
GAM98 GLRX		TTGGTGTAGGGGGCTGTAAGTTTT 1289 TATT TC_ C_ I	
		GGTGTAG GCTG AGTTTT	
		CCACATC CGAC TCAAAA	
		_____ CCC AT T	
GAM98 GLRX		TTGGTGTAGGGGGCTGTAAGTTTT 1289 TG TC_ C_ I	
		GTGTAG GCTG AGTTT	
		CACATC CGAC TCAAA	
		___ CCC AT I	
GAM98 MEIS1		ATTGTTG-A-TGACTGCAGTTTT 1280 _____ TAGTC I	
		TTGGTG GCTGCAGTTT	
		AACTAC TGACGTCAAA	
		TAAC _____ I	
GAM98 MEIS1		ATTGTTG-A-TGACTGCAGTTTT 1280 TA_ TAGTC	
		TTGGTG GCTGCAGTTTT	

		AACTAC TGACGTCAAAA			
		AAC _____			
GAM98	SIGLEC9	GGTG-AGTCTCTGCAGTTT	1281	T G I	
		GGTG AGTC CTGCAGTT			
		CCAC TCAG GACGTCAA			
		_ A A			
GAM98	SOX11	TGGCCTAGCAGCTGCAGTT	1287	G C II	
		TGGT TAGT GCTGCAGT			
		ACCG ATCG CGACGTCA			
		G T AI			
GAM98	SOX11	TGGCCTAGCAGCTGCAGTT	1287	TATTGGTG C T	
		TAGT GCTGCAGTT			
		ATCG CGACGTCAA			
		GG_____ T T			
GAM98	SP3	ATAGGTGAACT-GCTGCAGTT	1278	TATT T TC T	
		GGTG AG GCTGCAGTT			
		CCAC TT CGACGTCAA			
		AT__ _ GA T			
GAM98	SP3	ATAGGTGAACT-GCTGCAGTT	1278	TT_ T TC I	
		GGTG AG GCTGCAGT			
		CCAC TT CGACGTCA			
		TAT _ GA I			
GAM98	SPAG8	TACTGGTGTGAGAAGCTGCAGTT	1283	_ TC TTI	
		TATTGGTGT AG GCTGCAGTT			
		ATGACCACA TC CGACGTCAA			
		AC TT III			
GAM98	SPAG8	TACTGGTGTGAGAAGCTGCAGTT	1283	AT _ TC I	
		TGGTGT AG GCTGCAGT			
		ACCACA TC CGACGTCA			
		_ AC TT I			
GAM98	THY1	TTGGTTTTATTG-TGCAGTTTT	1292	_ GTAGTCGC I	
		TGGT TGCAGTTT			
		ACCA ACGTCAAA			
		A AAATAAC_ I			
GAM98	THY1	TTGGTTTTATTG-TGCAGTTTT	1292	TATT GTAGTCGC	
		GGT TGCAGTTTT			
		CCA ACGTCAAAA			
		_____ AAATAAC_			
GAM98	TLR4	ATTGGTGTATTCAAAGCAGTT	1279	TA G CT T	
		TTGGTGTA TCG GCAGTTT			

		AACCACAT AGT CGTCAAG		
		___ A TT I		
GAM98	TLR4	ATTGGTGTATTCAAAGCAGTT 1279	G CT I	
		TTGGTGTATCG GCAGT		
		AACCACAT AGT CGTCA		
		A TT I		
GAM98	TTID	TAATGGTGTAGTTG--GCTGTTTT 1284 T	C_ CAGI	
		TGGTGTAGT GCTG		
		ACCACATCA CGAC		
		T AC AAII		
GAM98	TTID	TAATGGTGTAGTTG--GCTGTTTT 1284 TAT	C_ CAGTTTT	
		TGGTGTAGT GCTG		
		ACCACATCA CGAC		
		ATT AC AAAAII		
GAM99	CDH10	GACATGTACCTAACAGAAGCG 1300	___ CC III	
		GACATGTACC ACAG GC		
		II		
		CTGTACATGG TGTC CG		
		AT TT CII		
GAM99	CDH10	GACATGTACCTAACAGAAGCG 1300 ACGA	___ CC C	
		CATGTACC ACAG GCG GC		
		III II		
		GTACATGG TGTC CGC CG		
		___ AT TT _		
GAM99	LASS1	CACGTACAGCCGCCGCGCGC 1297	CACA I	
		ATGTAC GCCGCGCG		
		TGCATG CGGCGCGC		
		TCGG I		
GAM99	MADH7	ACG-CGTGCACACACAGCCGC 1295	ACA _ GCG	
		ACG TGTAC CACAGCCGC		
		TGC ACGTG GTGTCGGCG		
		GC_ T III		
GAM99	MADH7	ACG-CGTGCACACACAGCCGC 1295	ACA _ I	
		CG TGTAC CACAGCCG		
		GC ACGTG GTGTCGGC		
		GC_ T I		
GAM99	PACE4	GAGATTTACTACACAGCCGC 1299	ACGACATG _ CG	
		TAC CACAGCCGCG		
		ATG GTGTCGGCGT		
		CTAA_ AT CI		
GAM99	PACE4	GAGATTTACTACACAGCCGC 1299	GACATG _ III	
		TAC CACAGCCG		

		ATG GTGTCGGC		
		CTCTAA AT GII		
GAM99	PKIB	CATG-ACTCCAGCCGCGCGC	1298	_ T CA I
		ATG AC CAGCCGCGCG		
		TAC TG GTCGGCGCGC		
		G _ AG I		
GAM99	PKIB	CATG-ACTCCAGCCGCGCGC	1298	ACGACATGT CA
		AC CAGCCGCGCG		
		TG GTCGGCGCGC		
		_____ AG		
GAM99	REQ	GGGGCTGGGCCCAAGGCAAGCAGA	1301	T T GC_ ____ TCGI
		GG GC GCCC GCAAGCAGA		
		CC CG CGGG CGTTCGTCT		
		_ _ ACC TTC CIII		
GAM99	RUNX1	TGGTTTG-GACAGCAAGCAGATC	1302	GCGC CC G
		TGGT GC GCAAGCAGATC		
		ACCA TG CGTTCGTCTAG		
		AACC T_ I		
GAM99	TFEB	CATGTACCAGGCACTGCCGC	1296	_ _ IIIG
		CATGTACCA CA GCCG		
		GTACATGGT GT CGGC		
		CC GA GIII		
GAM99	TFEB	CATGTACCAGGCACTGCCGC	1296	ACGA T CACA G
		CA GTAC GCCGCGC		
		GT CGTG CGGCGTG		
		ATG_ C A_ G		
GAM100	ADH5	TGGCAATGT-GAT-CTCGAAGTG	1313	G GGT G A
		TGG AA TGAT CTCGAAGTG		
		ACC TT ACTA GAGCTTCAC		
		G AC_ _ I		
GAM100	CDH11	AAGATTGATGCTC-AAGAGA	1305	TGGGAAGG AGTG
		TTGATGCTCGA		
		AACTACGAGTT		
		_____ CTCT		
GAM100	CLN2	TGGGAAGGTGGACGAT-GAAATG	1314	T CTC A
		TGGGAAGGT GATG GAAGTG		
		ACCCTTCCA CTGC CTTTAC		
		C TA_ I		
GAM100	CMAR	GAAGGTTGAGGC-CGCAGTGA	1307	TGGGAA T T A
		GGTTGA GC CG AGTG		

	CCAACT CG GC TCAC		
	_____ C _ G		
GAM100 FUT4	TGGGAAGGTACAGGAGGCTCGA 1310	T___ T	AGTGA
	TGGGAAGGT GA GCTCGA		
	ACCCTTCCA CT CGAGCT		
	TGTC C IIIAG		
GAM100 IL10RA	GGAAGCTCTGATGCTCG-AGTG 1308	TGGG G_	A A
	AAG TTGATGCTCGA GTG		
	TTC GACTACGAGCT CAC		
	_____ GA _ C		
GAM100 NFRKB	GAAGGTTGACCCT-GATAGT 1306	TGGGAA	G C _ G
	GGTTGAT CT GA AGT		
	CCAACTG GA CT TCA		
	_____ G _ A G		
GAM100 SKI	GGAAGGTTG-TGGACAAAGTG 1309	TG	A CT A
	GGAAGGTTG TG CGAAGTG		
	CCTTCCAAC AC GTTTCAC		
	_____ _ CT G		
GAM100 TNF	TGGGAAGGTTGGATGTTG 1312	_ C	AAGTG
	TGGGAAGGTTG ATG TCG		
	ACCCTTCCAAC TAC AGC		
	C A IIIAG		
GAM100 VAX2	TGGGAAGGTGCTG-TGCTCG 1311	_ A	AAGTG
	TGGGAAGGT TG TGCTCG		
	ACCCTTCCA AC ACGAGC		
	CG _ IIIAG		
GAM101 ANKRD3	TGAGCCAGCTTCACCTGGA 1321	_ C	II
	TGA CTA CTTACCTGG		
	ACT GGT GAAGTGGACC		
	C C TI		
GAM101 BAZ2A	CTACAGCTGCACTTGTGGAACATCA 1319	TAC T C_	I
	CT CAC TGGAACATC		
	GA GTG ACCTTGTAG		
	C_ C AAC I		
GAM101 CPO	ACTA---TCACCTGGAGCA 1318	CCT	AC
	ACTA TCACCTGGA		
	TGAT AGTGGACCT		
	_____ CG		
GAM101 DPP4	TGCCT-CTTTCAGTAGGAACATCA 1326	GA_ ACC	CT I
	CT TTCAC GGAACATC		

	GA AAGTG CCTTGTAG			
	ACG GA_ AT I			
GAM101 DUOX1	TGACTATGGCCACCTGGAACA	1324	CCT	I
	GACTA TCACCTGGAAC			
	CTGAT GGTGGACCTTG			
	ACC I			
GAM101 EIF4G2	TACCTTCACCGAGAAC-TCA	1320 _	T	ATCI
	ACCTTCACC GGAAC			
	TGGAAGTGG TCTTG			
	A C AGII			
GAM101 GNAS	TGACTTTGTCCACCTGGAAC	1323	ACC	I
	GACT TTCACCTGGAA			
	CTGA AGGTGGACCTT			
	AAC I			
GAM101 MGAM	TGATTAGCTTCAAGACCTGGAAC	1322	GACTAC	___ I
	CTTC ACCTGGAA			
	GAAG TGGACCTT			
	ATC___ TTC I			
GAM101 PCDH11Y	ACATGCACCTGGAAAACCA	1317	ACCTT	C II
	CACCTGGAA ATC			
	GTGGACCTT TGG			
	TGTAC T TI			
GAM101 SLC21A3	TGACTGACG-CACCTGGAAAATC	1325 _ _	CTT	CATI
	GACT AC CACCTGGAA			
	CTGA TG GTGGACCTT			
	A C C_ TTAI			
GAM102 ANKRD3	TGAGCCAGCTTCACCTGGA	1321 _	C	ACATC
	TGA CTA CTTACCTGGA			
	ACT GGT GAAGTGGACCT			
	C C IIIAC			
GAM102 BAZ2A	CTACAGCTGCACTTGTGGAACATCA	1319	TGACTAC T C_	II
	CT CAC TGGAACATCA			
	GA GTG ACCTTGTAGT			
	GTC_ C AAC GT			
GAM102 CPO	ACTA---TCACCTGGAGCA	1318	TGACTACCT	A
	TCACCTGGA CA			
	AGTGGACCT GT			
	AT_ C			
GAM102 DPP4	TGCCT-CTTTCACCTAGGAACATCA	1326	TGA ACC	CT I
	CT TTCAC GGAACATCA			

	GA AAGTG CCTTGTAGT		
	ACG GA_ AT I		
GAM102 DUOX1	TGACTATGGCCACCTGGAACA 1324	CCT	TCA
	TGACTA TCACCTGGAACA		
	ACTGAT GGTGGACCTTGT		
	ACC III		
GAM102 EIF4G2	TACCTTCACCGAGAAC-TCA 1320	TGACTACC	T A
	TTCACC GGAAC TC		
	AAGTGG TCTTG AG		
	_____ C _		
GAM102 GNAS	TGACTTTGTCCACCTGGAAC 1323	ACC	ATC
	TGACT TTCACCTGGAAC		
	ACTGA AGGTGGACCTTG		
	AAC III		
GAM102 MGAM	TGATTAGCTTCAAGACCTGGAAC 1322	C C ____	ATCAI
	TGA TA CTTC ACCTGGAAC		
	ACT AT GAAG TGGACCTTG		
	A C TTC IIIAC		
GAM102 SLC21A3	TGACTGACG-CACCTGGAAAATC 1325	_ CTT	C A
	TGACT AC CACCTGGAA ATC		
	ACTGA TG GTGGACCTT TAG		
	C C_ T I		
GAM103 ACTB	CAAGGGACTTCCTGTAACAATGCAT 1345	AAGG ____	C I
	GACTTCT GCAAT CA		
	CTGAAGG TGTTA GT		
	_____ ACAT C I		
GAM103 ACTB	CAAGGGACTTCCTGTAACAATGCAT 1345	TACA ____	C GII
	AGGGACTTCT GCAAT CAT		
	TCCCTGAAGG TGTTA GTA		
	_____ ACAT C GAI		
GAM103 COL9A1	CAAGTAGGACTTCTGTAATC 1343	CAA_	CAATIII
	GGGACTTCTG		
	TCCTGAAGAC		
	GTTCA ATTAGII		
GAM103 COL9A1	CAAGTAGGACTTCTGTAATC 1343	TACAA	C CAT
	GGGACTTCTG AATC		
	TCCTGAAGAC TTAG		
	TCA_ A TAI		
GAM103 HK1	AACGCACTGTCCTTGCAATCCA 1339	AAGGGA_ C	III
	CTT TGCAATCC		

	GGA ACGTTAGG	
	TTGCGTGACA _ TII	
GAM103 HK1	AACGCACTGTCCTTGCAATCCA 1339 TACAAG G _ _ TG	
	G ACT TCT GCAATCCA	
	I III III IIIIIII	
	C TGA AGG CGTTAGGT	
	_____ G C AA TG	
GAM103 INHBB	ACATGGGCAACTTCTGCAA 1340 A _ III	
	ACA GGG ACTTCTGCA	
	III III IIIIIII	
	TGT CCC TGAAGACGT	
	A GT TII	
GAM103 INHBB	ACATGGGCAACTTCTGCAA 1340 TACAA _ TCCAT	
	GGG ACTTCTGCAA	
	III IIIIIII	
	CCC TGAAGACGTT	
	GTA_ GT TIIIG	
GAM103 KIF5C	AAGTGGATCTTCTGCAA-CCAT 1338 TACAAG _ T G	
	GGA CTTCTGCAA CCAT	
	III IIIIIII III	
	CCT GAAGACGTT GGTA	
	A_____ A _ G	
GAM103 KIF5C	AAGTGGATCTTCTGCAA-CCAT 1338 AG _ T I	
	GGA CTTCTGCAA CCA	
	III IIIIIII III	
	CCT GAAGACGTT GGT	
	CA A _ I	
GAM103 NPTX2	ACAAGGGACATGGCCACTCCA 1342 TTCT AA_ I	
	CAAGGGAC GC TCC	
	IIIIII II III	
	GTTCCCTG CG AGG	
	TAC_ GTG I	
GAM103 NPTX2	ACAAGGGACATGGCCACTCCA 1342 TA TTCT AA_ TG	
	CAAGGGAC GC TCCA	
	IIIIII II III	
	GTTCCCTG CG AGGT	
	_ TAC_ GTG CI	
GAM103 PCDHB1	ACAAGCGCGCTCTCTGCAATC 1341 GGA_ _ III	
	ACAAG CT TCTGCAAT	
	IIII II IIIIIII	
	TGTTT GA AGACGTTA	
	GCGC G GII	
GAM103 PCDHB1	ACAAGCGCGCTCTCTGCAATC 1341 TA GGA_ _ CATG	
	CAAG CT TCTGCAATC	
	III II IIIIIII	
	GTTC GA AGACGTTAG	
	_ GCGC G TIII	
GAM103 RUNX1	CAAGGCAGAAATCTGCAATCC 1344 _ CT III	
	CAAGG GA TCTGCAATC	
	IIII II IIIIIII	

	GTTCC CT AGACGTTAG		
	GT TT GII		
GAM103 RUNX1	CAAGGCAGAAATCTGCAATCC 1344 TACAAG CT ATG		
	GGA TCTGCAATCC		
	III		
	TCT AGACGTTAGG		
	TCCG__ TT ATI		
GAM103 TIAL1	TATAAGG-ACTTCTGTACATC 1346 ACA _ ATI		
	AGGGACTTCTG CA		
	TTCCTGAAGAC GT		
	A__ A GTA		
GAM103 TIAL1	TATAAGG-ACTTCTGTACATC 1346 TACA _ _ CATG		
	AGGGACTTCTG CA ATC		
	TTCCTGAAGAC GT TAG		
	ATA_ A G IIIG		
GAM104 AQP1	CCTCCGCCCCGCCCTGCCCTGC 1369 __ CA I		
	CTGCCC GCCCCTGCCTCTG		
	GGCGGG CGGGGACGGGGAC		
	GA _ I		
GAM104 AQP1	CCTCCGCCCCGCCCTGCCCTGC 1369 AC CA I		
	CTGCCC GCCCCTGCCTCTGC		
	GGCGGG CGGGGACGGGGACG		
	GA _ G		
GAM104 AQP6	GCCCCTGCCCTGCCCTG 1384 A II		
	GCCCC GCCCCTGCCTCT		
	CGGGG CGGGGACGGGGA		
	A CI		
GAM104 AQP6	GCCCCTGCCCTGCCCTG 1384 AC A C G		
	CTGCCCC GCCCCTGC TCT		
	GACGGGG CGGGGACG AGG		
	_ A _ I		
GAM104 AQP6	GCTCC-GCCCCTGCCCTGC 1388 ____ A CTCTI		
	GCCCC GCCCCTGC		
	CGGGG CGGGGACG		
	GAGG A IIITC		
GAM104 AQP6	GCTCC-GCCCCTGCCCTGC 1388 ACCT A G		
	GCCCC GCCCCTGCCTCT		
	CGGGG CGGGGACGGGGA		
	G__ A I		
GAM104 AVPR2	CCTGGCCCCAGCCTGGTCCTTCCT 1358 _ ____ G IIIA		
	CCTG CCCCAGCC CCT CC		

	GGAC GGGGTCGG GGA GG		
	C ACCA A AIII		
GAM104 AVPR2	CCTGGCCCCAGCCTGGTCCTTCCT 1358 ACCT	_____ G	CTGCI
	GCCCCAGCC CCT CCT		
	CGGGGTCGG GGA GGA		
	GAC_ ACCA A AIIIC		
GAM104 BLTR2	ACCTGCCCCA-CTCCTGGCCTC 1352	G C _	TGC
	ACCTGCCCCA C CCTG CCTC		
	TGGACGGGGT G GGAC GGAG		
	_A C III		
GAM104 BLTR2	ACCTGCCCCA-CTCCTGGCCTC 1352	G C _	I
	CCTGCCCCA C CCTG CCT		
	GGACGGGGT G GGAC GGA		
	_A C I		
GAM104 BLTR2	CTTCCCTGCAGCC--TGCCTCT 1371 A_	CCC CC	G
	CCTGC AGCC TGCCTCT		
	GGACG TCGG ACGGAGA		
	AG _ _ A		
GAM104 BLTR2	CTTCCCTGCAGCC--TGCCTCT 1371 TGC	A C_	I
	CCC GC CCTGCCTC		
	GGG CG GGACGGAG		
	AA_ A TC I		
GAM104 CKAP1	CCCGCCCTGCCCCCTGCCTCTG 1367	CAG	I
	CTGCCC CCCCTGCCTCT		
	GGCGGG GGGGACGGAGA		
	ACG I		
GAM104 CKAP1	CCCGCCCTGCCCCCTGCCTCTG 1367 AC	CAG	C
	CTGCCC CCCCTGCCTCTG		
	GGCGGG GGGGACGGAGAC		
	_ ACG A		
GAM104 COMT	GCCCCAGCCCCAGTGCCTC 1383	_	III
	GCCCCAGCCCC TGCCT		
	CGGGGTCGGGG ACGGA		
	TC GII		
GAM104 COMT	GCCCCAGCCCCAGTGCCTC 1383 ACCT	CCCC	TG
	GCCCCAG TGCCTC		
	CGGGGTC ACGGAG		
	GT_ _ TC		
GAM104 CTSF	TGCCCCAGCCCAGTGCCCTCTGC 1390 ACCTGC	C_ _	I
	CCCAGCCC TGCC TCTGC		

	GGGTCGGG ACGG AGACG			
	_____ TC G A			
GAM104 CTSF	TGCCCCAGCCAGTGCCCTCTGC	1390 GC	C_ _ I	
	CCCAGCCC TGCC TCTG			
	GGGTCGGG ACGG AGAC			
	_____ TC G I			
GAM104 DVL1	CCTGCCCCCACCCTGCCTC	1365 AGC	I	
	CTGCCCC CCCTGCCT			
	GACGGGG GGGACGGA			
	GGT I			
GAM104 DVL1	CCTGCCCCCACCCTGCCTC	1365 AC AGC	G	
	CTGCCCC CCCTGCCTCT			
	GACGGGG GGGACGGAGG			
	_____ GGT I			
GAM104 EGR4	CCTGCCCCAG--CCTGTCTCTG	1368 CC C I		
	CCTGCCCCAGCC TG CTC			
	GGACGGGGTCGG AC GAG			
	_____ A A			
GAM104 EGR4	CCTGCCCCAG--CCTGTCTCTG	1368 AC CC C		
	CTGCCCCAGCC TG CTCTG			
	GACGGGGTCGG AC GAGAC			
	_____ A			
GAM104 EIF4G1	CCTGCCCCAGCTCCCACCCT	1362 C TG II		
	CCTGCCCCAGC CC CC			
	GGACGGGGTCG GG GG			
	A GT GA			
GAM104 EIF4G1	CCTGCCCCAGCTCCCACCCT	1362 AC C TG CTG		
	CTGCCCCAGC CC CCT			
	GACGGGGTCG GG GGG			
	_____ A GT AAI			
GAM104 EIF4G1	GCCCCAAGCCATCCTGCCTCT	1382 _ _ III		
	GCCCCA GCC CCTGCCTC			
	CGGGGT CGG GGACGGAG			
	T TA AII			
GAM104 EIF4G1	GCCCCAAGCCATCCTGCCTCT	1382 ACCTGCCCC _ GC		
	AGCC CCTGCCTCT			
	TCGG GGACGGAGA			
	GT_____ TA AG			
GAM104 FOXE3	CCTCTCCCAGCCCCCTTACTCTG	1361 ACCTGC GC_ CI		
	CCCAGCCCCT CTCTG			

	GGGTCGGGGG GAGAC		
	GAGA_ AAT AI		
GAM104 FOXE3	CCTCTCCCAGCCCCCTTACTCTG 1361 CTGC GC_ I		
	CCCAGCCCCT CTCT		
	GGGTCGGGGG GAGA		
	AGA_ AAT I		
GAM104 GIPR	ACTTGCTCCTGCAGCCCCTGCCACCGC1349_ CCC T I		
	CCTGC AGCCCCTGCC CTG		
	GGACG TCGGGGACGG GGC		
	CGA _ T I		
GAM104 GIPR	ACTTGCTCCTGCAGCCCCTGCCACCGC1349 A_ CCC T III		
	CCTGC AGCCCCTGCC CTGC		
	GGACG TCGGGGACGG GGCG		
	TGAACGA _ T III		
GAM104 H1F0	ACCGGGCTCTGCCTCTGCCTCTGC 1354 T_ CCCA C I		
	ACC GC GCC CTGCCTCTGC		
	TGG CG CGG GACGGAGACG		
	CC AGA_ A I		
GAM104 H1F0	ACCGGGCTCTGCCTCTGCCTCTGC 1354 CCTGCCCCA C I		
	GCC CTGCCTCTG		
	CGG GACGGAGAC		
	GGCCCGAGA A I		
GAM104 H1F0	CCCAGCCCC-GCCGGTCTG 1356 T TCTII		
	CCCAGCCCC GCC		
	GGGTCGGGG CGG		
	_ CCAGA		
GAM104 H1F0	CTGCCTCTGCCTCTGCCTCTGC 1380 CCA C I		
	TGCC GCC CTGCCTCTG		
	ACGG CGG GACGGAGAC		
	AGA A I		
GAM104 H1F0	CTGCCTCTGCCTCTGCCTCTGC 1380 ACCT CCA C		
	GCC GCC CTGCCTCTGC		
	CGG CGG GACGGAGACG		
	_ AGA A		
GAM104 H1F0	GCACCGGGCTCTGCCTCTGC 1385 ACCTGCCCCA C G		
	GCC CTGCCTCT		
	CGG GACGGAGA		
	GCCCGAGA_ A I		
GAM104 H1F0	GCACCGGGCTCTGCCTCTGC 1385 C_ CA CC I		
	CC GC CTGCCTCTG		

	GG CG GACGGAGAC	
	GT CC A_ I	
GAM104 HD	ACCAGCCC--GCCCCTGCCCCCGC 1353 T CA	
	ACC GCCC GCCCCTGCCTCTGC	
	TGG CGGG CGGGGACGGGGGCG	
	T _	
GAM104 HD	ACCAGCCC--GCCCCTGCCCCCGC 1353 T CA I	
	ACC GCCC GCCCCTGCCTCT	
	TGG CGGG CGGGGACGGGGG	
	T _ C	
GAM104 KCNK4	CCGGCCCTCAGCCCCTGTCT 1360 T _ CCII	
	CC GCCC CAGCCCCTG	
	GG CGGG GTCGGGGAC	
	C A AGAI	
GAM104 KCNK4	CCGGCCCTCAGCCCCTGTCT 1360 ACCT _ CC	
	GCCC CAGCCCCTG TCTG	
	CGGG GTCGGGGAC AGAC	
	GC_ A _	
GAM104 LZTR1	CTGCCCCAGCTCCTGCTCTCT 1375 ACCT C _ GC	
	GCCCCAGC CCTGC CTCT	
	CGGGGTCTG GGACG GAGA	
	_ A A GA	
GAM104 LZTR1	CTGCCCCAGCTCCTGCTCTCT 1375 T C _ I	
	GCCCCAGC CCTGC CTC	
	CGGGGTCTG GGACG GAG	
	_ A A I	
GAM104 MAPT	CTGCCC-AGCCCCTGCCTCGGC 1378 _ C TGI	
	TGCCC AGCCCCTGCCTC	
	ACGGG TCGGGGACGGAG	
	G _ CCI	
GAM104 MAPT	CTGCCC-AGCCCCTGCCTCGGC 1378 ACCTGC T	
	CCCAGCCCCTGCCTC GC	
	GGGTCTGGGGACGGAG CG	
	C_ C	
GAM104 MECP2	CTGCCCCAG-CCCTGGTCCTC 1374 CTG_ II	
	CTGCCCCAGCCC CCT	
	GACGGGGTCTGGG GGA	
	ACCA GI	
GAM104 MECP2	CTGCCCCAG-CCCTGGTCCTC 1374 ACCT CTG_	
	GCCCCAGCCC CCTCTG	

	CGGGGTCGGG GGAGGC			
	_____ ACCA			
GAM104 MMP2	GCCCCAGCCCCGCGCCGC 1387	T	I	
	CCCCAGCCCCTGCC CTG			
	GGGGTCGGGGGCGG GGC			
	C I			
GAM104 MMP2	GCCCCAGCCCCGCGCCGC 1387	ACCTGCCC		T
	CAGCCCCTGCC CTG			
	GTCGGGGGCGG GGC			
	C			
GAM104 MYO1E	ACCAGCCCCAGCCCCTGAC-CTGC 1350	T	_	C T I
	ACC GCCCC AGCCCCTG C CTGC			
	I			
	TGG CGGGG TCGGGGAC G GACG			
	T G T _ I			
GAM104 MYO1E	ACCAGCCCCAGCCCCTGAC-CTGC 1350	T	_	_ CTGI
	CC GCCCC AGCCCCTG CCT			
	GG CGGGG TCGGGGAC GGA			
	T G T C			
GAM104 NCOA6IP	CTGCCCCTGCCCTGCCCCCGC 1379	A		I
	TGCCCC GCCCCTGCCTCTG			
	ACGGGG CGGGGACGGGGGC			
	A I			
GAM104 NCOA6IP	CTGCCCCTGCCCTGCCCCCGC 1379	ACCT		A
	GCCCC GCCCCTGCCTCTGC			
	CGGGG CGGGGACGGGGGCG			
	A			
GAM104 OFD1	CCTGCCCTCAGAACCCTGCCTCTG 1359	AC	_ C_	CI
	CTGCCC CAG CCCTGCCTCTG			
	GACGGG GTC GGGACGGAGAC			
	_ A TT AI			
GAM104 OFD1	CCTGCCCTCAGAACCCTGCCTCTG 1359	CT	_ C_	I
	GCCC CAG CCCTGCCTCT			
	CGGG GTC GGGACGGAGA			
	_ A TT I			
GAM104 PCDHGA1	CCTGCCCTAGCTCCCTGCCTC 1363	AC	C _	GC
	CTGCCC AGC CCCTGCCTCT			
	GACGGG TCG GGGACGGAGG			
	_ A A II			
GAM104 PCDHGA1	CCTGCCCTAGCTCCCTGCCTC 1363	C	C _	I
	TGCCC AGC CCCTGCCT			

		ACGGG TCG GGGACGGA				
		— A A I				
GAM104 PCDHGA10		CCTGCCCTAGCTCCCTGCCTC	1363	AC	C _	GC
		CTGCCC AGC CCCTGCCTCT				
		GACGGG TCG GGGACGGAGG				
		— A A II				
GAM104 PCDHGA10		CCTGCCCTAGCTCCCTGCCTC	1363	C C _	I	
		TGCCC AGC CCCTGCCT				
		ACGGG TCG GGGACGGA				
		— A A I				
GAM104 PCDHGA11		CCTGCCCTAGCTCCCTGCCTC	1363	AC	C _	GC
		CTGCCC AGC CCCTGCCTCT				
		GACGGG TCG GGGACGGAGG				
		— A A II				
GAM104 PCDHGA11		CCTGCCCTAGCTCCCTGCCTC	1363	C C _	I	
		TGCCC AGC CCCTGCCT				
		ACGGG TCG GGGACGGA				
		— A A I				
GAM104 PCDHGA12		CCTGCCCTAGCTCCCTGCCTC	1363	AC	C _	GC
		CTGCCC AGC CCCTGCCTCT				
		GACGGG TCG GGGACGGAGG				
		— A A II				
GAM104 PCDHGA12		CCTGCCCTAGCTCCCTGCCTC	1363	C C _	I	
		TGCCC AGC CCCTGCCT				
		ACGGG TCG GGGACGGA				
		— A A I				
GAM104 PCDHGA2		CCTGCCCTAGCTCCCTGCCTC	1363	AC	C _	GC
		CTGCCC AGC CCCTGCCTCT				
		GACGGG TCG GGGACGGAGG				
		— A A II				
GAM104 PCDHGA2		CCTGCCCTAGCTCCCTGCCTC	1363	C C _	I	
		TGCCC AGC CCCTGCCT				
		ACGGG TCG GGGACGGA				
		— A A I				
GAM104 PCDHGA3		CCTGCCCTAGCTCCCTGCCTC	1363	AC	C _	GC
		CTGCCC AGC CCCTGCCTCT				
		GACGGG TCG GGGACGGAGG				
		— A A II				
GAM104 PCDHGA3		CCTGCCCTAGCTCCCTGCCTC	1363	C C _	I	
		TGCCC AGC CCCTGCCT				

		ACGGG TCG GGGACGGA				
		— A A I				
GAM104 PCDHGA4	CCTGCCCTAGCTCCCTGCCTC	1363 AC	C	_		GC
	CTGCCC AGC CCCTGCCTCT					
	GACGGG TCG GGGACGGAGG					
	— A A II					
GAM104 PCDHGA4	CCTGCCCTAGCTCCCTGCCTC	1363 C	C	_		I
	TGCCC AGC CCCTGCCT					
	ACGGG TCG GGGACGGA					
	— A A I					
GAM104 PCDHGA5	CCTGCCCTAGCTCCCTGCCTC	1363 AC	C	_		GC
	CTGCCC AGC CCCTGCCTCT					
	GACGGG TCG GGGACGGAGG					
	— A A II					
GAM104 PCDHGA5	CCTGCCCTAGCTCCCTGCCTC	1363 C	C	_		I
	TGCCC AGC CCCTGCCT					
	ACGGG TCG GGGACGGA					
	— A A I					
GAM104 PCDHGA6	CCTGCCCTAGCTCCCTGCCTC	1363 AC	C	_		GC
	CTGCCC AGC CCCTGCCTCT					
	GACGGG TCG GGGACGGAGG					
	— A A II					
GAM104 PCDHGA6	CCTGCCCTAGCTCCCTGCCTC	1363 C	C	_		I
	TGCCC AGC CCCTGCCT					
	ACGGG TCG GGGACGGA					
	— A A I					
GAM104 PCDHGA7	CCTGCCCTAGCTCCCTGCCTC	1363 AC	C	_		GC
	CTGCCC AGC CCCTGCCTCT					
	GACGGG TCG GGGACGGAGG					
	— A A II					
GAM104 PCDHGA7	CCTGCCCTAGCTCCCTGCCTC	1363 C	C	_		I
	TGCCC AGC CCCTGCCT					
	ACGGG TCG GGGACGGA					
	— A A I					
GAM104 PCDHGA8	CCTGCCCTAGCTCCCTGCCTC	1363 AC	C	_		GC
	CTGCCC AGC CCCTGCCTCT					
	GACGGG TCG GGGACGGAGG					
	— A A II					
GAM104 PCDHGA8	CCTGCCCTAGCTCCCTGCCTC	1363 C	C	_		I
	TGCCC AGC CCCTGCCT					

		ACGGG TCG GGGACGGA				
		— A A I				
GAM104	PCDHGA9	CCTGCCCTAGCTCCCTGCCTC	1363	AC	C _	GC
		CTGCCC AGC CCCTGCCTCT				
		GACGGG TCG GGGACGGAGG				
		— A A II				
GAM104	PCDHGA9	CCTGCCCTAGCTCCCTGCCTC	1363	C C	_ I	
		TGCCC AGC CCCTGCCT				
		ACGGG TCG GGGACGGA				
		— A A I				
GAM104	PCDHGB1	CCTGCCCTAGCTCCCTGCCTC	1363	AC	C _	GC
		CTGCCC AGC CCCTGCCTCT				
		GACGGG TCG GGGACGGAGG				
		— A A II				
GAM104	PCDHGB1	CCTGCCCTAGCTCCCTGCCTC	1363	C C	_ I	
		TGCCC AGC CCCTGCCT				
		ACGGG TCG GGGACGGA				
		— A A I				
GAM104	PCDHGB2	CCTGCCCTAGCTCCCTGCCTC	1363	AC	C _	GC
		CTGCCC AGC CCCTGCCTCT				
		GACGGG TCG GGGACGGAGG				
		— A A II				
GAM104	PCDHGB2	CCTGCCCTAGCTCCCTGCCTC	1363	C C	_ I	
		TGCCC AGC CCCTGCCT				
		ACGGG TCG GGGACGGA				
		— A A I				
GAM104	PCDHGB3	CCTGCCCTAGCTCCCTGCCTC	1363	AC	C _	GC
		CTGCCC AGC CCCTGCCTCT				
		GACGGG TCG GGGACGGAGG				
		— A A II				
GAM104	PCDHGB3	CCTGCCCTAGCTCCCTGCCTC	1363	C C	_ I	
		TGCCC AGC CCCTGCCT				
		ACGGG TCG GGGACGGA				
		— A A I				
GAM104	PCDHGB4	CCTGCCCTAGCTCCCTGCCTC	1363	AC	C _	GC
		CTGCCC AGC CCCTGCCTCT				
		GACGGG TCG GGGACGGAGG				
		— A A II				
GAM104	PCDHGB4	CCTGCCCTAGCTCCCTGCCTC	1363	C C	_ I	
		TGCCC AGC CCCTGCCT				

		ACGGG TCG GGGACGGA				
		— A A I				
GAM104 PCDHGB5	CCTGCCCTAGCTCCCTGCCTC	1363 AC	C	_		GC
	CTGCCC AGC CCCTGCCTCT					
	GACGGG TCG GGGACGGAGG					
	— A A II					
GAM104 PCDHGB5	CCTGCCCTAGCTCCCTGCCTC	1363 C	C	_		I
	TGCCC AGC CCCTGCCT					
	ACGGG TCG GGGACGGA					
	— A A I					
GAM104 PCDHGB6	CCTGCCCTAGCTCCCTGCCTC	1363 AC	C	_		GC
	CTGCCC AGC CCCTGCCTCT					
	GACGGG TCG GGGACGGAGG					
	— A A II					
GAM104 PCDHGB6	CCTGCCCTAGCTCCCTGCCTC	1363 C	C	_		I
	TGCCC AGC CCCTGCCT					
	ACGGG TCG GGGACGGA					
	— A A I					
GAM104 PCDHGB7	CCTGCCCTAGCTCCCTGCCTC	1363 AC	C	_		GC
	CTGCCC AGC CCCTGCCTCT					
	GACGGG TCG GGGACGGAGG					
	— A A II					
GAM104 PCDHGB7	CCTGCCCTAGCTCCCTGCCTC	1363 C	C	_		I
	TGCCC AGC CCCTGCCT					
	ACGGG TCG GGGACGGA					
	— A A I					
GAM104 PCDHGC3	CCTGCCCTAGCTCCCTGCCTC	1363 AC	C	_		GC
	CTGCCC AGC CCCTGCCTCT					
	GACGGG TCG GGGACGGAGG					
	— A A II					
GAM104 PCDHGC3	CCTGCCCTAGCTCCCTGCCTC	1363 C	C	_		I
	TGCCC AGC CCCTGCCT					
	ACGGG TCG GGGACGGA					
	— A A I					
GAM104 PCDHGC4	CCTGCCCTAGCTCCCTGCCTC	1363 AC	C	_		GC
	CTGCCC AGC CCCTGCCTCT					
	GACGGG TCG GGGACGGAGG					
	— A A II					
GAM104 PCDHGC4	CCTGCCCTAGCTCCCTGCCTC	1363 C	C	_		I
	TGCCC AGC CCCTGCCT					

	ACGGG TCG GGGACGGA		
	— A A I		
GAM104 PCDHGC5	CCTGCCCTAGCTCCCTGCCTC 1363 AC C _ GC		
	CTGCCC AGC CCCTGCCTCT		
	GACGGG TCG GGGACGGAGG		
	— A A II		
GAM104 PCDHGC5	CCTGCCCTAGCTCCCTGCCTC 1363 C C _ I		
	TGCCC AGC CCCTGCCT		
	ACGGG TCG GGGACGGA		
	— A A I		
GAM104 PODXL	CTTCCCCAGCCCCTCCCCCT 1377 ACCTG G		
	CCCCAGCCCCT CCTCTG		
	GGGGTCGGGGA GGGGAT		
	A _ G		
GAM104 PODXL	CTTCCCCAGCCCCTCCCCCT 1377 TG G I		
	CCCCAGCCCCT CCTC		
	GGGGTCGGGGA GGGG		
	AA G I		
GAM104 PPP2CA	ACCCGCCCCAGCCGGCTGCCGCT 1351 C_ T GCI		
	ACCTGCCCCAGCC CTGCC CT		
	TGGGCGGGGTCGG GACGG GA		
	CC C III		
GAM104 PPP2CA	ACCCGCCCCAGCCGGCTGCCGCT 1351 C C_ TCI		
	CTGCCCCAGCC CTGCC		
	GGCGGGGTCGG GACGG		
	— CC CGI		
GAM104 PRX	CCCAGCCCCCTCAGCCTCTGC 1355 _ III		
	CCCAGCCCCT GCCTCTG		
	GGGTCGGGGG CGGAGAC		
	AGT GII		
GAM104 PRX	CCCAGCCCCCTCAGCCTCTGC 1355 ACCTG _ C CT		
	CCC CAGCC CTGCCT GC		
	GGG GTCGG GACGGA CG		
	G _ A A AT		
GAM104 PRX	CCT-CCCCAGCCCCTTTGGCCTCAGC 1364 ACCTG _ T II		
	CCCCAGCCCCT GCCTC GC		
	GGGGTCGGGGA CGGAG CG		
	GA _ AAC T GI		
GAM104 PRX	CCT-CCCCAGCCCCTTTGGCCTCAGC 1364 G _ TGI		
	CCCCAGCCCCT GCCTC		

	GGGGTCGGGGA CGGAG	
	— AAC III	
GAM104 RARG	GCCACAGCCCCTGCCCATGC 1386 ACCTGCCC C	
	CAGCCCCTGCCT TG	
	GTCGGGGACGGG AC	
	— T	
GAM104 RARG	GCCACAGCCCCTGCCCATGC 1386 C _ CTGI	
	CC CAGCCCCTGCCT	
	GG GTCGGGGACGGG	
	— T TACI	
GAM104 ROCK2	CCGGGCCCACCGCCTGCCTCT 1366 ACCT CA _ C	
	GCCC GCC CCTGCCTCTG	
	CGGG TGG GGACGGAGAT	
	GCC_ _ C I	
GAM104 ROCK2	CCGGGCCCACCGCCTGCCTCT 1366 CT_ CA _ I	
	GCCC GCC CCTGCCTC	
	CGGG TGG GGACGGAG	
	GCC _ C I	
GAM104 RYR3	TGCCCCAGCCTCCGGCGCCTCTGC 1389 ACCTGC _ _ I	
	CCCAGCC CC TGCCTCTGC	
	GGGTCGG GG GCGGAGACG	
	— A CC A	
GAM104 RYR3	TGCCCCAGCCTCCGGCGCCTCTGC 1389 GCC _ _ I	
	CCAGCC CC TGCCTCTG	
	GGTCGG GG GCGGAGAC	
	— A CC I	
GAM104 SFN	CCCCAGCCCCAGGTGGCCTCAGC 1357 T_ TGIIG	
	CCCCAGCCCC GCCTC	
	GGGGTCGGGG CGGAG	
	TCCAC TCGII	
GAM104 SFN	CCCCAGCCCCAGGTGGCCTCAGC 1357 ACCT CC_ GC_ I	
	GCCCCAG CCT CTCTGC	
	CGGGGTC GGA GAGACG	
	— CACC GTC I	
GAM104 SLC6A9	CTGACGCATCCCCTGCCTCT 1376 ACCT CCCAG G	
	GC CCCCTGCCTCT	
	CG GGGGACGGAGA	
	CTG_ TA_ G	
GAM104 SLC6A9	CTGACGCATCCCCTGCCTCT 1376 T_ CCCAG I	
	GC CCCCTGCCTC	

	CG GGGGACGGAG			
	ACTG TA_____ I			
GAM104 TEM5	CTGCCCCAGTTCCACCTGCCCTCT	1372 ACCT	___ _ _	GCI
	GCCCCAG CC CCTGCC TCT			
	CGGGGTC GG GGACGG AGA			
	_____ AA T G GGI			
GAM104 TEM5	CTGCCCCAGTTCCACCTGCCCTCT	1372 TGCC	___ _	CI
	CCAG CC CCTGCCT			
	GGTC GG GGACGGG			
	_____ AA T AG			
GAM104 TFAP4	CTGCCCCGGCTCCCTCCAGCC	1373 A _		GCIIG
	CTGCCCC GC CCCT			
	GACGGGG CG GGGA			
	C A GGTCCG			
GAM104 TFAP4	CTGCCCCGGCTCCCTCCAGCC	1373 ACCT A _	_____	TGC
	GCCCC GC CCCT GCCTC			
	CGGGG CG GGGA CGGGG			
	_____ C A GGT			
GAM104 TRPV4	CCTGCCCCAGGCC-G--TCTGC	1370 AC		C TGCC
	CTGCCCCAG CCC TCTG			
	GACGGGGTC GGG AGAC			
	_____ C C_____			
GAM104 TRPV4	CCTGCCCCAGGCC-G--TCTGC	1370	_ _	CTCI
	CCTGCCCCAG CCC CTGC			
	GGACGGGGTC GGG GACG			
	C CA IIIC			
GAM104 VAV1	CTGTCACAGCCCCTGGCTCCGC	1381 ACCTGCCC		C
	CAGCCCCTG CTCTGC			
	GTCGGGGAC GAGGCG			
	CAGT_____ C			
GAM104 VAV1	CTGTCACAGCCCCTGGCTCCGC	1381 TGCCC		C I
	CAGCCCCTG CTCTG			
	GTCGGGGAC GAGGC			
	ACAGT C I			
GAM105 ACVR1B	ACTTCTGGTTCTTCCGGGCCAC	1399	_____	IIIG
	ACTTCTGG CCGGGCCA			
	TGAAGACC GGCCCGGT			
	AAGAA GIII			
GAM105 ACVR1B	ACTTCTGGTTCTTCCGGGCCAC	1399 TAACAAC	GG	GG
	TTCT CCGGGGCCAC			

	AAGA GGCCCGGTG	
	ACC____ A_ GA	
GAM105 ATP6V0C	ACAGCTCCGCGCAGGGCCACGG 1398 CAAC _ C I	
	TTCTG GC GGGCCACG	
	GAGGC CG CCCGGTGC	
	GTC_ G T I	
GAM105 ATP6V0C	ACAGCTCCGCGCAGGGCCACGG 1398 TAACAAC _ C	
	TTCTG GC GGGCCACGG	
	GAGGC CG CCCGGTGCC	
	TC____ G T	
GAM105 ATSV	AACTGCTCCACGGGCCACGG 1397 A__ GGC I	
	CTTCT CGGGCCACG	
	GAGGG GCCCGGTGC	
	GAC T__ I	
GAM105 ATSV	AACTGCTCCACGGGCCACGG 1397 TAACAA GGC	
	CTTCT CGGGCCACGG	
	GAGGG GCCCGGTGCC	
	C____ T__	
GAM105 DGSi	AACAGCTTCTGGCCCAGGCC 1395 A _ II	
	AACA CTTCTGGCC GGGC	
	TTGT GAAGACCGG TCCG	
	C G GI	
GAM105 DGSi	AACAGCTTCTGGCCCAGGCC 1395 TA A _ ACG	
	ACA CTTCTGGCC GGGCC	
	TGT GAAGACCGG TCCGG	
	_ C G AII	
GAM105 INHBB	CAACTTCGAGACGTGGCCGGGCCA 1400 _____ IIIT	
	CAACTTC TGGCCGGGCC G	
	GTTGAAG ACCGGCCCGG C	
	CTCTGC TIII	
GAM105 LFG	AACATCCACTGCAGCCGGGCCA 1394 ACAA T _ I	
	CT CTG GCCGGGCC	
	GG GAC CGGCCCGG	
	TA__ T GT I	
GAM105 LFG	AACATCCACTGCAGCCGGGCCA 1394 TA A T _ CGG	
	ACA CT CTG GCCGGGCCA	
	TGT GG GAC CGGCCCGGT	
	_ A T GT CII	
GAM105 LYZ	TAAGAACTGAATGTGGCCGGGC 1402 C TC__ CACGG	
	TAA AACT TGGCCGGGC	

	ATT TTGA ACCGGCCCG	
	C CTTAC III GG	
GAM105 LYZ	TAAGAACTGAATGTGGCCGGGC 1402 C TC___ III	
	TAA AACT TGGCCGGG	
	III III III III	
	ATT TTGA ACCGGCCC	
	C CTTAC GII	
GAM105 PPID	AACATTTTACTTGGCCGGG-CACGG 1393 ACA___ TC C I	
	ACT TGGCCGGGC ACG	
	III III III III	
	TGA ACCGGCCCG TGC	
	GTAAAA _ _ I	
GAM105 PPID	AACATTTTACTTGGCCGGG-CACGG 1393 TAACA___ TC C I	
	ACT TGGCCGGGC ACGG	
	III III III III	
	TGA ACCGGCCCG TGCC	
	TGTAAAA _ _ A	
GAM105 RAD1	AACAACCTTCTCGGCGGATCGCCA 1396 ACA _ C ___ I	
	ACTTCT GGC GG GCC	
	III III II III	
	TGAAGA CCG CC CGG	
	___ G _ TAG I	
GAM105 RAD1	AACAACCTTCTCGGCGGATCGCCA 1396 TA _ C ___ CGGI	
	ACAACCTTCT GGC GG GCCA	
	III III III II III	
	TGTTGAAGA CCG CC CGGT	
	___ G _ TAG TIII	
GAM105 TBX1	CAACTGCCGGCCGGGCGCGG 1401 T A I	
	AACT CTGGCCGGGCC CG	
	III III III II	
	TTGA GGCCGGCCCGG GC	
	C C I	
GAM105 TBX1	CAACTGCCGGCCGGGCGCGG 1401 TAACAA T A	
	CT CTGGCCGGGCC CGG	
	II III III III	
	GA GGCCGGCCCGG GCC	
	___ C C	
GAM106 BRCA1	TGTCC-AACACCCACTCTCGGGTC 1410 G G T G I	
	TG CC AAC CTCG TCTCGGGTC	
	II II III III III III	
	AC GG TTG GGGT AGAGCCCAG	
	A _ T G I	
GAM106 BRCA1	TGTCC-AACACCCACTCTCGGGTC 1410 GG_ G T G I	
	CC AAC CTCG TCTCGGGT	
	II III III III III	
	GG TTG GGGT AGAGCCCA	
	ACA _ T G I	
GAM106 CAPNS1	GGCCGCAACTCTCGG-GTCGG 1408 _ _ TCGI	
	GCCG AACTCTCGG TC	
	III III III II	

	CGGC TTGAGAGCC AG	
	G C CIII	
GAM106 CAPNS1	GGCCGCAACTCTCGG-GTCGG 1408 TG _ TC T	
	GCCG AACTCTCGG TCGGG	
	III IIIIII IIII	
	CGGC TTGAGAGCC AGCCT	
	_ G C_ I	
GAM106 GAS7	CCCAACT---GGTCTCGGG 1406 G CTC	
	CC AACT GGTCTCGG	
	II III IIIIII	
	GG TTGA CCAGAGCC	
	G _	
GAM106 GAS7	CCCAACT---GGTCTCGGG 1406 TGGCCGA ACTCTC	
	GGTCTCGG	
	IIIIII	
	CCAGAGCC	
	TTGA_____	
GAM106 SH3BP2	GA ACT---GTCTCGGGTC 1407 CTCG	
	GA ACT GTCTCGGGT	
	IIII IIIIII	
	CTTGA CAGAGCCCA	

GAM106 TBX1	GGGCGA---CGCGGTCTCGGG 1409 _ C ACTCT I	
	GGC GA CGGTCTCG	
	III II IIIIII	
	CCG CT GCCAGAGC	
	C _ GC___ C	
GAM106 TBX1	GGGCGA---CGCGGTCTCGGG 1409 T C ACTCT	
	GGC GA CGGTCTCGGG	
	III II IIIIII	
	CCG CT GCCAGAGCCC	
	_ _ GC___	
GAM106 TNFRSF6B	CCGAACATCTTAGGGTCTCGGG 1405 _ C___ III	
	CCGAAC TCT GGTCTCGG	
	IIII III IIIIII	
	GGCTTG AGA CCAGAGCC	
	T ATC CII	
GAM106 TNFRSF6B	CCGAACATCTTAGGGTCTCGGG 1405 TGGCCG _ C___ C	
	AAC TCT GGTCTCGGGT	
	III III IIIIII	
	TTG AGA CCAGAGCCCG	
	_____ T ATC T	
GAM107 ATRN	CTGAGGCCGGAGAAAGCTGT 1417 AGTTCTGA T _	
	GGCCGGAG AA CTGT	
	IIIIII II IIII	
	CCGGCCTC TT GACA	
	_____ T C	
GAM107 AVPR2	GTTCTGAGGGCCTGGAGGTGA-TGTG 1419 AG _ _ TAAC II	
	TTCTGAGG CC GGAG TGTG	
	IIIIII II IIII IIII	

	AAGACTCC GG CCTC ACAC		
	___ C A CACT GI		
GAM107 BGN	AGCTCTGAGGCCAAGGGAACATGTG 1416	AGT	_ II
	AGTTCTGAGGCCGG AAC TGTG		
	TCGAGACTCCGGTT TTG ACAC		
	CCC T II		
GAM107 BRCA2	AGTTCTTTTTTGCCGGAGTAAGCTG 1414	GA___	_ TGII
	AGTTCT GGCCGGAGTAA CTG		
	TCAAGA CCGCCTCATT GAC		
	AAAAA C IIIG		
GAM107 CFTR	TTCTGAGGCAGAGGTAAGTGT 1425 AGTT	C GA	G
	CTGAGGC G GTAAGTGT		
	GAAGTCCG C CATTGACA		
	___ T TC A		
GAM107 DGCR2	AGTTCTGAGGCCTGGCAGGAA 1415	_ _	TAAGTGTG
	AGTTCTGAGGCC GG AG		
	TCAAGACTCCGG CC TC		
	A G CTTIIIGT		
GAM107 ECH1	GTTCGGA---CGGAGTAAC 1420 TGA C		
	GTTC GG CGGAGTAA		
	CAAG CC GCCTCATT		
	___ T		
GAM107 ECH1	GTTCGGA---CGGAGTAAC 1420 GAGTTCTGA C		
	GG CGGAGTAAC		
	CC GCCTCATTG		
	AG___ T		
GAM107 ECH1	GTTCGGA---CGGAGTAAC-GTG 1422 AGTTCTGA C		_
	GG CGGAGTAAC TGT		
	CC GCCTCATTG ACG		
	AAG___ T C		
GAM107 EZH1	TTCTGAGGCCAGAGAAACAGT 1426 AGTT	T T G	
	CTGAGGCCGGAG AAC GT		
	GAAGTCCGGTCTC TTG CA		
	___ T T G		
GAM107 MX2	AGTATCTTAGGACACTGTAAGTGTG 1413	_ G C GA	II
	AGT TCT AGG CG GTAAGTGTG		
	TCA AGA TCC GT CATTGACAC		
	T A T GA II		
GAM107 PODXL	TTCTGAGGCGCACAGT--CTGTG 1424 AGTT	_ G AA	
	CTGAGGC CG AGT CTGTG		

	GACTCCG GT TCA GACAC		
	_____ C G _____		
GAM107 PTER	CTG-GGTCTGAGTAACTGT	1418 AGTTCTGAGGCCG	
	GAGTAACTG		
	CTCATTGAC		
	CAGA_____		
GAM107 PTP4A2	TTCTGAGGCC--AGTCTCGGTG	1427 AGTT	AGTAAC
	CTGAGGCCGG TGT		
	GACTCCGGTC ACA		
	_____ AGAGCC		
GAM107 SOX15	GTTCTGAGGCC-TACTGACTG	1421 _	GGAGTA I
	TTCTGAGGCC ACT		
	AAGACTCCGG TGA		
	C ATGAC_ I		
GAM107 SOX15	GTTCTGAGGCC-TACTGACTG	1421 AG	GGAGTA T
	TTCTGAGGCC ACTG		
	AAGACTCCGG TGAC		
	_____ ATGAC_ C		
GAM107 SOX15	GTTCTGAGGCC-TACTGACTG	1421 GAGT	GGAGTA
	TCTGAGGCC ACTG		
	AGACTCCGG TGAC		
	_____ ATGAC_		
GAM107 TMOD	GTTCTGAGG--GGA-AAATTGTG	1423 AG	CC T C
	TTCTGAGG GGAG AA TGT		
	AAGACTCC CCTT TT ACA		
	_____ _ _ A		
GAM108 ATF7	AGGGCTGAGTCTGAAGTAGTTAC	1431 GAG	T TAI
	CTGAGTCTGG GT		
	GACTCAGACT CA		
	_____ T TCA		
GAM108 CERD4	AGTGCTGCCAGTCTGGTGT	1430 AGA	_____
	GCTG AGTCTGGTG		
	CGAC TCAGACCAC		
	TCA GG AII		
GAM108 CERD4	AGTGCTGCCAGTCTGGTGT	1430 TGTCAGA	G TA
	GCT AGTCTGGTGT		
	CGG TCAGACCACA		
	GA_____ _ CC		
GAM108 COL19A1	TGTACAGAGCTGAGGCAGG	1438 _	TCT TGTTA
	TGT CAGAGCTGAG GG		

	ACA GTCTCGACTC CC		
	T CGT III CA		
GAM108 COL19A1	TGTACAGAGCTGAGGCAGG	1438	_ TCTGII
	TGT CAGAGCTGAG		
	ACA GTCTCGACTC		
	T CGTCCI		
GAM108 CSF1R	TCAGAGCTGGGCCGAGCTGTT	1437	TGTC A T _ AC
	AGAGCTG GTC GG TGTT		
	TCTCGAC CGG TC ACAA		
	_ C C G CT		
GAM108 CSF1R	TCAGAGCTGGGCCGAGCTGTT	1437	C A T GTI
	AGAGCTG GTC GGT		
	TCTCGAC CGG TCG		
	_ C C ACA		
GAM108 CTGF	TGTCAGAGCTGAGTCTGCTGTT	1442	G AC
	TGTCAGAGCTGAGTCTG TGTT		
	ACAGTCTCGACTCAGAC ACAA		
	G II		
GAM108 CTGF	TGTCAGAGCTGAGTCTGCTGTT	1442	G I
	GTCAGAGCTGAGTCTG TGT		
	CAGTCTCGACTCAGAC ACA		
	G I		
GAM108 CTLA1	GTCAGAGCT--GT-TGGTGTT	1436	AGTC I
	GTCAGAGCTG TGGTG		
	CAGTCTCGAC ACCAC		
	A _ A		
GAM108 CTLA1	GTCAGAGCT--GT-TGGTGTT	1436	TG AGTC
	TCAGAGCTG TGGTGTT		
	AGTCTCGAC ACCACAA		
	_ A _		
GAM108 EHF	TGCCTGAGCTGAGTTTTCTGTT	1441	A _ GTGTTAC
	TGTC GAGCTGAG TCTG		
	ACGG CTCGACTC AGAC		
	A AAA AAII CA		
GAM108 EHF	TGCCTGAGCTGAGTTTTCTGTT	1441	A _ GTGTI
	GTC GAGCTGAG TCTG		
	CGG CTCGACTC AGAC		
	A AAA AII T		
GAM108 EMP3	GTCAGAGCTGGAGTC-GGAGT	1434	_ T TGI
	TCAGAGCTG AGTC GG		

	AGTCTCGAC TCAG CC		
	C _ TCI		
GAM108 EMP3	GTCAGAGCTGGAGTC-GGAGT	1434 TG	_ T T A
	TCAGAGCTG AGTC GG GTT		
	AGTCTCGAC TCAG CC CAG		
	_ C _ T I		
GAM108 GOLGA5	CAGAGCTGAG-CT--TGTTA	1432	TC GTGTI
	CAGAGCTGAG TG		
	GTCTCGACTC AC		
	GA AATII		
GAM108 GOLGA5	CAGAGCTGAG-CT--TGTTA	1432 TGTCAG	T GG
	AGCTGAG CT TGTT		
	TCGACTC GA ACAA		
	_____ - -		
GAM108 KCNJ6	TGTCAGAGCTGCTGTATGG	1439	A_ C TGTTA
	TGTCAGAGCTG GT TGG		
	ACAGTCTCGAC CA ACC		
	GA T IIICA		
GAM108 KCNJ6	TGTCAGAGCTGCTGTATGG	1439	AGT II
	TGTCAGAGCTG CTG		
	ACAGTCTCGAC GAC		
	_____ AT		
GAM108 MAK	GTCAGAGCTGAGTCAGTGGT	1435	_
	GTCAGAGCTGAGTC TGG		
	CAGTCTCGACTCAG ACC		
	TC AII		
GAM108 MAK	GTCAGAGCTGAGTCAGTGGT	1435 TG	_ GTTA
	TCAGAGCTGAGTC TGGT		
	AGTCTCGACTCAG ACCA		
	_____ TC GIII		
GAM108 SLC25A14	TGTCAGAGC-GAG-CTCGTG	1440	T T G TT
	TGTCAGAGC GAG CT GTG		
	ACAGTCTCG CTC GA CAC		
	_ _ G II		
GAM108 SLC25A14	TGTCAGAGC-GAG-CTCGTG	1440 _	T T G I
	GTCAGAGC GAG CT GT		
	CAGTCTCG CTC GA CA		
	A _ _ G I		
GAM108 TNP2	GTCAGATTAAGCTGAGTCT	1433	_____ IIIA
	GTCAGA GCTGAGTC		

	CAGTCT CGACTCAG		
	AATT AIII		
GAM108 TNP2	GTCAGATTAAGCTGAGTCT 1433 TG	_____	GGTGT
	TCAGA GCTGAGTCT		
	AGTCT CGACTCAGA		
	___ AATT III CAT		
GAM109 AIM1	GGATGAGTTAAAATAATTCA 1459 G A		TTC
	GGA GAG TAAAATAATTCA		
	CCT CTC ATTTTATTAAGT		
	A A III		
GAM109 AIM1	GGATGAGTTAAAATAATTCA 1459 GAG A		I
	GAG TAAAATAATTC		
	CTC ATTTTATTAAG		
	CTA A I		
GAM109 CD2AP	AGGAGA--AAATAATTCATT 1448_ TA		I
	GGAGA AAATAATTCAT		
	CCTCT TTTATTAAGTA		
	T _ I		
GAM109 CD2AP	AGGAGA--AAATAATTCATT 1448 GGAG TA		
	GAGA AAATAATTCATT		
	CTCT TTTATTAAGTAA		

GAM109 COL4A6	GGAGGTAAAGATAACAATAATTCA 1457	_____ _	TTCTI
	GGAGG AGATAA AATAATTCA		
	CCTCC TCTATT TTATTAAGT		
	ATT G IIITC		
GAM109 COL4A6	GGAGGTAAAGATAACAATAATTCA 1457 GA	_	I
	GGAGATAA AATAATTC		
	TTTCTATT TTATTAAG		
	A_ G I		
GAM109 CPO	AGCAAATAAAATAATACATTC 1450 G		T I
	G AGATAAAATAAT CATT		
	I		
	C TTTATTTTATTA GTAA		
	G T I		
GAM109 CPO	AGCAAATAAAATAATACATTC 1450 GGAGG		T T
	AGATAAAATAAT CATT		
	TTTATTTTATTA GTAAG		
	G_____ T T		
GAM109 DGKI	AGTAGATAAAATAATATATT 1449 AGG		TCAI
	AGATAAAATAAT		

		TCTATTTTATTA		
		A__ TATA		
GAM109 DGKI		AGTAGATAAAATAATATATT	1449 GGAGG	TC C
		AGATAAAATAAT ATT		
		TCTATTTTATTA TAA		
		A__ TA T		
GAM109 EPS8		GGATGGGGATAAAATAATT-AGTCT	1456 _ A	CAT I
		GGA GG GATAAAATAATT TCT		
		CCT CC CTATTTTATTAA AGA		
		A C TC_ I		
GAM109 EPS8		GGATGGGGATAAAATAATT-AGTCT	1456 A A	CATI
		GG GATAAAATAATT		
		CC CTATTTTATTAA		
		A C TCAI		
GAM109 KLRC1		GAGCAAATAACATAATTCATT	1454 G A I	
		AG AGATAA ATAATTCAT		
		TC TTTATT TATTAAGTA		
		G G I		
GAM109 KLRC1		GAGCAAATAACATAATTCATT	1454 GG G A CT	
		AG AGATAA ATAATTCATT		
		TC TTTATT TATTAAGTAA		
		_ G G AI		
GAM109 KLRC2		GAGCAAATAACATAATTCATT	1454 G A I	
		AG AGATAA ATAATTCAT		
		TC TTTATT TATTAAGTA		
		G G I		
GAM109 KLRC2		GAGCAAATAACATAATTCATT	1454 GG G A CT	
		AG AGATAA ATAATTCATT		
		TC TTTATT TATTAAGTAA		
		_ G G AI		
GAM109 NDUFA6		GAGA-AAAATAATTCAATC	1452 T TTI	
		GAGA AAAATAATTCA		
		CTCT TTTTATTAAGT		
		_ TAG		
GAM109 NDUFA6		GAGA-AAAATAATTCAATC	1452 GGAGGAGAT T	
		AAAATAATTCA T		
		TTTTATTAAGT A		
		_____ T		
GAM109 OPHN1		AGGAGATAAAAGAGTTTAT	1447 TAATTCAII	
		AGGAGATAAAA		

	TCCTCTATTTT			
	CTCAAATAI			
GAM109 PLAG1	GAGAAGATAAAC--ATTCATTCT	1455	ATA	I
	GAGGAGATAAA ATTCATT			
	CTCTTCTATTT TAAGTAA			
	G__ G			
GAM109 PLAG1	GAGAAGATAAAC--ATTCATTCT	1455 GG	ATA	
	AGGAGATAAA ATTCATTCT			
	TCTTCTATTT TAAGTAAGA			
	__ G__			
GAM109 PSMD9	GGAGAGGAAAAAATAATTCA	1458	GA T	TTC
	GGAG GA AAAATAATTCA			
	CCTC CT TTTTATTAAGT			
	TC T III			
GAM109 PSMD9	GGAGAGGAAAAAATAATTCA	1458 __	TA	I
	GAGGAGA AAATAATTC			
	CTCCTTT TTTATTAAG			
	CT __ I			
GAM109 PTP4A2	AGGAGATTTCAAAATAATTCAATC	1446	GAGA_	TTI
	TAAAATAATTCA			
	GTTTTATTAAGT			
	CTAAA TII			
GAM109 PTP4A2	AGGAGATTTCAAAATAATTCAATC	1446	GGAG	__ T I
	GAGAT AAAATAATTCA TCT			
	CTCTA TTTTATTAAGT AGG			
	__ AAG T A			
GAM109 PYCS	AGGACGACAAAATAATTCAT	1445	GGAGGA	TC
	GATAAAATAATTCAT			
	CTGTTTTATTAAGTA			
	CTG__ TG			
GAM109 PYCS	AGGACGACAAAATAATTCAT	1445	_	II
	AGGA GATAAAATAATTCA			
	TCCT CTGTTTTATTAAGT			
	G AI			
GAM109 RAB1A	GGAGG--ATAAAATAGTTGAATCT	1461	GA	ATTCAT
	GGAGGA TAAAATA TCT			
	CCTCCT ATTTTAT AGA			
	_ CAACTT			
GAM109 RAB1A	GGAGG--ATAAAATAGTTGAATCT	1461	GA	ATTCATTI
	GGAGGA TAAAATA			

	CCTCCT ATTTTAT			
	___ CAACTTAG			
GAM109 SPRR2C	GAAGACATCAAAAATAATTCTTT	1453	G _	ATI
	GGA AT AAAATAATTC			
	TCT TA TTTTATTAAG			
	G G AII			
GAM109 SPRR2C	GAAGACATCAAAAATAATTCTTT	1453	GG G _	ATTCT
	AGGA AT AAAATAATTC			
	TTCT TA TTTTATTAAG			
	___ G G AAACI			
GAM109 SPTA1	GAGAGAGAGAGAAATAATTCA	1451	_ TA	TTCT
	GGAG GAGA AAATAATTCA			
	TCTC CTCT TTTATTAAGT			
	T C_ TIII			
GAM109 SPTA1	GAGAGAGAGAGAAATAATTCA	1451	__ _ TA	III
	GAG GAGA AAATAATTC			
	CTC CTCT TTTATTAAG			
	CT T C_ TII			
GAM109 STK38	GGAGGAGATAAATCAATGGATT	1460	A	TCATTCT
	GGAGGAGATAAA TAAT			
	CCTCCTCTATTT GTTA			
	A CCTAII			
GAM109 STK38	GGAGGAGATAAATCAATGGATT	1460	A	TCATI
	GAGGAGATAAA TAAT			
	CTCCTCTATTT GTTA			
	A CCTAI			
GAM110 ADCY6	CAGGGAAAGGGGTAAAAGG	1480	TGCAACAGGGGAT	
	GGGTAAAAGG			
	CCCATTTTCC			
	TTTC_____			
GAM110 EGFL5	CAGGGTTGTAGGGGTAAAAG	1479	TGCAACAGGGGAT	G
	GGGTAAAAG			
	CCCATTTTC			
	AACATC_____ A			
GAM110 GCSH	AACACTAGAGCCTAGTCTAA	1466	CCCA	II
	AACACTAGA GCCTA			
	TTGTGATCT CGGAT			
	___ CA			
GAM110 GCSH	AACACTAGAGCCTAGTCTAA	1466	TA _ C C	CTG
	AACTAGA CC AG CTAA			

	TGTGATCT GG TC GATT	
	___ C A A TII	
GAM110 GJB3	AACATCAGCCCCAGCCTAAC 1467 C A I	
	ACA TAG CCCAGCCTAA	
	TGT GTC GGGTCGGATT	
	A G I	
GAM110 GJB3	AACATCAGCCCCAGCCTAAC 1467 TA C A G	
	ACA TAG CCCAGCCTAACT	
	TGT GTC GGGTCGGATTGG	
	___ A G I	
GAM110 GPRK7	ACAGGGACATGATGGTAAAAGG 1473 TGCAACA G ___ G	
	GGG ATG GGTAAAAGG	
	CCT TAC CCATTTTCC	
	___ G TA G	
GAM110 HPCAL1	CACTAGACCATGCC---CTGT 1478 CA AACI	
	CACTAGACC GCCT	
	GTGATCTGG CGGG	
	TA ACAI	
GAM110 HPCAL1	CACTAGACCATGCC---CTGT 1478 TAACAC CA AACT	
	TAGACC GCCT	
	ATCTGG CGGG	
	___ TA ACAC	
GAM110 IL13RA1	CACCGGACCCAGCCCAGACTGT 1476 A TA _ I	
	C GACCCAGCCTA ACTG	
	G CTGGGTCGGGT TGAC	
	_GC C I	
GAM110 IL13RA1	CACCGGACCCAGCCCAGACTGT 1476 TAACACTA _	
	GACCCAGCCTA ACTGT	
	CTGGGTCGGGT TGACA	
	GC___ C	
GAM110 LAMC1	TAACACTAGTTCCAAGACTAACT 1481 AC C_ GTI	
	TAACACTAG CCAG CTAAC	
	ATTGTGATC GGTT GATTGA	
	AA CT III	
GAM110 LAMC1	TAACACTAGTTCCAAGACTAACT 1481 A AC C_ I	
	AACTAG CCAG CTAAC	
	TGTGATC GGTT GATTG	
	_ AA CT I	
GAM110 LMO2	TGAAACAGGGGA--GTAAAA 1485 C TGGG GG	
	TG AACAGGGGA TAAAA	

AC TTGTCCCCT ATTTT
 T CA_ II
 GAM110 MFAP2 AACATGGGGATGGGGAAAA 1465 TGCAACA T
 GGGGATGGG AAAAGG
 ||||| |||||
 CCCCTACCC TTTTTT
 TA_____ C
 GAM110 NEDD4L TGCAACAGGTCATTGGTAA 1484 GG G AAGG
 TGCAACAGG AT GGTAA
 ||||| || |||||
 ACGTTGTCC TA CCATT
 AG A IIIG
 GAM110 NOC4 CAC-AG-CCCAGCCTACCTG 1477 T A ACI
 CAC AG CCCAGCCTA
 ||| || |||||
 GTG TC GGGTCGGAT
 _ _ GGA
 GAM110 NOC4 CAC-AG-CCCAGCCTACCTG 1477 TAACACT A A
 AG CCCAGCCTA CT
 || ||||| ||
 TC GGGTCGGAT GA
 _____ _ G
 GAM110 PDE4B CAACAGGGGAAGGAAGTAAAA 1475 TGCA T _ GGG
 ACAGGGGA GG GTAAAA
 ||||| || |||||
 TGTCCCCT CC CATTTT
 _____ T TT ACI
 GAM110 PMP22 AACAGCCTAGACCCAGCCAAGCT 1464 AACA TAI
 CTAGACCCAGCC
 |||||
 GATCTGGGTCGG
 G_ TTC
 GAM110 PMP22 AACAGCCTAGACCCAGCCAAGCT 1464 TAACA TAA GTI
 CTAGACCCAGCC CT
 ||||| ||
 GATCTGGGTCGG GA
 TGTCG TTC GII
 GAM110 PON1 TGCAACAGGAGAATTGAAAAAG 1486 TG_ T GG
 TGCAACAGGGGA GG AAAAG
 ||||| || |||||
 ACGTTGTCCTCT CT TTTTC
 TAA _ II
 GAM110 PXF AAGAGAGGA--GGTAAAAGGG 1470 TGCAAC TG
 AGGGGA GGTAAGG
 |||| |||||
 TCTCCT CCATTTTCC
 _____ _
 GAM110 SIX2 ACAAGAGA-GGGTAAAAGG 1474 TGCAACAG T
 GGGA GGGTAAAAG
 ||| |||||

CTCT CCCATTTTC

GAM110	SLC25A13	AACAAGAGATGGACGTAAAAGGG	1469	TGCAAC	___	I
		AGGGGATGG GTAAAAGGG				
		TTCTCTACC CATTTTCCC				
		_____ TG T				
GAM110	SLC29A1	ACAGGGTGCATGATGGGTAAAA	1472	___	ACAGGG	GG
		TGCA GATGGGTAAAAG				
		ACGT CTACCCATTTTT				
		CC A_____ GA				
GAM110	TIMP3	TGGAACGAGGGGA-GGGTAAAAG	1483	C _	T	GG
		TG AAC AGGGGA GGGTAAAAG				
		AC TTG TCCCCT CCCATTTTC				
		C C _ II				
GAM110	TRPS1	ACAGGCAGGGCTGGGTAAAA	1471	TGCAA	GA	G
		CAGGG TGGGTAAAAG				
		GTCCC ACCCATTTTT				
		C_____ G_ G				
GAM110	UNG	TAACA--AGACCCAGCTTA	1482	CT	CTAACT	
		TAACA AGACCCAGC				
		ATTGT TCTGGGTCG				
		_____ AAT				
GAM110	UNG	TAACA--AGACCCAGCTTA	1482	CT	CTI	
		TAACA AGACCCAGC				
		ATTGT TCTGGGTCG				
		_____ AAT				
GAM110	ZNF264	AACAATGGAATGGGTAAAGAGG	1468	TGCAACAG		AG
		GGGATGGGTAAA GG				
		CCTTACCCATTT CC				
		TTA_____ CT				
GAM111	EGR2	CTTGTCCTTTTGCTGT-CCCCAC	1490	TCTG C		GA
		GTC TTTTGCTGT CCCAC				
		CAG AAAACGACA GGGTG				
		AA_ A G_				
GAM111	EGR2	CTTGTCCTTTTGCTGT-CCCCAC	1490	TG_ C		GA I
		GTC TTTTGCTGT CCA				
		CAG AAAACGACA GGGT				
		GAA A G_ I				
GAM111	EIF4EBP2	TTTTGCTGTGTACC	1493	T	CCI	
		TCC TTTGCTGTGA				

	AGG GAACGACACT			
	C CGI			
GAM111 EIF4EBP2	TTTTGCTGTGTACC	1493	TCTGG T	GACCC
	TCC TTTGCTGT			
	AGG GAACGACA			
	AAAAG C CA			
GAM111 FMN2	GTGACCCAC	1491	II	
	GTGACCCA			
	CACTGGGT			
	GI			
GAM111 KLRC4	TGTTCATTTTGCTGTTGACC	1492	G C _ II	
	TG TC TTTTGCTGT GAC			
	AC AG AAAACGACA CTG			
	A T A GI			
GAM111 KLRC4	TGTTCATTTTGCTGTTGACC	1492	TCTGG C _ CA	
	TC TTTTGCTGT GACC			
	AG AAAACGACA CTGG			
	A _ T A TT			
GAM111 PLAB	TTTTGCTGTGTACC	1493	T CCI	
	TCC TTTGCTGTGA			
	AGG GAACGACACT			
	C CGI			
GAM111 PLAB	TTTTGCTGTGTACC	1493	TCTGG T GACCC	
	TCC TTTGCTGT			
	AGG GAACGACA			
	AAAAG C CA			
GAM111 PSCDBP	CTGGTGCACCTGCTG	1489	ACII	
	TTTTGCTGTG			
	AAAACGACAC			
	ATGG			
GAM112 DDX11	TGGCCTCTCTCCTGGCCACAGGC	1508	_ GA TGI	
	TGGCCTCTC CCTGG ACGGGC			
	ACCGGAGAG GGACC TGTCCG			
	A GG			
GAM112 EHD2	TGCCCTCTCC-TGGGAACG	1510	G C GGC	
	TG CCTCTCC TGGGAACG			
	AC GGAGAGG ACCCTTGC			
	G _			
GAM112 GNA11	CCCCTCCCTGGGAA-GGCCT	1498	TGGCCT AC	
	CTCCCTGGGA GGGCT			

GAGGGACCCT TCCGG

GAM112 HSF4	CCTCTCCCTGCGCCGGGGC	1497 TGGCCT	GGAAC
	CTCCCTG GGGCT		
	GAGGGAC CCCGG		
	_____ GCGGC		
GAM112 ISG20	GCCTCTAGTCCCTGCGGAACGGGCTG	1499 TGGC	___ _ II
	CTC TCCCTG GGAACGGGCTG		
	GAG AGGGAC CCTTGCCCGAC		
	_____ ATC G CT		
GAM112 ITGB1	GGCCTCTCCC-G---CGGGCTG	1506 TG	TGGGAA
	GCCTCTCCC CGGGC		
	CGGAGAGGG GCCCG		
	_____ C _____		
GAM112 KHK	GCCTCTCCCTGTGGGGAAC	1502 TGGC	___ GGCT
	CTCTCCCT GGGAACG		
	GAGAGGGA CCCTTGT		
	_____ CAC GIII		
GAM112 LAMA4	CCTCTCCCTGGCCGTTCTGGGACTG	1496 TGGCCT	GAA___ _ I
	CTCCCTGG CGGG CTG		
	GAGGGACC GCCC GAC		
	_____ GGCAA T C		
GAM112 MAFG	TGGCCTCTCCCAGG--CTGGGCTG	1514	T AAC
	TGGCCTCTCCC GGG GGGCTG		
	ACCGGAGAGGG TCC CCCGAC		
	_____ GA_		
GAM112 MAP3K14	TGGCAATC-CCCTGGGAAC-GGCTG	1507	C_ T G I
	TGGC TC CCCTGGGAACGG CTG		
	ACCG AG GGGACCCTTGCC GAC		
	TT _ _ I		
GAM112 MMP19	TGCCCTCTCCCTG---CAGGCTG	1513 G	GGAA
	TG CCTCTCCCTG CGGGCT		
	AC GGAGAGGGAC GTCCGA		
	G _____		
GAM112 NR1D1	GCCTTTCCTGGGACAGAGGGCT	1503 TGGC C	AC___ GI
	CT TCCCTGGGA GGGCT		
	GA AGGGACCCT CCCGA		
	_____ A GTCT GA		
GAM112 PLD2	TGACCTCTCCCTG---ACGGG	1511	GGA C
	TGGCCTCTCCCTG ACGGG		

	ACTGGAGAGGGAC TGCCC		
	_____ I		
GAM112 RS1	GCCTCTCCC-AGGAAGGGGC 1504 TGGC T C		
	CTCTCCC GGGAA GGGCT		
	GAGAGGG TCCTT CCCGG		
	_____ _ C		
GAM112 SLC7A8	TGGCCTCTCCTCTCTGAAGGGGC 1509 _ GG C TGI		
	TGGCCTCTCC CT GAA GGGC		
	ACCGGAGAGG GA CTT CCCG		
	A GA C		
GAM112 SNL	GCCTCTCCCACGTGGGAGAGGGGCTG 1500 TGGC ____ AC_ II		
	CTCTCCC TGGGA GGGCTG		
	GAGAGGG ACCCT CCCGAC		
	_____ TGC CTC AA		
GAM112 SOLH	TGGCAGCTCCCTGGG--CGGG 1512 CT AA CT		
	TGGC CTCCCTGGG CGGG		
	ACCG GAGGGACCC GCCC		
	TC ____ II		
GAM112 STAT1	GCCTCTCCC--GAGCGCGCTG 1505 TGGC T AA G		
	CTCTCCC GGG CG GCT		
	GAGAGGG CTC GC CGA		
	_____ _ _ G		
GAM112 WHSC1	GCCTCTCCCGAGTGGCGACGGCGCTG 1501 TGGC ____ GA _ II		
	CTCTCCC TGG ACGG GCTG		
	GAGAGGG ACC TGCC CGAC		
	_____ CTC GC G TC		
GAM113 ABCD1	AGGGCGAGGG-TTACGCAGG 1518 TAG ____ _ TTAGTAGG		
	GAGGG CG AGGGC		
	CTCCC GC TCCCG		
	G_ AAT G CG ITGG		
GAM113 CAPON	TAGGAGGGCGGCAGGG--GAGGAGGT 1523 ____ CTT T I		
	TAGGAGGGCG AGGG AG AGGT		
	ATCCTCCCGC TCCC TC TCCA		
	CG C_ C I		
GAM113 DISC1	TAGCATGGCAAGGGCTTAGCATGGT 1524 TA AG_ _ II		
	GG GGCGAGGGCTTAGTA GGT		
	TC CCGTTCCCGAATCGT CCA		
	A_ GTA A II		
GAM113 GAS41	AGGAGGGCGAG--TTACTTGG 1517 TA G_ AGTAGG		
	GGAGGGCGAG GCTT		

	CCTCCCGCTC TGAA		
	___ AA CCCII		
GAM113 HOXC5	GAGGGCGAGG--TTAGAGGGT 1519 TAGGAG GC TA		
	GGCGAGG TTAG GG		
	CCGCTCC AATC CC		
	_____ TC		
GAM113 NR3C2	GGACGAGCGAGGGGCTCAG-AGG 1520 TAGGA T		
	GGGCGAGGGGCTTAG AGGT		
	CTCGCTCCCGAGTC TCCG		
	TG_____		
GAM113 OTP	GGCGGGCGAGGGGGGTCGTAGG 1521 TAGGA CTTA_		
	GGGCGAGGG GTAGGT		
	CCCGCTCCC CATCCG		
	G_____ CCCAG		
GAM113 SIAT7D	GGGCGAGGGCAGGACGTAGGT 1522 TAGG G TTA		
	AGGGC AGGGC GTAGGT		
	TCCCG TCCTG CATCCA		
	_____ - _____		
GAM114 ADCY6	GGCGCCTGTAATCCCAGCT-ACT 1565 G A_ CACI		
	GC TGATCCCAGCT		
	CG ATTAGGGTCGA		
	G GAC TIII		
GAM114 ADCY6	GGCGCCTGTAATCCCAGCT-ACT 1565 TAGGG A_ C G		
	GC TGATCCCAGCT ACT		
	CG ATTAGGGTCGA TGA		
	G_ GAC _ G		
GAM114 AQP6	AGGCGCCTGTAATCCCAGCT-ACT 1531 GG A_ CAI		
	GC TGATCCCAGCT		
	CG ATTAGGGTCGA		
	G_ GAC TII		
GAM114 AQP6	AGGCGCCTGTAATCCCAGCT-ACT 1531 TA G A_ C GI		
	GG GC TGATCCCAGCT ACT		
	CC CG ATTAGGGTCGA TGA		
	_ G GAC _ AI		
GAM114 AQP6	AGGCGCCTGTAATCCCAGCT-ACT 1531 TA G A_ C GI		
	GG GC TGATCCCAGCT ACT		
	CC CG ATTAGGGTCGA TGA		
	_ G GAC _ GI		
GAM114 ARCN1	ATGATCCCAGTGCCTGACTG 1551 _ C III		
	ATGATCCCAG CT ACT		

	TACTAGGGTC GA TGA			
	ACG C CII			
GAM114 ATP1A2	GGCACGATCTCAGCTCACTG 1555	C	I	
	GCATGATC CAGCTCACT			
	CGTGCTAG GTCGAGTGA			
	A I			
GAM114 ATP1A2	GGCACGATCTCAGCTCACTG 1555	TAGGGGCAT	C	
	GATC CAGCTCACT			
	CTAG GTCGAGTGA			
	G_____ A			
GAM114 AXUD1	AGTGTGCACAT-GGCACCTGT 1549	GA	CC	
	AGTGTGCACGTGG ACCTGT			
	TCACACGTGTACC TGGACA			
	G_ II			
GAM114 BLTR2	AGTAGGC-CTTGGGAACCT 1548	T ACG	GTC	
	AGTG GC TGGGAACCT			
	TCAT CG ACCCTTGGA			
	C GA_ III			
GAM114 C1orf1	AGGGGCATGATCTCAACTCACTG 1534	C	I	
	GGGGCATGATC CAGCTCACT			
	CCCCGTACTAG GTTGAGTGA			
	A I			
GAM114 C1orf1	AGGGGCATGATCTCAACTCACTG 1534	TA	C	I
	GGGGCATGATC CAGCTCACTG			
	CCCCGTACTAG GTTGAGTGAC			
	_____ A C			
GAM114 CIT	TGAGCACGTGGGCGCTTGGGTCCC 1574	AGTGT	AACCT_	I
	GCACGTGGG GTCCC			
	CGTGCACCC CAGGG			
	T_____ GCGAACC G			
GAM114 CPT2	AGTGGTGTGATCTCAGCTCACTG 1545	GG CA	C	I
	GG TGATC CAGCTCACT			
	CC ACTAG GTCGAGTGA			
	CA AC A I			
GAM114 CPT2	AGTGGTGTGATCTCAGCTCACTG 1545	TAGG CA	C	I
	GG TGATC CAGCTCACTG			
	CC ACTAG GTCGAGTGAC			
	CA_ AC A G			
GAM114 DDOST	GGCGTGATCTCAGCTCACTG 1561	A C	I	
	GC TGATC CAGCTCACT			

	CG ACTAG GTCGAGTGA	
	C A I	
GAM114 DDOST	GGCGTGATCTCAGCTCACTG 1561 TAGGGGCA C	
	TGATC CAGCTCACT	
	ACTAG GTCGAGTGA	
	_____ A	
GAM114 DGKI	AGTGGTGTGATCTCAGCTCACTG 1545 GG CA C I	
	GG TGATC CAGCTCACT	
	CC ACTAG GTCGAGTGA	
	CA AC A I	
GAM114 DGKI	AGTGGTGTGATCTCAGCTCACTG 1545 TAGG CA C I	
	GG TGATC CAGCTCACTG	
	CC ACTAG GTCGAGTGAC	
	CA__ AC A G	
GAM114 FGFR1	AGTGGCGTGATCTCAGCTCACTG 1544 GG A C I	
	GGC TGATC CAGCTCACT	
	CCG ACTAG GTCGAGTGA	
	CA C A I	
GAM114 FGFR1	AGTGGCGTGATCTCAGCTCACTG 1544 TAGG A C I	
	GGC TGATC CAGCTCACTG	
	CCG ACTAG GTCGAGTGAC	
	CA__ C A G	
GAM114 FGFR2	GGCATGATCTCGGCTCACTG 1560 CCA I	
	GCATGATC GCTCACT	
	CGTACTAG CGAGTGA	
	AGC I	
GAM114 FOLR1	AGGGTTCCCGTTT-AACCTGTCCC 1550 T GCA GGG I	
	AG GT CGT AACCTGTCCC	
	TC CA GCA TTGGACAGGG	
	C AGG AG_ I	
GAM114 GALNT7	GGCATGATCTCAGCTCACTG 1557 C I	
	GCATGATC CAGCTCACT	
	CGTACTAG GTCGAGTGA	
	A I	
GAM114 GALNT7	GGCATGATCTCAGCTCACTG 1557 TAGGGGCA C	
	TGATC CAGCTCACT	
	ACTAG GTCGAGTGA	
	_____ A	
GAM114 HDAC4	GTGGGCACGTGGGCACGCTG 1568 AG T A _ CC	
	TG GCACGTGGG AC CTGT	

	AC CGTGCACCC TG GACG	
	__ C G C II	
GAM114 HIP1	GGCGTGATCTCAGCTCACTG 1561 A C I	
	GC TGATC CAGCTCACT	
	II IIII IIIIIII	
	CG ACTAG GTCGAGTGA	
	C A I	
GAM114 HIP1	GGCGTGATCTCAGCTCACTG 1561 TAGGGGCA C	
	TGATC CAGCTCACT	
	IIII IIIIIII	
	ACTAG GTCGAGTGA	
	_____ A	
GAM114 HR	TGAGCACCTGGTCTACCTGTCCC 1573 AGTGT G GA_ I	
	GCAC TGG ACCTGTCCC	
	IIII III IIIIIII	
	CGTG ACC TGGACAGGG	
	T_____ G AGA G	
GAM114 HYAL4	GGGCATGATGGCATGCTC-CTG 1562 CC _ A I	
	GGCATGAT CA GCTC CT	
	IIIIII II IIII II	
	CCGTACTA GT CGAG GA	
	CC A _ I	
GAM114 IGF1	GGTGCCTGTAATCCCAGCT-ACT 1566 G A__ CACI	
	GC TGATCCCAGCT	
	II IIIIIIIII	
	CG ATTAGGGTCGA	
	A GAC TIII	
GAM114 IGF1	GGTGCCTGTAATCCCAGCT-ACT 1566 TAGGG A__ C	
	GC TGATCCCAGCT ACTG	
	II IIIIIIIII IIII	
	CG ATTAGGGTCGA TGAC	
	A__ GAC _	
GAM114 IL10	AGGGGCATGATATCAGCTCACTG 1533 CC I	
	GGGGCATGAT CAGCTCACT	
	IIIIIIII IIIIIII	
	CCCCGTACTA GTCGAGTGA	
	TA I	
GAM114 IL10	AGGGGCATGATATCAGCTCACTG 1533 TA CC I	
	GGGGCATGAT CAGCTCACTG	
	IIIIIIII IIIIIII	
	CCCCGTACTA GTCGAGTGAC	
	_____ TA G	
GAM114 IPP	AGTGGCATGATCGTAGCTCACT 1532 GG CC I	
	GGCATGATC AGCTCAC	
	IIIIIIII IIIII	
	CCGTACTAG TCGAGTG	
	CA CA I	
GAM114 IPP	AGTGGCATGATCGTAGCTCACT 1532 TAGG CC	
	GGCATGATC AGCTCACTG	
	IIIIIIII IIIIIII	

	CCGTACTAG TCGAGTGAT			
	CA__ CA			
GAM114 IRAK4	AGTGGCACGATCTCAGCTCACTG 1537 GG	C	I	
	GGCATGATC CAGCTCACT			
	CCGTGCTAG GTCGAGTGA			
	CA A I			
GAM114 IRAK4	AGTGGCACGATCTCAGCTCACTG 1537 TAGG	C	I	
	GGCATGATC CAGCTCACTG			
	CCGTGCTAG GTCGAGTGAC			
	CA__ A G			
GAM114 JRK	AGGTGCCAAG-TCCCAGCTCA 1527 G ATGA	I		
	GG GC TCCCAGCTC			
	CC CG AGGGTCGAG			
	A GTTC I			
GAM114 JRK	AGGTGCCAAG-TCCCAGCTCA 1527 TA G ATGA	CT		
	GG GC TCCCAGCTCA			
	CC CG AGGGTCGAGT			
	_ A GTTC TI			
GAM114 KAI1	GCACGATCTCAGCTCACTG 1552	C	II	
	GCATGATC CAGCTCACT			
	CGTGCTAG GTCGAGTGA			
	A CI			
GAM114 KCNJ5	AGTGGCATGATCTTGGCTCACTG 1543 GG	CCA	I	
	GGCATGATC GCTCACT			
	CCGTACTAG CGAGTGA			
	CA AAC I			
GAM114 KCNJ5	AGTGGCATGATCTTGGCTCACTG 1543 TAGG	CCA	I	
	GGCATGATC GCTCACTG			
	CCGTACTAG CGAGTGAC			
	CA__ AAC G			
GAM114 KLK5	GGGGGATTTGCTCCCAGCTCA 1563 _ CA_ A	III		
	GGGG TG TCCCAGCTC			
	CCCC AC AGGGTCGAG			
	C TAA G TII			
GAM114 KLK5	GGGGGATTTGCTCCCAGCTCA 1563 TA CA A	CTG		
	GGGG TG TCCCAGCTCA			
	CCCT AC AGGGTCGAGT			
	_ AA G CGI			
GAM114 MBD4	AGTGGCATGATCATGGCTCACTG 1540 GG	CCA	I	
	GGCATGATC GCTCACT			

	CCGTACTAG CGAGTGA	
	CA TAC I	
GAM114 MBD4	AGTGGCATGATCATGGCTCACTG 1540 TAGG CCA I	
	GGCATGATC GCTCACTG	
	CCGTACTAG CGAGTGAC	
	CA__ TAC G	
GAM114 MEF2A	AGGCGCCTGTAATCCCAGCT-ACT 1531 GG A__ CAI	
	GC TGATCCCAGCT	
	CG ATTAGGGTCGA	
	G_ GAC TII	
GAM114 MEF2A	AGGCGCCTGTAATCCCAGCT-ACT 1531 TA G A__ C GI	
	GG GC TGATCCCAGCT ACT	
	CC CG ATTAGGGTCGA TGA	
	__ G GAC _ GI	
GAM114 MEFV	GGCGCCTGTAATCCCAGCT-ACT 1565 G A__ CACI	
	GC TGATCCCAGCT	
	CG ATTAGGGTCGA	
	G GAC TIII	
GAM114 MEFV	GGCGCCTGTAATCCCAGCT-ACT 1565 TAGGG A__ C G	
	GC TGATCCCAGCT ACT	
	CG ATTAGGGTCGA TGA	
	G__ GAC _ A	
GAM114 MERTK	TGGACGTCCCGAACCTGTCC 1571 AGTGTGCA GG_	
	CGT GAACCTGTCC	
	GCA CTTGGACAGG	
	_____ GGG	
GAM114 MRPL49	GGCGCCTGTAATCCCAGCT-ACT 1565 G A__ CACI	
	GC TGATCCCAGCT	
	CG ATTAGGGTCGA	
	G GAC TIII	
GAM114 MRPL49	GGCGCCTGTAATCCCAGCT-ACT 1565 TAGGG A__ C G	
	GC TGATCCCAGCT ACT	
	CG ATTAGGGTCGA TGA	
	G__ GAC _ G	
GAM114 MYCL2	AGGCGCCTGCGATCCCAGCT-ACT 1530 GG AT__ CAI	
	GC GATCCCAGCT	
	CG CTAGGGTCGA	
	G_ GACG TII	
GAM114 MYCL2	AGGCGCCTGCGATCCCAGCT-ACT 1530 TA G AT__ C GI	
	GG GC GATCCCAGCT ACT	

	CC CG CTAGGGTCGA TGA	
	__ G GACG __ GI	
GAM114 NCALD	GGCAAGAATTTCAGCTCACT 1554 T TCC II	
	GGCA GA CAGCTCAC	
	CCGT CT GTCGAGTG	
	T TAA AI	
GAM114 NPHS1	AGTGGCGTGATCTCAGCTCACTG 1544 GG A C I	
	GGC TGATC CAGCTCACT	
	CCG ACTAG GTCGAGTGA	
	CA C A I	
GAM114 NPHS1	AGTGGCGTGATCTCAGCTCACTG 1544 TAGG A C I	
	GGC TGATC CAGCTCACTG	
	CCG ACTAG GTCGAGTGAC	
	CA__ C A G	
GAM114 PAICS	AGTGGCATGATCCAGGCTCACTG 1541 GG CA I	
	GGCATGATCC GCTCACT	
	CCGTACTAGG CGAGTGA	
	CA TC I	
GAM114 PAICS	AGTGGCATGATCCAGGCTCACTG 1541 TAGG CA I	
	GGCATGATCC GCTCACTG	
	CCGTACTAGG CGAGTGAC	
	CA__ TC G	
GAM114 PHEMX	AGGGGCCTCAGACCGCAGCTCACTG 1528 GG AT__ C I	
	GGC GATC CAGCTCACT	
	CCG CTGG GTCGAGTGA	
	__ GAGT C I	
GAM114 PHEMX	AGGGGCCTCAGACCGCAGCTCACTG 1528 TA AT__ C II	
	GGGGC GATC CAGCTCACTG	
	CCCCG CTGG GTCGAGTGAC	
	__ GAGT C GI	
GAM114 PLOD3	TACGCGCCTGGATCCCAGCTC 1569 AGGG AT_ I	
	GC GATCCCAGCT	
	CG CTAGGGTCGA	
	GCG_ GAC I	
GAM114 PLOD3	TACGCGCCTGGATCCCAGCTC 1569 TAGGG AT_ ACTG	
	GC GATCCCAGCTC	
	CG CTAGGGTCGAG	
	ATGCG GAC G	
GAM114 PMSCL1	GTTCAACA-GGAAACCTGTCC 1567 AGTGTG T	
	CACG GGGAACCTGTCC	

GTGT CCTTTGGACAGG

GAM114 PSMB2	AGTGGCATGATCTCGGCTCACTG 1542 GG CCA I
	GGCATGATC GCTCACT
	CCGTACTAG CGAGTGA
	CA AGC I
GAM114 PSMB2	AGTGGCATGATCTCGGCTCACTG 1542 TAGG CCA I
	GGCATGATC GCTCACTG
	CCGTACTAG CGAGTGAC
	CA__ AGC G
GAM114 PSMD5	AGTGGCAAGATCTCAGCTCACTG 1535 GG T C I
	GGCA GATC CAGCTCACT
	CCGT CTAG GTCGAGTGA
	CA T A I
GAM114 PSMD5	AGTGGCAAGATCTCAGCTCACTG 1535 TAGG T C I
	GGCA GATC CAGCTCACTG
	CCGT CTAG GTCGAGTGAC
	CA__ T A G
GAM114 PTGFRN	AGTGCTGCTGGTAGGAACCTGT 1546 _ AC CCC
	AGTG TGC GTGGGAACCTGT
	TCAC ACG CATCCTTGGACA
	G AC
GAM114 RANBP3	AGTGTGGGCGTCACGTGGGAACGTGGCC1547 C T C
	AGTGTG CACGTGGGAAC TG CC
	TCACAC GTGCACCCTTG AC GG
	CCGCA C C C
GAM114 SIP	AGTGGCATCATCATAGCTCACTG 1538 GG G CC I
	GGCAT ATC AGCTCACT
	CCGTA TAG TCGAGTGA
	CA G TA I
GAM114 SIP	AGTGGCATCATCATAGCTCACTG 1538 TAGG G CC I
	GGCAT ATC AGCTCACTG
	CCGTA TAG TCGAGTGAC
	CA__ G TA G
GAM114 SLC1A4	TGTATGTGA-AACCTGTCC 1572 AGTGTGCAC G
	GTGG AACCTGTC
	CACT TTGGACAG
	A_____
GAM114 SLC2A6	GGCATGATCTCAGCTCATTG 1558 C CTI
	GCATGATC CAGCTCA

	CGTACTAG GTCGAGT		
	A AAI		
GAM114 SLC2A6	GGCATGATCTCAGCTCATTG 1558 TAGGGGCA C CT		
	TGATC CAGCTCA		
	ACTAG GTCGAGT		
	_____ A AA		
GAM114 SMAC	GGCGCCTGCAATCCCAGCT-ACT 1564 G AT__ CACI		
	GC GATCCCAGCT		
	CG TTAGGGTCGA		
	G GACG TIII		
GAM114 SMAC	GGCGCCTGCAATCCCAGCT-ACT 1564 TAGGG AT__ C G		
	GC GATCCCAGCT ACT		
	CG TTAGGGTCGA TGA		
	G__ GACG _ G		
GAM114 SUDD	GCATGATCTCAGCTCACTG 1553 C II		
	GCATGATC CAGCTCACT		
	CGTACTAG GTCGAGTGA		
	A CI		
GAM114 SWAP70	GGCATGATCTCAGCTCGCTG 1559 C A I		
	GCATGATC CAGCTC CT		
	CGTACTAG GTCGAG GA		
	A C I		
GAM114 SWAP70	GGCATGATCTCAGCTCGCTG 1559 TAGGGGCA C A		
	TGATC CAGCTC CT		
	ACTAG GTCGAG GA		
	_____ A C		
GAM114 TBX1	AGTGGCATGATCATAGCTTACTG 1539 GG CC C I		
	GGCATGATC AGCT ACT		
	CCGTACTAG TCGA TGA		
	CA TA A I		
GAM114 TBX1	AGTGGCATGATCATAGCTTACTG 1539 TAGG CC C I		
	GGCATGATC AGCT ACTG		
	CCGTACTAG TCGA TGAC		
	CA__ TA A G		
GAM114 TNFSF10	TAGTGGCATGATCTCACCACACTG 1570 G CCA _ I		
	TAG GGCATGATC GCT CACTG		
	ATC CCGTACTAG TGG GTGAC		
	A AG_ T I		
GAM114 TNFSF10	TAGTGGCATGATCTCACCACACTG 1570 AGG CCA _ I		
	GGCATGATC GCT CACT		

	CCGTACTAG TGG GTGA			
	TCA AG_ T I			
GAM114 TPMT	AGTGGCACGATCTCAGCTCACTG 1537 GG C I			
	GGCATGATC CAGCTCACT			
	CCGTGCTAG GTCGAGTGA			
	CA A I			
GAM114 TPMT	AGTGGCACGATCTCAGCTCACTG 1537 TAGG C I			
	GGCATGATC CAGCTCACTG			
	CCGTGCTAG GTCGAGTGAC			
	CA_ A G			
GAM114 TRAF5	GGCGCCTGTAATCCCAGCT-ACT 1565 G A_ CACI			
	GC TGATCCCAGCT			
	CG ATTAGGGTCTGA			
	G GAC TIII			
GAM114 TRAF5	GGCGCCTGTAATCCCAGCT-ACT 1565 TAGGG A_ C G			
	GC TGATCCCAGCT ACT			
	CG ATTAGGGTCTGA TGA			
	G_ GAC _ G			
GAM114 UBE2B	GGCATAATCACAGCTCACTG 1556 C I			
	GCATGATC CAGCTCACT			
	CGTATTAG GTCGAGTGA			
	T I			
GAM114 UBE2G2	AGTGGCGTGATCTCAGCTCACTG 1544 GG A C I			
	GGC TGATC CAGCTCACT			
	CCG ACTAG GTCGAGTGA			
	CA C A I			
GAM114 UBE2G2	AGTGGCGTGATCTCAGCTCACTG 1544 TAGG A C I			
	GGC TGATC CAGCTCACTG			
	CCG ACTAG GTCGAGTGAC			
	CA_ C A G			
GAM114 VDR	GGCACGATCTCAGCTCACTG 1555 C I			
	GCATGATC CAGCTCACT			
	CGTGCTAG GTCGAGTGA			
	A I			
GAM114 VDR	GGCACGATCTCAGCTCACTG 1555 TAGGGGCAT C			
	GATC CAGCTCACT			
	CTAG GTCGAGTGA			
	G_ A			
GAM114 VHL	AGTGGCACCATCTCAGCTCACTG 1536 GG G C I			
	GGCAT ATC CAGCTCACT			

	CCGTG TAG GTCGAGTGA		
	CA G A I		
GAM114 VHL	AGTGGCACCATCTCAGCTCACTG 1536 TAGG G C I		
	GGCAT ATC CAGCTCACTG		
	CCGTG TAG GTCGAGTGAC		
	CA__ G A G		
GAM114 VHL	AGGCGCCTGTAATCCCAGCTCA 1529 GGG A__ I		
	GC TGATCCCAGCTC		
	CG ATTAGGGTCGAG		
	G__ GAC I		
GAM114 VHL	AGGCGCCTGTAATCCCAGCTCA 1529 TA G A__ CTG		
	GG GC TGATCCCAGCTCA		
	CC CG ATTAGGGTCGAGT		
	__ G GAC CII		
GAM114 ZNF133	AGGCGCCTGTAATCCCAGCT-ACT 1531 GG A__ CAI		
	GC TGATCCCAGCT		
	CG ATTAGGGTCGA		
	G_ GAC TII		
GAM114 ZNF133	AGGCGCCTGTAATCCCAGCT-ACT 1531 TA G A__ C GI		
	GG GC TGATCCCAGCT ACT		
	CC CG ATTAGGGTCGA TGA		
	__ G GAC _ GI		
GAM114 ZNF14	AGTGGCGTGATCTCAGCTCACTG 1544 GG A C I		
	GGC TGATC CAGCTCACT		
	CCG ACTAG GTCGAGTGA		
	CA C A I		
GAM114 ZNF14	AGTGGCGTGATCTCAGCTCACTG 1544 TAGG A C I		
	GGC TGATC CAGCTCACTG		
	CCG ACTAG GTCGAGTGAC		
	CA__ C A G		
GAM115 ACADSB	TCTAAATAAATTTTCATCAGTTTT 1586 CAC GCTG I		
	TCT TAAGT ATCAGTTTT		
	AGA ATTTA TAGTCAAAA		
	TTT AAAG I		
GAM115 BCL2L2	TCTAGCTAAG-CTGATCAGT 1585 CA GT TT		
	TCT CTAA GCTGATCAGT		
	AGA GATT CGACTAGTCA		
	TC _ II		
GAM115 CD28	TCACTAAGTACATGGTAAGTT 1580 TCTC _ ATC TT		
	ACTAAGTGC TG AGTT		

	TGATTCATG AC TCAA	
	_____ T CAT CC	
GAM115 CD79A	TCACTAAGTGGCCCTGA-CAG 1579 TCTC	____ T TTT
	ACTAAGTG CTGA CAG	
	TGATTCAC GACT GTC	
	_____ CGG _ TAI	
GAM115 CYP7A1	TCTCACTAA--GCTGTCCAG 1584	GT A TT
	TCTCACTAA GCTG TCAG	
	AGAGTGATT CGAC GGTC	
	_____ A II	
GAM115 EIF4G2	TCTCTCAAAA--CTGATCAGTTTT 1587	____ CTAAGT
	TCTCA GCTGATCAGTTTT	
	AGAGT TGACTAGTCAAAA	
	AG TT_____	
GAM115 FGF7	CAC-AAGTCCAGCTTGATCAGTTTT 1577 TCTCA	A GC I
	CTA GT TGATCAGTTTT	
	GGT CG ACTAGTCAAAA	
	TTCA_ _ A_ A	
GAM115 FOLH1	TCTCACTAATGCCTCGCTTATCAG 1583	_ _ _ G TTTT
	TCTCACTAA GT GCT ATCAG	
	AGAGTGATT CG CGA TAGTC	
	A GAG A IIITT	
GAM115 LANCL1	TCTTACTGTAAGTGCTGAT 1581 C	____ CAGTTT
	TCT ACT AAGTGCTGAT	
	AGA TGA TTCACGACTA	
	A CA IIITTT	
GAM115 NRIP1	TCTGACCACAGTGCTGATCA 1582 C	_ GTTT
	TCT ACTA AGTGCTGATCA	
	AGA TGGT TCACGACTAGT	
	C G IIIT	
GAM115 SNX6	CTCACTAAGAGC--ATCAG 1578 TC	T TG TT
	TCACTAAG GC ATCAG	
	AGTGATTC CG TAGTC	
	_____ T _ TI	
GAM115 TGFBR2	TCTTCCTAAG--C--ATCAGTTTT 1588 CA	GCTG
	TCT CTAAGT ATCAGTTT	
	AGA GATTCG TAGTCAAA	
	AG _____	
GAM116 AADAC	TAAAGTATACAAG-AATGTAATATTT 1609	_ TAAG ATTTII
	TAAAGTATA AGG GTAA	

	ATTTCATAT TTC CATT		
	G TTA_ ATAAAI		
GAM116 ATP8A2	AAG-ATCAGGTAAGGTGAA	1602 TAAAGTATA	AAAT
	AGGTAAGGT		
	TCCATTCCA		
	CTAG_____CTTC		
GAM116 BACH1	AAAAAATAAGGTAATGTTATTTT	1600 TAAAGTAT	ATTTI
	AAGGTAAGGTAA		
	TTTTATTCCATT		
	T_____ACAAT		
GAM116 BCAT1	TAAAG-ACAATATAAGGTAAAT	1611 T G	TT
	TAAAG ATAA GTAAGGTAAAT		
	ATTTC TGTT TATTCCATTTA		
	_ A _ II		
GAM116 CAV1	AAATAAAAAGGTAAGGAAAA	1595 TAA T_	T TT
	AGTA AAGGTAAGG AAA		
	TTAT TTCCATTCC TTT		
	___ TT T TI		
GAM116 COG5	TAAAGTATAAGTGCTAAAGAGGTAAAT	1610 _ A___	TTIII
	TAAAGTATAAG GT AGGTAAAT		
	ATTTCATATTC CG TCCATTTA		
	A ATTC IIIT		
GAM116 COL19A1	AAAGTATCTG--AAGGTAAAT	1598 TA AAGGT	T
	AAGTAT AAGGTAAAT		
	TTCATA TTCCATTTA		
	___ GAC_ T		
GAM116 COL4A4	TAAAGTATATGAAAAATAGATT	1612 A T	AATTTI
	TAAAGTATA GG AAGGTA		
	ATTTCATAT CC TTTTAT		
	A T CTAII		
GAM116 EGR3	AGTATAAGGTACTATAAAT	1605 TAAAGT	AG
	ATAAGGTA GTAAATT		
	TATTCCAT TATTTAG		
	_____GA		
GAM116 EPB72	TAGAGAATGAG-TAAGGTAAGTTT	1615 TAAAGTATAA	ATTTI
	GGTAAGGTAA		
	TCATTCCATT		
	ATCTCTTAC_ CAAAI		
GAM116 FGF5	TAAAGTATAA-ATTAGTTCAATTT	1613 GTA GTA	I
	TAAAGTATAAG AG AATTT		

	ATTTCATATTT TC TTAAA	
	AA_ AAG I	
GAM116 GPR23	AAAGTATAACAGGGAGGATAAAT 1591 TA _ TA _ TTI	
	AAGTATAA GG AGG TAAAT	
	TTCATATT TC TCC ATTTA	
	_ G CC T TII	
GAM116 KERA	TAAAGTATAACAAAAAG-ATATTT 1614 GGT_ AATTTI	
	TAAAGTATAA AAGGTA	
	ATTTCATATT TTCTAT	
	GTTT AAIII	
GAM116 MYCN	TAAAGTATACAGGCAGTGTA 1608 _ AG ATTT	
	TAAAGTATA AGGTA GTAA	
	ATTTCATAT TCCGT CATT	
	G CA IIIT	
GAM116 OSR1	AAACTCTAAGGTAAGCGGTAA 1594 TAAAGTA _ ATTT	
	TAAGGTAA GGTA	
	ATTCCATT CCATT	
	TTGAG_ CG CIII	
GAM116 OSR1	AAG-AGAAAATAAGGTAAA 1601 TAAAGTAT T	
	AAGGTAAGGTAAA	
	TTTTATTCCATTT	
	CTC_ T	
GAM116 PPP3R1	AAAATGTAAT-TAAGGTAAAT 1596 TAAA TAAGG T	
	GTA TAAGGTAAAT	
	CAT ATTCCATTTA	
	TTTA TA_ T	
GAM116 PTPN12	AGTATAAGG-CAGGTAGAT 1604 TAAAGT A AAT	
	ATAAGGTA GGTA	
	TATTCCGT CCAT	
	_ CTA	
GAM116 RFXAP	AAGTATAA-GAAAAATAATTTT 1603 TAAA T ATTT	
	GTATAAGG AAGGTAA	
	CATATTCT TTTTATT	
	_ AAAA	
GAM116 RFXAP	AAAGTATAAGAAAAAGGTA 1592 TA T_ AATT	
	AAGTATAAGG AAGGTA	
	TTCATATTCT TTCCAT	
	_ TT AIII	
GAM116 SPF30	AAAATATAAGGATAAAAAGGTAAAT 1593 TA T_ TTII	
	AAGTATAAGG AAGGTAAAT	

	TTTATATTCC TTCCATTTA	
	___ TATTT CIII	
GAM116 SPO11	TAAAGTATAAAGGCAAAGGAAAAT 1607	_ T TTTI
	TAAAGTATAA GGTAAGG AAA	
	ATTCATATT CCGTTTC TTT	
	T C TAI	
GAM116 TCTEL1	AAAGTATAAAGTATGGAAAATT 1599 TA	A T T
	AAGTATAAAGGTA GG AAATT	
	TTCATATTTTCAT CC TTAA	
	___ A T T	
GAM116 USP7	AAAGTATAACTGAAGG-AAAT 1597 TA	GGT T T
	AAGTATAA AAGG AAAT	
	TTCATATT TTCC TTAA	
	___ GAC _ T	
GAM116 ZNF24	GTAAAAGGAAATAAGGGTAAATTT 1606 TAAAGTATA	_ I
	AGGTAAGG TAAATTT	
	TTTATTCC ATTAAA	
	TTCC___ C A	
GAM117 AHR	GACAATTTATACACATTGAAATGGG 1631 ACAACAG	C I
	ACACATTGA ATGG	
	TGTGTAAC TACC	
	TTAAATA T I	
GAM117 AHR	GACAATTTATACACATTGAAATGGG 1631 TG CAG___	C II
	ACAA ACACATTGA ATGGG	
	TGTT TGTGTAAC TACCC	
	___ AAATA T AI	
GAM117 AKAP13	ACAACAGAC-C-TTTACATG 1623	ACATTG I
	ACAACAGAC ACA	
	TGTTGTCTG TGT	
	GAAA_ A	
GAM117 AKAP13	ACAACAGAC-C-TTTACATG 1623	ACATTG I
	ACAACAGAC ACA	
	TGTTGTCTG TGT	
	GAAA_ A	
GAM117 AKAP13	ACAACAGAC-C-TTTACATG 1623 TGAC	ACATTG
	AACAGAC ACATG	
	TTGTCTG TGTAC	
	___ GAAA_	
GAM117 AKAP13	ACAACAGAC-C-TTTACATG 1623 TGAC	ACATTG
	AACAGAC ACATG	

		TTGTCTG TGTAC		
		_____ GAAA__		
GAM117 ARHGEF7	TGA-AACAGACACAGTTATAT	1639 C	TTGACATGG	
	TGA AACAGACACA			
	ACT TTGTCTGTGT			
	_____ CAATATAII			
GAM117 ARHGEF7	TGA-AACAGACACAGTTATAT	1639 _ C	TTGACAI	
	GA AACAGACACA			
	CT TTGTCTGTGT			
	A _ CAATATI			
GAM117 BCAR1	ACAGC-GACTC-TTGACATGGG	1625 TGACAACA ACA		
	GAC TTGACATGG			
	CTG AACTGTACC			
	TCG_____ AG_			
GAM117 BCAR1	ACAGC-GACTC-TTGACATGGG	1625 CA AC A_ I		
	ACAG AC TTGACATGG			
	TGTC TG AACTGTACC			
	_____ GC AG I			
GAM117 CACNA1C	ACATGAGAAGCATTGACAT	1622 AC CA II		
	ACA AGA CATTGACA			
	TGT TCT GTAACGT			
	AC TC AI			
GAM117 CACNA1C	ACATGAGAAGCATTGACAT	1622 TGACAAC CA GG		
	AGA CATTGACAT			
	TCT GTAACGTGA			
	TAC_____ TC AC			
GAM117 CBS	TGACAACAGAATC--TGTCATGGG	1642 CACA A		
	TGACAACAGA TTG CATGGG			
	ACTGTTGTCT GAC GTACCC			
	TA_ A			
GAM117 CBS	TGACAACAGAATC--TGTCATGGG	1642 _ CACA A I		
	GACAACAGA TTG CATGG			
	CTGTTGTCT GAC GTACC			
	A TA_ A I			
GAM117 CD3Z	TGACAACAGAAGCCAAATTTACA	1636 CA_ TTG_ TGGGI		
	TGACAACAGA CA ACA			
	ACTGTTGTCT GT TGT			
	TCG TTAAA IIIGG			
GAM117 CDKN2C	GACACACAGACACACATACAT	1630 _ A TG I		
	ACA CAGACACAT ACA			

	TGT GTCTGTGTG TGT	
	G _ TA I	
GAM117 CDKN2C	GACACACAGACACACATACAT 1630 TG _ TG GGG	
	ACA ACAGACACAT ACAT	
	TGT TGTCTGTGTG TGTA	
	_ G TA AII	
GAM117 DIAPH2	GAAAACAGATACATTGACA 1633 C C II	
	GA AACAGA ACATTGAC	
	CT TTGTCT TGTAAGT	
	T A TI	
GAM117 DIAPH2	GAAAACAGATACATTGACA 1633 TGAC C TGG	
	AACAGA ACATTGACA	
	TTGTCT TGTAAGT	
	TT_ A TII	
GAM117 EMX2	TGACAAAATATTGACATTGACAT 1638 CAGAC_ GGGI	
	TGACAA ACATTGACAT	
	ACTGTT TGTAAGT	
	TTATAAC IIIG	
GAM117 ETF1	GACATCAGGTTACACATTGACA 1632 A _ III	
	GACA CAG ACACATTGAC	
	CTGT GTC TGTGTAAGT	
	A CAA TII	
GAM117 ETF1	GACATCAGGTTACACATTGACA 1632 TG A _ TGGG	
	ACA CAG ACACATTGACA	
	TGT GTC TGTGTAAGT	
	_ A CAA CIII	
GAM117 IL11RA	ACAGACACATGGTCACACATGG 1626 TG_ IIC	
	ACAGACACAT ACATG	
	TGTCTGTGTA TGTAC	
	CCAGTG CIII	
GAM117 IL11RA	ACAGACACATGGTCACACATGG 1626 TG ACAG_ T GG	
	ACA ACACAT GACATG	
	TGT TGTGTA CTGTGT	
	G_ ACCAG C II	
GAM117 IL17BR	TGACACCTGCTAC-TTGACATGG 1641 ACAGAC A G	
	TGACA AC TTGACATGG	
	ACTGT TG AACTGTACC	
	GGACGA _ I	
GAM117 IL17BR	TGACACCTGCTAC-TTGACATGG 1641 _ ACAGAC A I	
	GACA AC TTGACATG	

	CTGT TG AACTGTAC		
	A GGACGA _ I		
GAM117 KDR	GACA-CAGACACATT--CTTGGG	1635	A GACATI
	GACA CAGACACATT		
	CTGT GTCTGTGTAA		
	_ GAACCC		
GAM117 KDR	GACA-CAGACACATT--CTTGGG	1635	TG A GACA
	ACA CAGACACATT TGG		
	TGT GTCTGTGTAA ACC		
	_ _ GA_		
GAM117 LRAT	AATACACACACTGACATGGG	1619	ACAG I
	ACACATTGACATGG		
	TGTGTGACTGTACC		
	TATG I		
GAM117 LRAT	AATACACACACTGACATGGG	1619	TGACAACAG
	ACACATTGACATGG		
	TGTGTGACTGTACC		
	G_		
GAM117 MEN1	ACAGACACA--GGCTTGGG	1627	TTGACATGGI
	ACAGACACA		
	TGTCTGTGT		
	CCGAACCCII		
GAM117 NCALD	ACCACAGACACACTTGCCCATG	1621	CA GA_ I
	ACAGACACATT CAT		
	TGTCTGTGTGA GTA		
	_ ACGG I		
GAM117 NCALD	ACCACAGACACACTTGCCCATG	1621	TGACA GA_ GG
	ACAGACACATT CATG		
	TGTCTGTGTGA GTAC		
	G_ ACGG AG		
GAM117 PNUTL1	AACAGACACAATGACCTGGG	1618	T A I
	ACAGACACA TGAC TGG		
	TGTCTGTGT ACTG ACC		
	T G I		
GAM117 PNUTL1	AACAGACACAATGACCTGGG	1618	TGACAACA T A
	GACACA TGAC TGG		
	CTGTGT ACTG ACC		
	_ T G		
GAM117 PTGFRN	ACAGACACATT--CTTGGG	1628	GACA I
	ACAGACACATT TGG		

		TGTCTGTGTAA ACC			
		GA__ C			
GAM117 SDC2		GACAACAGATAAATTAACA 1634	CAC	II	
		GACAACAGA ATTGAC			
		CTGTTGTCT TAATTG			
		ATT TI			
GAM117 SDC2		GACAACAGATAAATTAACA 1634 TG	CAC	TGG	
		ACAACAGA ATTGACA			
		TGTTGTCT TAATTGT			
		__ ATT TII			
GAM117 SLC29A1		GACACACAGACACATACACA 1629 _	TGACII		
		GACA ACAGACACAT			
		CTGT TGTCTGTGTA			
		G TGTGTI			
GAM117 SLC29A1		GACACACAGACACATACACA 1629 TG _	TG		
		ACA ACAGACACAT ACATGG			
		TGT TGTCTGTGTA TGTGTC			
		_ G _			
GAM117 SMP1		TGACAA-ATACTTACATTGACA 1637	CAG _	TGGG	
		TGACAA AC ACATTGACA			
		ACTGTT TG TGTAAGTGT			
		TA_ AA IIIG			
GAM117 SMP1		TGACAA-ATACTTACATTGACA 1637 G	CAG _	I	
		ACAA AC ACATTGAC			
		TGTT TG TGTAAGTGT			
		_ TA_ AA I			
GAM117 SUV39H1		ACAGACAGACACATAGATCTGG 1620 CA	T CA I		
		ACAGACACAT GA TG			
		TGTCTGTGTA CT AC			
		TC T AG I			
GAM117 SUV39H1		ACAGACAGACACATAGATCTGG 1620 TGACA	T CA G		
		ACAGACACAT GA TGG			
		TGTCTGTGTA CT ACC			
		TC__ T AG G			
GAM117 UPF3A		TGCCAAAA-ATACATTGACAT 1640 GA_ C C	I		
		CAA AGA ACATTGACA			
		GTT TTT TGTAAGTGT			
		ACG _ A I			
GAM117 UPF3A		TGCCAAAA-ATACATTGACAT 1640 TGA C C	GG		
		CAA AGA ACATTGACAT			

	GTT TTT TGTAAGTGTG	
	ACG _ A _ _ II	
GAM117 ZNF255	ACAATAGATG--TTGACATGGG 1624 _ C CACA I	
	CAA AGA TTGACATGG	
	GTT TCT AACTGTACC	
	T A AC_ _ I	
GAM117 ZNF255	ACAATAGATG--TTGACATGGG 1624 TGACAAC CACA	
	AGA TTGACATGG	
	TCT AACTGTACC	
	TTA_ _ AC_ _	
GAM118 AHR	GACAATTTATACACATTGAAATGGG 1631 TG CAG_ _ C II	
	ACAA ACACATTGA ATGGG	
	TGTT TGTGTAAGT TACCC	
	_ AAATA T AI	
GAM118 AKAP13	ACAACAGAC-C-TTTACATG 1623 TGAC ACATTG	
	AACAGAC ACATG	
	TTGTCTG TGTAC	
	_ GAAA_ _	
GAM118 AKAP13	ACAACAGAC-C-TTTACATG 1623 TGAC ACATTG	
	AACAGAC ACATG	
	TTGTCTG TGTAC	
	_ GAAA_ _	
GAM118 ARHGEF7	TGA-AACAGACACAGTTATAT 1639 C TTGACATGG	
	TGA AACAGACACA	
	ACT TTGTCTGTGT	
	_ CAATATAII	
GAM118 BCAR1	ACAGC-GACTC-TTGACATGGG 1625 TGACAACA ACA	
	GAC TTGACATGG	
	CTG AACTGTACC	
	TCG_ _ AG_	
GAM118 CACNA1C	ACATGAGAAGCATTGACAT 1622 TGACAAC CA GG	
	AGA CATTGACAT	
	TCT GTAAGTGTG	
	TAC_ _ TC AC	
GAM118 CBS	TGACAACAGAATC--TGTCATGGG 1642 CACA A	
	TGACAACAGA TTG CATGGG	
	ACTGTTGTCT GAC GTACCC	
	TA_ _ A	
GAM118 CD3Z	TGACAACAGAAGCCAAATTTACA 1636 CA_ TTG_ _ TGGGI	
	TGACAACAGA CA ACA	

	ACTGTTGTCT GT TGT		
	TCG TTAAA IIIIGG		
GAM118 CDKN2C	GACACACAGACACACATACAT 1630 TG _ TG GGG		
	ACA ACAGACACAT ACAT		
	III IIIIIII III		
	TGT TGTCTGTGTG TGTA		
	_ G TA AII		
GAM118 DIAPH2	GAAAACAGATACATTGACA 1633 TGAC C TGG		
	AACAGA ACATTGACA		
	IIII IIIIIII		
	TTGTCT TGTAAGTGT		
	TT_ A TII		
GAM118 EMX2	TGACAAAATATTGACATTGACAT 1638 CAGAC_ GGGI		
	TGACAA ACATTGACAT		
	IIII IIIIIII		
	ACTGTT TGTAAGTGT		
	TTATAAC IIIIG		
GAM118 ETF1	GACATCAGGTTACACATTGACA 1632 TG A _ TGGG		
	ACA CAG ACACATTGACA		
	III III IIIIIII		
	TGT GTC TGTGTAAGTGT		
	_ A CAA CIII		
GAM118 IL11RA	ACAGACACATGGTCACACATGG 1626 TG ACAG_ T GG		
	ACA ACACAT GACATG		
	III IIIIIII		
	TGT TGTGTA CTGTGT		
	G_ ACCAG C II		
GAM118 IL17BR	TGACACCTGCTAC-TTGACATGG 1641 ACAGAC A G		
	TGACA AC TTGACATGG		
	IIII II IIIIIII		
	ACTGT TG AACTGTACC		
	GGACGA _ I		
GAM118 KDR	GACA-CAGACACATT--CTTGGG 1635 TG A GACA		
	ACA CAGACACATT TGG		
	III IIIIIII III		
	TGT GTCTGTGTAA ACC		
	_ _ GA_		
GAM118 LRAT	AATACACACACTGACATGGG 1619 TGACAACAG		
	ACACATTGACATGG		
	IIIIIIIIII		
	TGTGTGACTGTACC		
	G_		
GAM118 NCALD	ACCACAGACACACTTGCCCATG 1621 TGACA GA_ GG		
	ACAGACACATT CATG		
	IIIIIIII III		
	TGTCTGTGTGA GTAC		
	G_ ACGG AG		
GAM118 PNU TL1	AACAGACACAATGACCTGGG 1618 TGACAACA T A		
	GACACA TGAC TGG		
	IIII III III		

		CTGTGT ACTG ACC			
		_____ T G			
GAM118 SDC2		GACAACAGATAAATTAACA	1634 TG	CAC	TGG
		ACAACAGA ATTGACA			
		TGTTGTCT TAATTGT			
		___ ATT TII			
GAM118 SLC29A1		GACACACAGACACATACACA	1629 TG _		TG
		ACA ACAGACACAT ACATGG			
		TGT TGTCTGTGTA TGTGTC			
		___ G ___			
GAM118 SMP1		TGACAA-ATACTTACATTGACA	1637	CAG ___	TGGG
		TGACAA AC ACATTGACA			
		ACTGTT TG TGTAAGTGT			
		TA_ AA IIIG			
GAM118 SUV39H1		ACAGACAGACACATAGATCTGG	1620 TGACA		T CA G
		ACAGACACAT GA TGG			
		TGTCTGTGTA CT ACC			
		TC___ T AG G			
GAM118 UPF3A		TGCCAAAA-ATACATTGACAT	1640 TGA	C C	GG
		CAA AGA ACATTGACAT			
		GTT TTT TGTAAGTGT			
		ACG _ A II			
GAM118 ZNF255		ACAATAGATG--TTGACATGGG	1624 TGACAAC		CACA
		AGA TTGACATGG			
		TCT AACTGTACC			
		TTA___ AC___			
GAM119 BLTR2		ACAACAGACAGTGAGAGAGAGTTG	1677 AA	T _ T	C I
		CAACAGACA TG G GAGGG TG			
		GTTGTCTGT AC C CTCTC AC			
		___ C T T A A			
GAM119 EPHB1		AAGAAAAGAATGTCATTGGTGAGG	1670 AACAACAGA___		GCTGI
		CATTGGTGAGG			
		GTAACCACTCC			
		TTCTTTTCTTACA	IIIGT		
GAM119 EPHB2		AACAACAGATGCTGGAGAGG	1673	CA T	GCT
		AACAACAGA TTGG GAGG			
		TTGTTGTCT GACC CTCC			
		AC T III			
GAM119 EPHB4		AACAGACA-TGATGATGGGC	1676 AACAAC	T _	
		AGACAT GGTGA GGGCT			

TCTGTA CTA CT CCGG
 _____ A
 GAM119 LHX3 CAACAGACATCTGTGGGTGC 1682 AACA G A _ T
 ACAGACATT GTG GG GC
 ||||| ||| ||
 TGTCTGTAG CAC CC CG
 _____ A _ A T
 GAM119 MMP15 CAGACAGGGTGTGTGAGGGCTG 1683 AACAAACAGACAT _
 TG GTGAGGGCTG
 || |||||
 AC CACTCCCGAC
 TCCC _____ A
 GAM119 PIK3R3 AACAAACAGATCATTCTTTAGG 1671 _ GGTG GCTG
 AACAAACAGA CATT AGG
 ||||| ||| ||
 TTGTTGTCT GTAA TCC
 A GAAA |||G
 GAM119 PLXNA1 ACACGCATGCGGTGAGGGCTG 1680 AACAAACAGA _
 CAT TGGTGAGGGCTG
 ||| |||||
 GTA GCCACTCCCGAC
 C _____ C
 GAM119 PPP1R2 AACAGAGCAGACATTGGTGA 1669 A_ GGGCT
 AACA CAGACATTGGTGA
 ||| |||||
 TTGT GTCTGTAACCACT
 CTC |||GT
 GAM119 RBBP2 AACAGCAGACATTGGGGTCAGGGCTG 1672 A _ G ||
 AACA CAGACATT GGT AGGGCTG
 ||| ||||| ||| |||||
 TTGT GTCTGTAA CCA TCCCGAC
 C CC G ||
 GAM119 SLC26A4 CAACAGACACCTTGGTCAAGG 1681 AACA _ _ CTG
 ACAGACAT TGGT GAGGG
 ||||| ||| |||||
 TGTCTGTG ACCA CTTCC
 _____ GA G CTI
 GAM119 SPOCK ACACACACTTTGTGAGGGCTG 1679 AACAAACAG G_
 ACATT GTGAGGGCTG
 ||| |||||
 TGTGA CACTCCCGAC
 _____ AA
 GAM119 SRY AACATAAGAAA--GTGAGGGCTG 1675 AAC GACATT
 AACA GGTGAGGGCTG
 ||| |||||
 TTGT TCACTCCCGAC
 _____ ATTCTT
 GAM119 TBX6 AACAAACAGAC--TGGTGTGGCCTG 1674 AT A G
 AACAAACAGAC TGGTG GG CTG
 ||||| |||| |||

	TTGTTGTCTG ACCAC CC GAC	
	— A G	
GAM119 VANGL2	ACAAAAGTTGTTGGTGAGG 1678 AA C ACA GCT	
	CAA AG TTGGTGAGG	
	GTT TC AACCACTCC	
	— T AAC AII	
GAM120 DRD1	TGAAAATACATG-TCTTCTCGC 1697 T ATG I	
	GA GATA GTCTTCTCG	
	CT TTAT CAGAAGAGC	
	T GTA I	
GAM120 DRD1	TGAAAATACATG-TCTTCTCGC 1697 TGTGAT ATG C	
	GATA GTCTTCTCGC	
	TTAT CAGAAGAGCG	
	TT— GTA A	
GAM120 FGF12	TGATGATAAATGGT-TCCTGGC 1696 _ C CGI	
	GATGATAA TGGT TTCT	
	CTACTATT ACCA AGGA	
	T _ CCI	
GAM120 FGF12	TGATGATAAATGGT-TCCTGGC 1696 T TA C C C	
	GTGATGA ATGGT TTCT GC	
	TACTATT TACCA AGGA CG	
	_ _ _ C A	
GAM120 GRB14	ATGATAATG---TTTTCGCC 1686 _ GTCTTC	
	TGATAATG TCGC	
	ACTATTAC AGCG	
	T AAA—	
GAM120 HRH1	TGTAAT--TGAAGGTCTTCTC 1698 GATAAT GC	
	TGTGAT GGTCTTCTC	
	ACATTA CCAGAAGAG	
	ACTT_ II	
GAM120 HRH1	TGTAAT--TGAAGGTCTTCTC 1698 _ GATAAT I	
	GTGAT GGTCTTCT	
	CATTA CCAGAAGA	
	A ACTT_ I	
GAM120 HUNK	GATAATGCTGCCTTCTCGCC 1688 _ III	
	GATAATG GTCTTCTCGC	
	CTATTAC CGGAAGAGCG	
	GA GII	
GAM120 IKBKAP	TGAGTGGAATGGTCTTCTC 1693 _ AT II	
	TGA TG AATGGTCTTCT	

	ACT AC TTACCAGAAGA	
	C CT GI	
GAM120 IKBKAP	TGAGTGGAAATGGTCTTCTC 1693 T AT T GC	
	GTG GA AATGGTCTTCTC	
	CAC CT TTACCAGAAGAG	
	T _ _ AC	
GAM120 MAOB	GTGAGGACTAAATGGTCTT 1690 T _	
	GTGA GAT AATGGTCT	
	CACT CTG TTACCAGA	
	C AT AII	
GAM120 MAOB	GTGAGGACTAAATGGTCTT 1690 TG T _ CTCGC	
	TGA GAT AATGGTCTT	
	ACT CTG TTACCAGAA	
	_ C AT AIIIC	
GAM120 NLGN1	TGATAATGGTGTACCTGCC 1695 CTT TC II	
	TGATAATGGT C GC	
	ACTATTACCA G CG	
	CAT GA GI	
GAM120 PLA2G5	GTGATGATAA---TCTGATCGC 1692 _ TTCTI	
	GTGATGATAA TGGTC	
	CACTACTATT ACTAG	
	AG CGIII	
GAM120 PLA2G5	GTGATGATAA---TCTGATCGC 1692 TG ATG TC	
	TGATGATA GTCT TCGC	
	ACTACTAT TAGA AGCG	
	_ _ CT	
GAM120 SPAM1	GTGATGATAGTCATGGTTTTTTC 1691 TG _ C C CCI	
	TGATGATA ATGGT TT TCG	
	ACTACTAT TACCA AA AGT	
	_ CAG A A	
GAM120 SYNGR1	GATAATGGTGTCTACTTCTC 1687 _ IG	
	GATAATGGT CTTCT	
	CTATTACCA GAAGA	
	CGAT GIII	
GAM120 TMSB4Y	TGAGAAAGCCCTTCTCGCC 1694 TAAT _ II	
	TGA GGTC TTCTCGC	
	ACT TCGG AAGAGCG	
	CTT_ G GI	
GAM120 YY1	GTGGTCGAGAAGGGTCTTCTC 1689 TGA T T I	
	TGA AA GGTCTTCT	

	GCT TT CCAGAAGA		
	CCA C C I		
GAM120 YY1	GTGGTCGAGAAGGGTCTTCTC	1689	TGTGA T T GCC
	TGA AA GGTCTTCTC		
	GCT TT CCAGAAGAG		
	ACCA_ C C AII		
GAM121 LAMB3	GTGATCCCCAGAAAGGACC	1701	GTTATA TG II
	CC GAAAGGAC		
	GG CTTTCCTG		
	CACTAG GT GI		
GAM121 LAMB3	GTGATCCCCAGAAAGGACC	1701	TGTTATA TG GTG
	CC GAAAGGACC		
	GG CTTTCCTGG		
	ACTAG__ GT AII		
GAM122 APPL	TGTTATAGAACTTCTTTTGAAA	1711	__ A AGACT
	TGTTATAGA TT TTTGGAA		
	ACAATATCT AG AAACCTT		
	TGA A IIITC		
GAM122 CD53	ATAGTTTTTTTCTGGAAAGACT	1704	TGTTATAGATTA
	TTTGGAAAGACT		
	AGACCTTTCTGA		
	AAAAA_____		
GAM122 DIAPH2	TGTGATAGTACCTTATTTGGAAA	1710	T A__ GACTI
	TGT ATAG TTATTTGGAAA		
	ACA TATC AATAAACCTTT		
	C ATGG IIITC		
GAM122 FVT1	TGTTCAA-ATTATTTGGAAA	1714	A GAC
	TGTT TAGATTATTTGGAAA		
	ACAA GTTTAATAAACCTTT		
	__		
GAM122 HRMT1L1	ATAATTTATTTGG-AAGAC	1706	TGTTATAGA A
	TTATTTGGAA GA		
	AATAAACCTT CT		
	A_____		
GAM122 JAK2	TTATAGATTAACATGGAAG	1717	TGTT TT__ C
	ATAGATTA TGGAAAGA		
	TATCTAAT ACCTTTTT		
	__ TGAT I		
GAM122 NDUFAB1	TTATAGATTTATTTTCAAAGA	1716	TGTT _ GG CT
	ATAGATT ATTT AAAGA		

	TATCTAA TAAA TTTCT		
	_____ A AG CA		
GAM122 NRCAM	TGTTATAGATTTTCATATTTGGA 1712	_____	AAGACTI
	TGTTATAGAT TATTTGGA		
	ACAATATCTA ATAAACCT		
	AAAGT IIITCAG		
GAM122 POLK	TTATAGATT-TGTGGAAAG 1720 TGTT ATT A		
	ATAGATT TGGAAG		
	TATCTAA ACCTTTC		
	_____ AC_ A		
GAM122 RCN2	ATGGAGTATTTAGGAAAGACT 1705 TGTTATAGAT _		
	TATTT GGAAAGACT		
	ATAAA CCTTTCTGA		
	TC_____ T		
GAM122 RFXAP	TTAAATGTTATTTGGAAAGA 1721 TGTTATAGA C		
	TTATTTGGAAAGA		
	AATAAACCTTTCT		
	TTTAC_____ A		
GAM122 ROS1	TGCTATATGAATTATTTGG 1709 _ AAAGAC		
	TGTTATA GATTATTTGG		
	ACGATAT TTAATAAACC		
	AC IIITCA		
GAM122 SCN3A	TTATTAGATTACTTTTTGGAAAG 1715 TGTTA _ ACTI		
	TAGATTAT TTGGAAAG		
	ATCTAATG AACCTTTC		
	TA_____ AAA GTII		
GAM122 SLC1A2	GTTATAAAGCATTATTTGGCAAAGAC 1707 _ TAT _ _ TII		
	TGT AG ATTATTTGG AAAGAC		
	ATA TC TAATAAACC TTTCTG		
	A TT_ G G TII		
GAM122 SULT1C1	TTATATCTTACTTTGGAAAGA 1719 TGTT GA _ CT		
	ATA TTATTT GGAAAGA		
	TAT AATGAA CCTTTCT		
	_____ AG A TA		
GAM122 TEX15	TAAAAAATATTTGGAAAACT 1708 TGTTAT T		
	AGA TATTTGGAAAGACT		
	TTT ATAAACCTTTTGA		
	_____ T		
GAM122 ZNF192	TTAAAGGTTAATTTTGGAAAG 1718 TGTTATAGATTA A		
	TTTGGAAAG CT		

		AAACCTTTC GG		
		TTTCCAATTA__		
GAM122 ZNF192		TGTTCCAAAT-ATTTGGAA	1713	ATA T AGA
		TGTT GA TATTTGGAA		
		ACAA TT ATAAACCTT		
		GG_ T		
GAM123 ASS		AGGCCCCAGCTCC-TCATTG	1727	TTAG AA G
		GCCCCAGCTCC CATTG		
		CGGGGTCGAGG GTAAC		
		_____ A_ A		
GAM123 C10orf2		TTAGGCCCCAGCTC--ACAT	1732	_ ACATTG
		TTAGGCCCCAGCTC CA		
		AATCCGGGGTCGAG GT		
		T AIIIGG		
GAM123 C5		TTCGGCCCCAG--CAAACATT	1733	TTA TCC GG
		GGCCCCAGC AACATT		
		CCGGGGTCG TTGTAA		
		AAG T__		
GAM123 DAG1		AGCCCTCACCTGGAACATTGGG	1729	TTAGG _ G CC
		CCC CA CT AACATTGGG		
		GGG GT GA TTGTAACCC		
		_____ A G CC		
GAM123 ED1		AGGCCTGCTGCTCCAACATTG	1724	TTAG CCA_ GG
		GCC GCTCCAACATTG		
		CGG CGAGGTTGTAAC		
		_____ ACGA AC		
GAM123 EFNB1		AGGCCCCAGC-CCAAGACTGGG	1730	TTAG T C
		GCCCCAGC CCAA ATTGGG		
		CGGGGTCG GGTT TGACCC		
		_____ _ C		
GAM123 FUS1		TAGGCCCCAG-GCAAAC-TTGG	1731	TT CTC CA
		AGGCCCCAG CAA TTGG		
		TCCGGGGTC GTT AACC		
		_ C_ TG		
GAM123 KCNK5		AGGCCCCAG-GCCACATAGG	1728	TTAG CT A T
		GCCCCAG CCA CAT GG		
		CGGGGTC GGT GTA CC		
		_____ CG _ T		
GAM123 MLC1		AGGCAC-AGACTAGCCAACATTGG	1725	TTAG CC _ _ GI
		GC CAG CT CCAACATTGG		

	CG GTC GA GGTGTGAACC	
	____ T_ T TC GG	
GAM123 MVK	AGGCCCCAGCACCTGAGCATTGG 1726 TTAG T AA__ I	
	GCCCCAGC CC CATTGGG	
	CGGGGTCG GG GTAACCT	
	____ T ACTC G	
GAM124 BTG1	AGATCTCAA--T-AGCTGCA 1738 TTAG ACTC	
	ATCTCAA AGCTGCA	
	TAGAGTT TCGACGT	
	____ A____	
GAM124 DAB1	AGAAATGACACTCTGAGCTGCACA 1736 TTA_ CTCAA __ I	
	GAT ACTC AGCTGCACA	
	CTG TGAG TCGACGTGT	
	TTTA ____ AC A	
GAM124 HYAL1	AGAT-TCCACCCCAGCTGCAC 1739 TTAGATC AAA	
	TC CTCAGCTGCAC	
	AG GGGTCGACGTG	
	TA____ GTG	
GAM124 RPH3AL	CTCAAAGCTGTCAGCTGCA 1740 TTAGATCTCAAAC C	
	TCAGCTGCA	
	AGTCGACGT	
	CGAC____ C	
GAM124 TAF11	AGCTCGGAAACCCGAGCTGCACA 1737 TTAGAT __ _ I	
	CTC AAACCTC AGCTGCACA	
	GAG TTTGGG TCGACGTGT	
	____ CC C C	
GAM125 AR	GGCTGGCAGCGCTGGGCCGA 1769 CAACAGGAT CA	
	GC CGCTGGGCCG	
	CG GCGACCCGGC	
	____ TC	
GAM125 BCL9	ACTGCAGTGCTCATCCTGGAGG 1748 _ A II	
	ACT CGGTGT CGTCCTGGAGG	
	TGA GTCACG GTAGGACCTCC	
	C A II	
GAM125 BCL9	ACTGCAGTGCTCATCCTGGAGG 1748 CT A I	
	CGGTGT CGTCCTGGAG	
	GTCACG GTAGGACCTC	
	AC A I	
GAM125 CARD10	CACCAGGGT-CCACGCTGG 1757 CAA ATG GCC	
	CAGG CCACGCTGG	

	GTCC GGTGCGACC		
	GTG CA_ III		
GAM125 CEBPD	AGGCTGTCACCTCGCTGGGCC	1751 CAACAGGAT A	GA
	GCC CGCTGGGCC		
	III		
	TGG GCGACCCGG		
	ACAG_____ A GT		
GAM125 CSH2	ACAGGATGCCACGC-GGGC	1746 CAAC	T
	AGGATGCCACGC GGGCC		
	TCCTACGGTGCG CCCGG		
	_____ -		
GAM125 CSH2	ACAGGATGCCACGC-GGGC	1746 CAAC	T C
	AGGATGCCACGC GGGC		
	TCCTACGGTGCG CCCG		
	_____ - T		
GAM125 CSHL1	ACAGGATGCCACGC-GGGC	1747 CAAC	T
	AGGATGCCACGC GGGCC		
	TCCTACGGTGCG CCCGG		
	_____ -		
GAM125 CSHL1	ACAGGATGCCACGC-GGGC	1747 CAAC	T G
	AGGATGCCACGC GGGCC		
	TCCTACGGTGCG CCCGG		
	_____ - G		
GAM125 ESR1	CAACCAGG--GCCACGCTGGG	1753 CAA_ AT	CCG
	CAGG GCCACGCTGGG		
	GTCC CGGTGCGACCC		
	GTTG _ III		
GAM125 FNTB	CAGGACCCAGCACGCTGGGC	1762 CAA_ GATGC	CG
	CAG CACGCTGGGC		
	GTC GTGCGACCCG		
	CTGG _____ CC		
GAM125 GH1	ACAGGGATGCCAC-CCGGGC	1744 CAACA	G CG
	GGATGCCAC CTGGGC		
	CCTACGGTG GGCCCG		
	TC_____ TC		
GAM125 GH1	ACAGGGATGCCAC-CCGGGC	1744 CAACA	G CG
	GGATGCCAC CTGGGC		
	CCTACGGTG GGCCCG		
	TC_____ TC		
GAM125 GH2	ACAGGGATGCCAC-CCGGGC	1744 CAACA	G CG
	GGATGCCAC CTGGGC		

	CCTACGGTG GGCCCG	
	TC___ _ TC	
GAM125 HIP12	ACAGGATGCCTGACCCTCGTCC 1745 CAAC ___ G _GG A	
	AGGATGCC AC CT G CCG	
	TCCTACGG TG GA C GGT	
	___ AC G G AG I	
GAM125 HIVEP3	CAAGAG-ATGCCACGCTGG 1756 CAACA GCC	
	GGATGCCACGCTGG	
	TCTACGGTGCGACC	
	GTTC_	
GAM125 HUNK	CAACAGGATG-AACACAGGGCC 1758 CC T GA	
	CAACAGGATG ACGC GGGCC	
	GTTGTCCTAC TGTG CCCGG	
	T_ T	
GAM125 IRS2	GGACGCGCTCGCTGGGCCG 1768 CAACAGGAT CA	
	GC CGCTGGGCCG	
	CG GCGACCCGGC	
	G_____ A_	
GAM125 JPH2	CAGGATGCCA-GCAGAGGCTGA 1764 CAACAG C T_ C	
	GATGCCA GC GGGC GA	
	CTACGGT CG TCCG CT	
	_____ _ TC A	
GAM125 MTMR1	CAGGGTCTCCACGCTGGGC 1761 CAACA ATG CG	
	GG CCACGCTGGGC	
	CC GGTGCGACCCG	
	_____ AGA AC	
GAM125 NUCB1	CTGGGCCTAGGTCCTGGAG 1766 ACTC G C G	
	GGT TA GTCCTGGAG	
	CCG AT CAGGACCTC	
	AC_ G C A	
GAM125 NUCB1	CTGGGCCTAGGTCCTGGAG 1766 CTC G C	
	GGT TA GTCCTGGA	
	CCG AT CAGGACCT	
	GAC G C CI	
GAM125 OTX1	CAACAGGATCGGGACCACGGAGGGC 1754 _____ CT CGAII	
	CAACAGGAT GCCACG GGGC	
	GTTGTCCTA TGGTGC CCCG	
	GCCC CT IIIAG	
GAM125 PACE4	CAGGGTTCGCCA-GCTGGGCCG 1759 CAACAGGA C A	
	TGCCA GCTGGGCCG	

	GCGGT CGACCCGGC		
	CCAA_____C		
GAM125 PROS1	CAATCAGGA-GCCACGCTG	1752 CAA_ T	GGCC
	CAGGA GCCACGCTG		
	GTCCT CGGTGCGAC		
	GTTA _ IIIA		
GAM125 RNH	CAGGATGCCAGGATCCTGGACC	1763 CAACAG CG_____GA	
	GATGCCA CTGGGCC		
	CTACGGT GACCTGG		
	_____CCTAG GC		
GAM125 SORL1	CAGGAGAGCCG-GCTGGGCCG	1760 CAACA T AC	
	GGA GCC GCTGGGCCG		
	TCT CGG CGACCCGGC		
	C_____C_		
GAM125 SPK	AACTGTGATGCCACGCT---CCGA	1743 CAACAG GGG	
	GATGCCACGCT CCGA		
	CTACGGTGCGA GGCT		
	TGACA_ _____		
GAM125 STXBP1	CAGGTGGGCGCGCTGGGCC	1765 CAACA AT CA	
	GG GC CGCTGGGCCG		
	CC CG GCGACCCGGT		
	CA_____C_		
GAM125 SURF6	ACTCAGAGGGTGTCTGGAG	1749 TGTAC GI	
	ACTCGG GTCCTGGAG		
	TGAGTC CAGGACCTC		
	TCCCA II		
GAM125 SURF6	ACTCAGAGGGTGTCTGGAG	1749 TGTAC I	
	CTCGG GTCCTGGA		
	GAGTC CAGGACCT		
	TCCCA I		
GAM125 UBASH3A	ACTCGGTGTACATGCTGCAGG	1750 C G I	
	ACTCGGTGTACGT CTG AGG		
	TGAGCCACATGTA GAC TCC		
	C G I		
GAM125 UBASH3A	ACTCGGTGTACATGCTGCAGG	1750 C G I	
	CTCGGTGTACGT CTG AG		
	GAGCCACATGTA GAC TC		
	C G I		
GAM125 WIF1	CTCCCTCTA-GTCCTGGAGG	1767 A_ GGTGTAC	
	CTC GTCCTGGAGG		

		GAG CAGGACCTCC	
		AGG AT_____	
GAM125 WIF1	CTCCCTCTA-GTCCTGGAGG	1767 TCGGTGTAC	I
	GTCCTGGAG		
	CAGGACCTC		
	GAGGGAGAT	I	
GAM125 ZNF14	CACCATGTTGACCACGCTGGTCTCGA	1755 CAA GGA _	GC_ II
	CA TG CCACGCTGG CGA		
	GT AC GGTGCGACC GCT		
	GTG ACA T AGA II		
GAM126 ABL1	GGCCCAGTCTGGGGCTATTTG	1773 A _ _	III
	GGC CA TC GGGCTATTT		
	CCG GT AG CCCGATAAA		
	G C AC CII		
GAM126 ABL1	GGCCCAGTCTGGGGCTATTTG	1773 TG A _ _	AACAC
	GC CA TC GGGCTATTTG		
	CG GT AG CCCGATAAAC		
	_ G C AC CIIIC		
GAM126 BCL11A	GGCAGAGTCAAGTGCTATTTGAACAC	1774 GCA_ TCGG	I
	CA GCTATTTGAACA		
	GT CGATAAACTTGT		
	CTCA TCA_ I		
GAM126 BCL11A	GGCAGAGTCAAGTGCTATTTGAACAC	1774 TG CA_ _	II
	GCA TCG G GCTATTTGAACAC		
	CGT AGT C CGATAAACTTGTG		
	_ CTC T A GI		
GAM126 LARS2	CACATATTGGTTATTTGAACA	1772 A CG_ C	I
	CAT GG TATTTGAAC		
	GTA CC ATAAACTTG		
	_ TAA A I		
GAM126 LARS2	CACATATTGGTTATTTGAACA	1772 TGGCACATC GC	C
	GG TATTTGAACA		
	CC ATAAACTTGT		
	TATAA_ A_ A		
GAM126 LPL	TGGCACATCAGGAACAATTT	1777	CTATTIII
	TGGCACATCGGG		
	ACCGTGTAGTCC		
	TTGTTAAA		
GAM126 LPL	TGGCACATCAGGAACAATTT	1777	CTATTTG
	TGGCACATCGGG	AACA	

ACCGTGTAGTCC TTGT

GAM126 RNF26 GGCCCTTCTG--TATTTGAAC 1776 TG ACA GGGC A
GC TC TATTTGAAC
|| || |||||
CG AG ATAACTTG
__ GGA AC__ G

GAM126 SLC20A1 TGGAACC-CGGGCTATTTTACACA 1778 C A GA I
TGG AC TCGGGCTATTT ACAC
||| || ||||| |||
ACC TG GGCCCGATAAA TGTG
T _ A_ T

GAM126 SLC20A1 TGGAACC-CGGGCTATTTTACACA 1778 C A GAACI
GG AC TCGGGCTATTT
|| || |||||
CC TG GGCCCGATAAA
T _ ATGTG

GAM126 SLC4A7 TGCCAAATTTTGCAATTTGAACAC 1779 G A TCGG__ T I
GC CA GC ATTTGAACA
|| || || |||||
CG GT CG TAACTTGT
__ _ TTAAAA T I

GAM126 SLC4A7 TGCCAAATTTTGCAATTTGAACAC 1779 TG A TCGG__ T I
GC CA GC ATTTGAACAC
|| || || |||||
CG GT CG TAACTTGTG
A_ _ TTAAAA T I

GAM126 TRPM1 GGCACCTCCTAGGCTATTTG 1775 A __ III
GGCAC TC GGGCTATTT
|||| || |||||
CCGTG AG TCCGATAAA
A GA CII

GAM126 TRPM1 GGCACCTCCTAGGCTATTTG 1775 TG A __ AACA
GCAC TC GGGCTATTTG
|||| || |||||
CGTG AG TCCGATAAAC
__ A GA CIII

GAM127 GNAL GAGATGGTCTGGTCTCTTCG 1782 CA____ IIIC
GAGATGGTC CTC
||||| |||
CTCTACCAG GAAG
ACCAGA CIII

GAM127 GNAL GAGATGGTCTGGTCTCTTCG 1782 TG CA____ ACCTGC
AGATGGTC CTCG
||||| |||
TCTACCAG GAAGC
__ ACCAGA CIIIC

GAM127 MYCL2 TGAGGTAATGGTCCACGTTGA 1784 __ TTCGACCTGCC
TGAG ATGGTCCAC
||| |||||

	ACTC TACCAGGTG		
	CAT CAACTIIICCG		
GAM127 MYCL2	TGAGGTAATGGTCCACGTTGA 1784	___	TTCGIII
	TGAG ATGGTCCAC		
	ACTC TACCAGGTG		
	CAT CAACTII		
GAM127 OAS3	GAAGGTACCCAACTGCGACCTGCC 1783	TGAGAT _ _ T	I
	GGT CC ACT CGACCTGCC		
	CCA GG TGA GCTGGACGG		
	_____ T GT C T		
GAM127 OAS3	GAAGGTACCCAACTGCGACCTGCC 1783	ATGG _ T	I
	TCCA CT CGACCTGC		
	GGGT GA GCTGGACG		
	CAT_ T C I		
GAM127 SLC6A6	TGGTCCAC-TC-ACCTCCC 1785	CG GCI	
	TGGTCCACTT ACCT		
	ACCAGGTGAG TGGA		
	_ GGG		
GAM127 SLC6A6	TGGTCCAC-TC-ACCTCCC 1785	TGAGATGGTC GA TG	
	CACTTC CC		
	GTGGAG GG		
	GTGA_____ _ GT		
GAM128 ARHC	GCTCACTCGGCGTA-G-CCTG 1798	C T GA	
	GCTCACTCGGTGTA G CCTG		
	CGAGTGAGCCGCAT C GGAC		
	_ _		
GAM128 CHRNA2	GCTCACTC---GTCCATCCT 1796	GTGTA GG	
	GCTCACTCG CGTCCT		
	CGAGTGAGC GTAGGA		
	AG_____		
GAM128 DBCCR1	GCTCCATTCTGTGGA-GTCCTGGAG 1793	AC_ G TAC	I
	GCTC TC GTG GTCCTGGAG		
	CGAG AG CAC CAGGACCTC		
	GTA A CT_ I		
GAM128 EPHB4	CTCACTCGG-GTAGGATCC 1791	GC T C_ TGG	
	TCACTCGG GTA GTCC		
	AGTGAGCC CAT TAGG		
	_ _ CC CII		
GAM128 FUT8	CTCACTTCCTGGA-GTCCTGGAG 1790	GC _ GG TAC	I
	TCACT C TG GTCCTGGAG		

	AGTGA G AC CAGGACCTC	
	___ A GG CT_ G	
GAM128 GPD1	GCTCCCTGGG---A-GTCCTGGAG 1800	A TC TGTAC
	GCTC C GG GTCCTGGA	
	CGAG G CC CAGGACCT	
	_ GA CT__	
GAM128 HS3ST4	GCTCCCTAGG---A-GTCCTGGAG 1799	A C TGTAC
	GCTC CT GG GTCCTGGA	
	CGAG GA CC CAGGACCT	
	G T T__	
GAM128 IBSP	GCTTCCTCTG-GCA-GTCCTGGAG 1801	CA GGT C
	GCT CTC GTA GTCCTGGAG	
	CGA GAG CGT CAGGACCTC	
	AG AC_ _	
GAM128 LMCD1	GCTCACTCGGAATTGCATTCTGGA 1795	TGTA_ C GI
	GCTCACTCGG CGT CTGGA	
	CGAGTGAGCC GTA GACCT	
	TTAAC A	
GAM128 LY64	TCATTCGGTGTACTTGCCTAGA 1802	GCTCAC GT_
	TCGGTGTAC CCTGGAG	
	AGCCACATG GGATCTT	
	TA__ AAC	
GAM128 MSI1	GCTCACTC-GTG---GTCCT 1797	G TAC G
	GCTCACTCG TG GTCCT	
	CGAGTGAGC AC CAGGA	
	_ _ _ I	
GAM128 PAX5	CACTTGCTGGG-GTCCTGGAG 1789	GCTCACTCG GTAC
	GT GTCCTGGA	
	CG CAGGACCT	
	AA__ ACCC	
GAM128 SNTB1	CTCACTCGGT---CCTCCTG 1792	GC GTACG
	TCACTCGGT TCCTGG	
	AGTGAGCCA AGGACT	
	_ GG__	
GAM128 SURF6	ACTCAGAGGGTGTCTCTGGAG 1749	GCTCACTC T AC
	GG GT GTCCTGGA	
	CC CA CAGGACCT	
	TCT__ _ _	
GAM128 TYK2	GCTCAGCTGAGGGTGAGTCCTGGAG 1794	_ C__ TAC
	GCTCA CT GGTG GTCCTGGAG	

	CGAGT GA CCAC CAGGACCTC		
	C CTC T__ II		
GAM128 UBASH3A	CACTCGGTGTACATGCTGCAG 1788 GCTCAC	C G	
	TCGGTGTACGT CTG AG		
	II		
	AGCCACATGTA GAC TC		
	_____ C G		
GAM129 ASH1	AGGTATCTAGGAAGAAGCC 1806 TGAG	___ CGGA	
	GTATCTA AAGAGGCC		
	CATAGAT TTCTTCGG		
	_____ CC AGII		
GAM129 DRD5	AGCTATGGTAAAGAGGCC 1805 TGA_ TCTA	GGA	
	GGTA AAGAGGCC		
	CCAT TTCTCCGGG		
	GATA _____ GGI		
GAM129 MNT	TGAGGTATCTGTGCAGGCCCGG 1811	AAAG AA	
	TGAGGTATCT AGGCCCGG		
	ACTCCATAGA TCCGGGCC		
	CACG II		
GAM129 RANBP3	TGAAGTCCC-AAAGAGGCC 1809	A GGA	
	TGAGGT TCTAAAGAGGCC		
	ACTTCA GGGTTTCTCCGGG		

GAM129 RGS6	GAAGTATCTAAA-AGCGCC 1808 TG	AG CGG	
	AGGTATCTAAAG GCC		
	TTCATAGATTTT CGG		
	_____ CG TII		
GAM129 SEC22L1	AGGGATCCAACACTGGCCCGGAA 1807 TGA T	AGA_ I	
	GG ATCTAA GGCCCGGAA		
	CC TAGGTT CCGGGCCTT		
	_____ GTGA C		
GAM129 WHSC1	TGAGTTAGCCAA-GAGGCC 1810	G T A GGA	
	TGAG TA CTAA GAGGCC		
	ACTC AT GGTT CTCCGGG		
	A C _		
GAM130 CNGB3	ATGTTCTGGGTGTTAGCAA 1815	GA _ II	
	ATG CTGG TGTTAGCA		
	TAC GACC ACAATCGT		
	AA C TI		
GAM130 DVL3	CATGGA CTGG-GTTGGGAA 1818	T AGCAI	
	CATGGA CTGG GTT		

	GTACCTGACC CAA			
	_ CCCTT			
GAM130 EIF2C1	GGCAGATGGA---GTGTTAGCA	1822	_ C	CTG
	GCA ATGGA GTGTTAGC			
	CGT TACCT CACAATCG			
	C C _			
GAM130 EIF2C1	GGCAGATGGA---GTGTTAGCA	1822	TG C	CTG
	GCA ATGGA GTGTTAGCA			
	CGT TACCT CACAATCGT			
	_ C _			
GAM130 EIF4EBP2	GGAATATGAA-TGGTGTTAG	1821	GCAC_ C	I
	ATGGA TGGTGTTA			
	TACTT ACCACAAT			
	CCTTA _ I			
GAM130 EIF4EBP2	GGAATATGAA-TGGTGTTAG	1821	TGGCAC C	CA
	ATGGA TGGTGTTAG			
	TACTT ACCACAATC			
	CTTA_ _ CI			
GAM130 KCNK10	CACATGGACCCTTGCTAACAA	1816	GG	I
	ACATGGACT TGTTAGCA			
	TGTACCTGG ACGATTGT			
	GA I			
GAM130 KCNK10	CACATGGACCCTTGCTAACAA	1816	TGGCAC	GG
	ATGGACT TGTTAGCAA			
	TACCTGG ACGATTGTT			
	GA			
GAM130 MAPK4	TGGCACATGAGGAGTGGTGT	1824	_ C	TAGCA
	TGGCACAT GGA TGGTGT			
	ACCGTGTA CCT ACCACA			
	CT C IIIAA			
GAM130 MAPK4	TGGCACATGAGGAGTGGTGT	1824	_ C	III
	TGGCACAT GGA TGGTG			
	ACCGTGTA CCT ACCAC			
	CT C AII			
GAM130 MEN1	GCACATGGA--GAGGTTAGC	1819	CT	GTTAI
	GCACATGGA GGT			
	CGTGTACCT CCA			
	CT ATCGI			
GAM130 MEN1	GCACATGGA--GAGGTTAGC	1819	TGGC	CT T
	ACATGGA GG GTTAGC			

		TGTACCT TC CAATCG		
		_____ C _ _		
GAM130 NT5E	GGCACATG	---GGTGTT-GCAA 1823	ACTG	A
	GGCACATGG	GTGTT GC		
	CCGTGTACC	CACAA CG		
		_____ _		
GAM130 NT5E	GGCACATG	---GGTGTT-GCAA 1823 TG	ACTG	A
	GCACATGG	GTGTT GC		
	CGTGTACC	CACAA CG		
		_____ _		
GAM130 RAD54L	CAGGAACTGGT	TTTGAA 1817 T	AGCA	I
	CA G	GA		
	GT CTTGACCACAA			
	C	ACCTT		
		_____ _		
GAM130 SFRP4	ACATGCTTACTG-TGTTAGCAA	1814 CATGG_ G		I
	ACTG TGTTAGCA			
	TGAC ACAATCGT			
	TACGAA _	I		
		_____ _		
GAM130 SFRP4	ACATGCTTACTG-TGTTAGCAA	1814 TGGCACATGG G		
	ACTG TGTTAGCAA			
	TGAC ACAATCGTT			
	CGAA_____ _			
		_____ _		
GAM130 SUFU	GGCAGCAGAGAGCAGTGT	TTAGCAA 1820 __ CAT CT		I
	GCA GGA GGTGT	TTAGCA		
	CGT TCT TCACAATCGT			
	GT C_ CG	I		
		_____ _		
GAM130 SUFU	GGCAGCAGAGAGCAGTGT	TTAGCAA 1820 TG _ T CT		I
	GCA CA GGA GGTGT	TTAGCAA		
	CGT GT TCT TCACAATCGTT			
	_ C C CG	T		
		_____ _		
GAM131 CDH13	GTACAGACTAAGTGAAATTG	1829 TC__		
	GTACAG AGTGAAATT			
	CATGTC TCACTTTAA			
	TGAT	CII		
		_____ _		
GAM131 CDH13	GTACAGACTAAGTGAAATTG	1829 TGTGTA TC__		AA
	CAG AGTGAAATTG			
	GTC TCACTTTAAC			
	_____ TGAT	AT		
		_____ _		
GAM131 CORO1C	TGTACAGTCA-TCAAAATGA	1834 _	GT	TGI
	GTACAGTCA GAAAT			

		CATGTCAGT TTTTA		
		A AG CII		
GAM131 CORO1C		TGTACAGTCA-TCAAAATGA 1834 TGTG GT T A		
		TACAGTCA GAAAT GA		
		ATGTCAGT TTTTA CT		
		AG _ G		
GAM131 CRIM1		GTATACAGTCAGTTATATT 1832 GAAATII		
		GTGTACAGTCAGT		
		CATATGTCAGTCA		
		ATATAAI		
GAM131 CRIM1		GTATACAGTCAGTTATATT 1832 TG GAAATTGAA		
		TGTACAGTCAGT		
		ATATGTCAGTCA		
		ATATAAAII		
GAM131 EPB41L2		GTGCACAGTCAGTGAAGTT 1833 ATII		
		GTGTACAGTCAGTGAA		
		CACGTGTCAGTCACTT		
		GAAI		
GAM131 EPB41L2		GTGCACAGTCAGTGAAGTT 1833 TG ATTGAA		
		TGTACAGTCAGTGAA		
		ACGTGTCAGTCACTT		
		GAAGII		
GAM131 ESR1		AGACAGTGCAAAATTGAAG 1828 T III		
		AG CAGTG AAATTGAA		
		TC GTCAC TTAACTT		
		T GT CII		
GAM131 F2R		TGTGTACAGTGTGTAAAAT 1841 CA TGAA		
		TGTGTACAGT GTGAAAT		
		ACACATGTCA CATTTTA		
		CA IIIG		
GAM131 F2R		TGTGTACAGTGTGTAAAAT 1841 CA II		
		TGTGTACAGT GTGAAA		
		ACACATGTCA CATTTT		
		CA AI		
GAM131 KCNJ10		TGTGTT-AGTCACTCCAAATTGAAG 1839 AC GTG_ I		
		TGTGT AGTCA AAATTGAAG		
		ACACA TCAGT TTAACTTC		
		A_ GAGG I		
GAM131 KCNJ10		TGTGTT-AGTCACTCCAAATTGAAG 1839 AC GTG_ I		
		GTGT AGTCA AAATTGAA		

	CACA TCAGT TTAACTT			
	A_ GAGG I			
GAM131 KIAA0442	TGTGTACAGGTA-TGAAAT 1840	TCA	TGA	
	TGTGTACAG GTGAAAT			
	ACACATGTC TACTTTA			
	CA_ III			
GAM131 KIAA0442	TGTGTACAGGTA-TGAAAT 1840	TCA	I	
	TGTGTACAG GTGAAA			
	ACACATGTC TACTTT			
	CA_ A			
GAM131 LNK	TGTG-ACAGTGTGAGTGA 1836	T _	TTGAA	
	TGTG ACA GTCAGTGA 1836			
	ACAC TGT CAGTCACTTT			
	_ CA IIIGA			
GAM131 LNK	TGTG-ACAGTGTGAGTGA 1836	T _	II	
	TGTG ACA GTCAGTGAA			
	ACAC TGT CAGTCACTT			
	_ CA TI			
GAM131 MECP2	GTACAGACAAAATTGAAATTGA 1830	T _	III	
	GTACAG CAG TGAAATTG			
	CATGTC GTT ACTTTAAC			
	T TTA TII			
GAM131 MECP2	GTACAGACAAAATTGAAATTGA 1830	TGTGTA T _	AG	
	CAG CAG TGAAATTGA			
	GTC GTT ACTTTAACT			
	_ _ T TTA CC			
GAM131 OTC	GTGCATCAG-CACTTAAATTGAAG 1831	A T GTG	I	
	TGTGT CAG CA AAATTGAAG			
	ACGTA GTC GT TTAACTTC			
	_ _ GAA C			
GAM131 OTC	GTGCATCAG-CACTTAAATTGAAG 1831	_ T GTG	I	
	TGTA CAG CA AAATTGAA			
	ACGT GTC GT TTAACTT			
	A _ GAA I			
GAM131 PPP2R4	TGTGGCTACAGTCAG-GAAA 1835	_	T TTGAA	
	TGTG TACAGTCAG GAAA			
	ACAC ATGTCAGTC CTTT			
	CG _ IIIGA			
GAM131 PPP2R4	TGTGGCTACAGTCAG-GAAA 1835	_	T II	
	TGTG TACAGTCAG GAA			

	ACAC ATGTCAGTC CTT		
	CG _ TI		
GAM131 SNCA	TGTATTCACTTCAGTGAAAGGGAAG 1837	A G_	TT II
	TGTGT CA TCAGTGAAA GAAG		
	II		
	ACATA GT AGTCACTTT CTTC		
	A GA CC II		
GAM131 SNCA	TGTATTCACTTCAGTGAAAGGGAAG 1837	GTG_ AG	TT I
	TAC TCAGTGAAA GAA		
	GTG AGTCACTTT CTT		
	ATAA A_ CC I		
GAM131 SP100	TGTGTACAGGCAGCTTAAAT 1838	T GAAAI	
	TGTGTACAG CAGT		
	ACACATGTC GTCG		
	C AATTTA		
GAM131 SP100	TGTGTACAGGCAGCTTAAAT 1838	T GAAATTGAA	
	TGTGTACAG CAGT		
	ACACATGTC GTCG		
	C AATTTA		
GAM131 WHSC1L1	ACAGTCCATGTTGAAATTGA 1827	AG__	
	ACAGTC TGAAATTG		
	TGTCAG ACTTTAAC		
	GTACA TII		
GAM131 WHSC1L1	ACAGTCCATGTTGAAATTGA 1827	TGTGTA GTCAG	A
	CA TGAAATTGA		
	GT ACTTTAACT		
	G__ ACA_ A		
GAM132 EFG1	TAGCATTCATTAGGTTGAT 1849	ATGAI	
	TAGCATTCATTG		
	ATCGTAAGTAAT		
	CCAACTA		
GAM132 EFG1	TAGCATTCATTAGGTTGAT 1849	TT A__ TCTTG	
	AGCATTCATTG TGAT		
	TCGTAAGTAAT ACTA		
	_ CCA CIIT		
GAM132 GSTM3	ATTCATATCTTGATGATTCT 1847	_	IIIA
	ATTCAT TGATGATTCT		
	TAAGTA ACTACTAAG		
	TAGA A		
GAM132 GSTM3	ATTCATATCTTGATGATTCT 1847	TTAGCAT A	G
	TC TTGATGATTCTT		

		AG AACTACTAAGAG		
		AT_____ G		
GAM132 ISL1	AGCATTTCATTCTTGATTC	1844	GA_	II
	AGCATTTCATT TGATT			
	TCGTAAGTAA ACTAA			
	AGA GI			
GAM132 ISL1	AGCATTTCATTCTTGATTC	1844	TTAG	GA_ TTG
	CATTTCATT TGATTC			
	GTAAGTAA ACTAAG			
	_____ AGA TCI			
GAM132 MAPK1	ATTCATAAA-GATTCTTGT	1848	TGAT	I
	ATTCAT GATTCTTG			
	TAAGTA CTAAGAAC			
	TTT_ A			
GAM132 MS4A1	TTTGCATTCATTCACTATTGCTGT	1855	TA	G G _ TI
	GCATTCATT AT ATT CT			
	CGTAAGTAA TG TAA GA			
	A_ G A C CI			
GAM132 MS4A1	TTTGCATTCATTCACTATTGCTGT	1855	TTA	G G C I
	GCATTCATT AT ATT TTGT			
	CGTAAGTAA TG TAA GACA			
	AAA G A C I			
GAM132 MYCBP	TTTATTGATGATTCTATGT	1856	TTC	TGII
	ATTGATGATTCT			
	TAACTACTAAGA			
	AAA TACA			
GAM132 NR2E1	TTAGCATTCATTCAT-CTCCTTG	1854		G GA T
	TTAGCATTCATT AT TTCTTG			
	AATCGTAAGTAA TA AGGAAC			
	G G_ I			
GAM132 NR2E1	TTAGCATTCATTCAT-CTCCTTG	1854	_	G GA I
	TAGCATTCATT AT TTCTT			
	ATCGTAAGTAA TA AGGAA			
	A G G_ I			
GAM132 PCDHB4	TTAGCATTCATGGAACATT	1853		T TGATII
	TTAGCATTCAT GA			
	AATCGTAAGTA CT			
	C TGTAAl			
GAM132 PCDHB4	TTAGCATTCATGGAACATT	1853		T TGATTCTTG
	TTAGCATTCAT GA			

	AATCGTAAGTA CT		
	C TGTAIIIT		
GAM132 PROS1	AGCATTTCATCTAT-A-TCTT 1846	GATG CI	
	AGCATTTCATT ATT		
	III		
	TCGTAAGTAG TAG		
	ATA_ AA		
GAM132 PROS1	AGCATTTCATCTAT-A-TCTT 1846 TTAG	GATGAT	
	CATTTCATT TCTT		
	III		
	GTAAGTAG AGAA		
	____ ATAT__		
GAM132 SOX11	AGAATTCATTAAGATGATTCT 1845 C	___ III	
	AG ATTTCATT GATGATTC		
	TC TAAGTAA CTAATAAG		
	T TT AII		
GAM132 SOX11	AGAATTCATTAAGATGATTCT 1845 TTAGC	___ T	
	ATTCATT GATGATTCTTG		
	TAAGTAA CTAATAAGAGT		
	T____ TT I		
GAM132 STATH	TTTGCATTGCTCTTTGATGATTCTT 1852 TA__ AT A	I	
	GC TC TTGATGATTCT		
	CG AG AACTACTAAGA		
	GTAA __ A I		
GAM132 STATH	TTTGCATTGCTCTTTGATGATTCTT 1852 TTA	___ A GTII	
	GCAT TC TTGATGATTCTT		
	CGTA AG AACTACTAAGAA		
	AAA ACG A IIIT		
GAM132 TZFP	TAGCATTTCAGTGGTATGGTTGTT 1850 TT	T ATG TC I	
	AGCATTCA TG AT TTGT		
	TCGTAAGT AC TA AACA		
	___ C CA_ CC A		
GAM132 VPS41	TTAGCAAATCCTATTGATGA-TCTT 1851	___ _ CTTGTI	
	TTAGCA TTC ATTGATGATT		
	AATCGT AGG TAACTACTAG		
	TT A AIIIT		
GAM132 VPS41	TTAGCAAATCCTATTGATGA-TCTT 1851 TA	___ _ CTI	
	GCA TTC ATTGATGATT		
	CGT AGG TAACTACTAG		
	___ TT A AII		
GAM133 AQP1	GGTCAG-GCAGTAAGTCCG 1869 TGGCCA	C TT	
	GGGCAGTAAG CCG		

	TCCGTCATTG GGC		
	CAG___ A TI		
GAM133 BAIAP3	GGCCAGGGCGGTAGGCGCCG 1868 TG	A A _ TG	
	GCCAGGGC GTA GC CCGT		
	CGGTCCCG CAT CG GGCG		
	___ C C C II		
GAM133 CYLN2	GGCCAGGGCTGTA---CCGTT 1871 TG	A AGC	
	GCCAGGGC GTA CCGTT		
	CGGTCCCG CAT GGCAA		
	___ A ___		
GAM133 GNA11	GCCAGGGCAGGGTGGCCGT 1864 TGGC	TAAGC TG	
	CAGGGCAG CCGT		
	GTCCCGTC GGCA		
	___ CCACC CG		
GAM133 HD	TGGCCAGGG-AACCAGCCCG 1874	C TA TTG	
	TGGCCAGGG AG AGCCCG		
	ACCGGTCCC TT TCGGGC		
	_ GG III		
GAM133 IL11	GCCAGGGCAG-AAGTCTGT 1863 TGGC	T CCC T	
	CAGGGCAG AAG G T		
	GTCCCGTC TTC C A		
	___ _ AGA _		
GAM133 KRT16	TGGCCAGG---GTCAGCTCGT 1875	_ AAGCCCGTT	
	TGGCCAGGG CAGT		
	ACCGGTCCC GTCG		
	A AGCAIIIGG		
GAM133 MGAM	GCCAGGGCAGGATGTAGCCC 1862 TGGC	TA___ GTTG	
	CAGGGCAG AGCCC		
	GTCCCGTC TCGGG		
	___ CTACA GGII		
GAM133 MTMR3	TGCCCAGGGCAGT--GCTC-TTGG 1878 G	AA CCG	
	TG CCAGGGCAGT GC TTGG		
	AC GGTCCCGTCA CG AACC		
	G _ AG_		
GAM133 P2RY6	TGCCCAGGGCAG--AGCCC 1873 G	TA GTT	
	TG CCAGGGCAG AGCCC		
	AC GGTCCCGTC TCGGG		
	G _ III		
GAM133 PAH	GGCCAGGGCAGCCTGCCGGATG 1872 TG	AA CGT G	
	GCCAGGGCAGT GCC TG		

	CGGTCCCGTCG CGG AC		
	— GA CCT G		
GAM133 PARN	GGCCAGGGCATACGGCAAGCCC 1866 TG	—	GTTGG
	GCCAGGGCA GTAAGCCC		
	CGGTCCCGT CGTTCGGG		
	— ATGC AIII		
GAM133 PMP22	CAGGGCAGTCAGAGACCCG 1859 TGGC	GG TAA	TG
	CAG CAG GCCCGT		
	GTC GTC TGGGCG		
	C— A_ TC_ TC		
GAM133 PYCR1	TGGCCAGGGCA-AAAGCCAGCTGG 1879	T C I	
	TGGCCAGGGCAG AAGCC GTTGG		
	ACCGGTCCCGTT TTCGG CGACC		
	— T I		
GAM133 RAB26	GGCC-GGGCTGCAAGGCCCGTTGG 1867 TG	A A _	I
	GCC GGGC GTAAG CCCGTTGG		
	CGG CCCG CGTTC GGGCAACC		
	— _ A C C		
GAM133 SLC22A12	GGCCAGGGCAACGGGCCTGTT 1870 TG	TAA C GG	
	GCCAGGGCAG GCC GTT		
	CGGTCCCGTT CGG CAA		
	— GCC A AI		
GAM133 SYCP1	TGGCCTGAAAAGAAAGCCCGTT 1877	A C T	GG
	TGGCC GGG AG AAGCCCGTT		
	ACCGG CTT TC TTCGGGCAA		
	A T T II		
GAM133 SYNGR1	TGGCCAGGGAAG--AGCACGT 1876	C TA C TG	
	TGGCCAGGG AG AGC CGT		
	ACCGGTCCC TC TCG GCA		
	T _ T II		
GAM133 TMEM1	GGCCAGGGCTCTGAGTAAGCGGCGTCGG1865 TG	—	C_
	GCCAGGGC AGTAAGC CGTTGG		
	CGGTCCCG TCATTTCG GCAGCC		
	— AGAC CC TII		
GAM133 TNP1	CCAGGGCAG--AGCCCGCTGG 1861 TGGCCA	TA	
	GGGCAG AGCCCGTTG		
	CCCGTC TCGGGCGAC		
	— —		
GAM133 UBTF	CCAGGGCAGT--GCCTGTT 1860 TGGCCA	AA C	
	GGGCAGT GCC GTT		

	CCCGTCA CGG CAA	
	_____ A	
GAM134 BRCA1	GTTTCACCATGTTGGCCAGG 1885 TG A I	
	TCACCAT TTGGCCAG	
	AGTGGTA AACCGGTC	
	AA C I	
GAM134 BRCA1	GTTTCACCATGTTGGCCAGG 1885 TGCAGTGT A	
	CACCAT TTGGCCAG	
	GTGGTA AACCGGTC	
	_____ C	
GAM134 CPT2	GTTTCACCATGTTGGCCAGG 1885 TG A I	
	TCACCAT TTGGCCAG	
	AGTGGTA AACCGGTC	
	AA C I	
GAM134 CPT2	GTTTCACCATGTTGGCCAGG 1885 TGCAGTGT A	
	CACCAT TTGGCCAG	
	GTGGTA AACCGGTC	
	_____ C	
GAM134 CYP1A2	CAGGGTCCCCTATGTTGGCCAGG 1883 A G C A I	
	GT TCAC AT TTGGCCAG	
	CA GGTG TA AACCGGTC	
	C G A C I	
GAM134 CYP1A2	CAGGGTCCCCTATGTTGGCCAGG 1883 TGCA G C A I	
	GT TCAC AT TTGGCCAGG	
	CA GGTG TA AACCGGTCC	
	CC_ G A C G	
GAM134 CYP4F3	GTTTCACCATATTGGCCAGG 1884 TG I	
	TCACCATATTGGCCAG	
	AGTGGTATAACCGGTC	
	AA I	
GAM134 CYP4F3	GTTTCACCATATTGGCCAGG 1884 TGCAGTGT	
	CACCATATTGGCCAG	
	GTGGTATAACCGGTC	

GAM134 DNASE2	GTTTCACCATGTTGGCCAGG 1885 TG A I	
	TCACCAT TTGGCCAG	
	AGTGGTA AACCGGTC	
	AA C I	
GAM134 DNASE2	GTTTCACCATGTTGGCCAGG 1885 TGCAGTGT A	
	CACCAT TTGGCCAG	

		GTGGTA AACCGGTC			
		_____ C			
GAM134 EGFL4		GTTTCACCATATTGGCCAGG	1884	TG	I
		TCACCATATTGGCCAG			
		AGTGGTATAACCGGTC			
		AA I			
GAM134 EGFL4		GTTTCACCATATTGGCCAGG	1884	TGCAGTGT	
		CACCATATTGGCCAG			
		GTGGTATAACCGGTC			

GAM134 FGFR2		GTTTCACCATGTTGGCCAGG	1885	TG A I	
		TCACCAT TTGGCCAG			
		AGTGGTA AACCGGTC			
		AA C I			
GAM134 FGFR2		GTTTCACCATGTTGGCCAGG	1885	TGCAGTGT A	
		CACCAT TTGGCCAG			
		GTGGTA AACCGGTC			
		_____ C			
GAM134 FUT6		GTTTCACCATATTGGCCAGG	1884	TG	I
		TCACCATATTGGCCAG			
		AGTGGTATAACCGGTC			
		AA I			
GAM134 FUT6		GTTTCACCATATTGGCCAGG	1884	TGCAGTGT	
		CACCATATTGGCCAG			
		GTGGTATAACCGGTC			

GAM134 HIP1		GTTTCACCATGTTGGCCAGG	1885	TG A I	
		TCACCAT TTGGCCAG			
		AGTGGTA AACCGGTC			
		AA C I			
GAM134 HIP1		GTTTCACCATGTTGGCCAGG	1885	TGCAGTGT A	
		CACCAT TTGGCCAG			
		GTGGTA AACCGGTC			
		_____ C			
GAM134 IL17R		GTTTCACCATGTTGGCCAGG	1885	TG A I	
		TCACCAT TTGGCCAG			
		AGTGGTA AACCGGTC			
		AA C I			
GAM134 IL17R		GTTTCACCATGTTGGCCAGG	1885	TGCAGTGT A	
		CACCAT TTGGCCAG			

		GTGGTA AACCGGTC			
		_____ C			
GAM134 IRAK4	GTTTCACCATGTTGGCCAGG	1885 TG	A	I	
	TCACCAT TTGGCCAG				
	AGTGGTA AACCGGTC				
	AA C I				
GAM134 IRAK4	GTTTCACCATGTTGGCCAGG	1885 TGCAGTGT	A		
	CACCAT TTGGCCAG				
	GTGGTA AACCGGTC				
	_____ C				
GAM134 LAMC2	GTTTCACCATGTTGGCCAGG	1885 TG	A	I	
	TCACCAT TTGGCCAG				
	AGTGGTA AACCGGTC				
	AA C I				
GAM134 LAMC2	GTTTCACCATGTTGGCCAGG	1885 TGCAGTGT	A		
	CACCAT TTGGCCAG				
	GTGGTA AACCGGTC				
	_____ C				
GAM134 LEP	GTTTCACCATGTTGGCCAGG	1885 TG	A	I	
	TCACCAT TTGGCCAG				
	AGTGGTA AACCGGTC				
	AA C I				
GAM134 LEP	GTTTCACCATGTTGGCCAGG	1885 TGCAGTGT	A		
	CACCAT TTGGCCAG				
	GTGGTA AACCGGTC				
	_____ C				
GAM134 OPA3	AGTTTCACCATGTTGGCCAGG	1882 G	A	I	
	GT TCACCAT TTGGCCAG				
	CA AGTGGTA AACCGGTC				
	A C I				
GAM134 OPA3	AGTTTCACCATGTTGGCCAGG	1882 TGCAGTG	A		
	TCACCAT TTGGCCAGG				
	AGTGGTA AACCGGTCC				
	A_____ C				
GAM134 PAICS	GTTTCACCATGTTGGCCAGG	1885 TG	A	I	
	TCACCAT TTGGCCAG				
	AGTGGTA AACCGGTC				
	AA C I				
GAM134 PAICS	GTTTCACCATGTTGGCCAGG	1885 TGCAGTGT	A		
	CACCAT TTGGCCAG				

	GTGGTA AACCGGTC			
	_____ C			
GAM134 PDE4C	GTTTCACCATGTTGGCCAGG	1885 TG	A	I
	TCACCAT TTGGCCAG			
	AGTGGTA AACCGGTC			
	AA C I			
GAM134 PDE4C	GTTTCACCATGTTGGCCAGG	1885 TGCAGTGT	A	
	CACCAT TTGGCCAG			
	GTGGTA AACCGGTC			
	_____ C			
GAM134 PSMB2	GTTTCACCATGTTGGCCAGG	1885 TG	A	I
	TCACCAT TTGGCCAG			
	AGTGGTA AACCGGTC			
	AA C I			
GAM134 PSMB2	GTTTCACCATGTTGGCCAGG	1885 TGCAGTGT	A	
	CACCAT TTGGCCAG			
	GTGGTA AACCGGTC			
	_____ C			
GAM134 TCF7	GTTTCACCATGTTGGCCAGG	1885 TG	A	I
	TCACCAT TTGGCCAG			
	AGTGGTA AACCGGTC			
	AA C I			
GAM134 TCF7	GTTTCACCATGTTGGCCAGG	1885 TGCAGTGT	A	
	CACCAT TTGGCCAG			
	GTGGTA AACCGGTC			
	_____ C			
GAM134 UPK1B	GTTTCACCATGTTGGCCAGG	1885 TG	A	I
	TCACCAT TTGGCCAG			
	AGTGGTA AACCGGTC			
	AA C I			
GAM134 UPK1B	GTTTCACCATGTTGGCCAGG	1885 TGCAGTGT	A	
	CACCAT TTGGCCAG			
	GTGGTA AACCGGTC			
	_____ C			
GAM134 VHL	GTTTCACCATGTTGGCCAGG	1885 TG	A	I
	TCACCAT TTGGCCAG			
	AGTGGTA AACCGGTC			
	AA C I			
GAM134 VHL	GTTTCACCATGTTGGCCAGG	1885 TGCAGTGT	A	
	CACCAT TTGGCCAG			

	GTGGTA AACCGGTC			
	_____ C			
GAM134 VHL	GTTTTACCATGTTGGCCAGG	1886	TGCAGTGTC	A
	ACCAT TTGGCCAG			
	TGGTA AACCGGTC			
	A_____ C			
GAM134 VHL	GTTTTACCATGTTGGCCAGG	1886	TGTC	A I
	ACCAT TTGGCCAG			
	TGGTA AACCGGTC			
	AAAA C I			
GAM135 B3GAT1	GGCCACGGGCGGCGGCAGCAC	1895	TGA CCAC	TG
	GG CGGCGGCAGTACG			
	CC GCCGCCGTCGTGT			
	GTG C_____ CC			
GAM135 DLG1	AGCCCACCGCGCTCCCGCAGT	1889	TGAGG	_____ ACGTG
	CCACCGGCG GCAGT			
	GGTGGCCGC CGTCA			
	G_____ AGGG AGIII			
GAM135 EIF1A	TGCGTCCACGCTCGGCGGCAG	1896	AGG	_____ TACGTG
	TG CCAC CGGCGGCAG			
	AC GGTG GCCGCCGTC			
	GCA CGA III GTG			
GAM135 EVC	GCCACCGGCAGC-CTACATG	1894	TGAGGCCA	AG
	CCGGCGGC TACGT			
	GGCCGTCG ATGTA			
	_____ G_			
GAM135 HR	GATGCCACCGGCTGC-GCACG	1893	TGAG	G A T
	GCCACCGGC GC GTACG			
	CGGTGGCCG CG CGTGC			
	TA_____ A _ C			
GAM135 MYO9A	GAGGCCACCGAGGGTCGGACG	1892	TG	C CAGT TG
	AGGCCACCGG GG ACG			
	TCCGGTGGCT CC TGC			
	_____ C AGCC CI			
GAM135 PTEN	GAGGCCTGGCAGCGGCGGCAG	1890	TG	AC_____ ACGTG
	AGGCC CGGCGGCAGT			
	TCCGG GCCGCCGTCG			
	_____ ACCGTC III GT			
GAM135 SURF6	GAGGCCACCGTCTTCTGTCCCGTG	1891	TG	GCGGCA A_ I
	AGGCCACCG GT CGTG			

		TCCGGTGGC CA GCAC		
		___ AGAAGA GG C		
GAM135 TNFRSF14		TGAGGCCACAAGAGTCAG-ACG 1897	C C _ T TG	
		TGAGGCCAC GG GG CAG ACG		
		ACTCCGGTG TC TC GTC TGC		
		T _ A _ II		
GAM136 CHI3L1		TGAGCTCAAATCTGTGTGTT 1905	TTTTTCTA	
		TGAGCTCAAATCTGT		
		ACTCGAGTTTAGACA		
		CACAAIII		
GAM136 COL10A1		GAGCTCTATTTCTGTTTTTT 1902 TG	AAA_ CTA	
		AGCTC TCTGTTTTTT		
		TCGAG AGACAAAAAA		
		___ ATAA AII		
GAM136 DSC3		AGCTC---TCTCTTTTTTCTA 1900 TGAG	AAA G	
		CTC TCT TTTTTTCT		
		GAG AGA AAAAAAGA		
		___ _ G		
GAM136 GALR1		AGCTCAAAT-T-TTTTTTCTA 1901 TGAG	CTG	
		CTCAAAT TTTTTTCTA		
		GAGTTTA AAAAAAGAT		
		___ A_		
GAM136 NCOA3		GAGCTCAAAGCTGGTCCTTTCT 1903 TG	T _ AG	
		AGCTCAA CTG TTTTTTCT		
		TCGAGTTT GAC AGGAAAGA		
		___ C C AI		
GAM136 NFIB		TGTGTTCAAA-CTGTTTTTT 1906 TGAGC	T CTA	
		TCAA CTGTTTTTT		
		AGTTT GACAAAAAA		
		ACACA _ III		
GAM136 RGS1		GAGCTCCA--CTGTTTTTT 1904 TG	AAAT CT	
		AGCTC CTGTTTTTT		
		TCGAG GACAAAAAA		
		___ GT_ TI		
GAM137 ALDH3A2		ACA-AGAATGACAGGTGATGCT 1912 _ T	T A I	
		CA AGAATGACA GT ATGC		
		GT TCTTACTGT CA TACG		
		T _ C C I		
GAM137 ALDH3A2		ACA-AGAATGACAGGTGATGCT 1912 TGACAT	T A	
		AGAATGACA GT ATGCT		

		TCTTACTGT CA TACGA		
		T_____ C C		
GAM137 APG5L		ACA-AGAAATGAAATGTAATGC 1910 TA C I		
		CA GAATGA ATGTAATG		
		II		
		GT TTTACT TACATTAC		
		TC T I		
GAM137 APG5L		ACA-AGAAATGAAATGTAATGC 1910 TGACATA C T		
		GAATGA ATGTAATGC		
		TTTACT TACATTACG		
		TTC_____ T T		
GAM137 BACH1		CATA-AATG---TGTAATGCT 1914 ATA ACA		
		GAATG TGTAATGC		
		TTTAC ACATTACG		
		GTA _____		
GAM137 CALCB		GACATAGAATTAAATATAA 1919 GAC II		
		GACATAGAAT ATGTA		
		CTGTATCTTA TATAT		
		ATT TI		
GAM137 CALCB		GACATAGAATTAAATATAA 1919 TG GAC TGC		
		ACATAGAAT ATGTAA		
		TGTATCTTA TATATT		
		_____ ATT TII		
GAM137 DXF68S1E		ACATACATATG-CATGTAATGC 1909 TG GAA A		
		ACATA TG CATGTAATGCT		
		TGTAT AC GTACATTACGG		
		TA _____		
GAM137 DXF68S1E		ACATACATATG-CATGTAATGC 1909 GA_ A I		
		CATA ATG CATGTAATG		
		GTAT TAC GTACATTAC		
		GTA _ I		
GAM137 EFG1		GACATAGAATTACCTTTGAAT 1917 TG G ATGTAATGCT		
		ACATAGAAT AC		
		TGTATCTTA TG		
		_____ A GAAACTTATI		
GAM137 ISL1		ACATAGAATTAGACATATAAT 1911 _ III		
		ACATAGAAT GACATGTAA		
		TGTATCTTA CTGTATATT		
		AT AII		
GAM137 ISL1		ACATAGAATTAGACATATAAT 1911 TGAC _ GCT		
		ATAGAAT GACATGTAAT		

		TATCTTA CTGTATATTA		
		____ AT AGI		
GAM137 MKKS		CATAGAATG--ATTTAATG 1913		CATGTAATI
		CATAGAATGA		
		GTATCTTACT		
		AAATTACII		
GAM137 NRG1		GACATAGAATCATCTGAAA 1918		GACATGTAI
		GACATAGAAT		
		CTGTATCTTA		
		GTAGACTTTI		
GAM137 NRG1		GACATAGAATCATCTGAAA 1918 TG		GACATGTAATGC
		ACATAGAAT		
		TGTATCTTA		
		— GTAGACTTTGII		
GAM137 NT5C2		TGATATACAATACCATGTAATGC 1920	C G A	TI
		TGA ATA AATG CATGTAATGC		
		ACT TAT TTAT GTACATTACG		
		A G G II		
GAM137 NT5C2		TGATATACAATACCATGTAATGC 1920	C G A	I
		GA ATA AATG CATGTAATG		
		CT TAT TTAT GTACATTAC		
		A G G I		
GAM137 RBBP5		GAGATAGGAAATGACATGTCAAATG 1915	CATA	AATI
		GAATGACATGT		
		TTTACTGTACA		
		CC_ GTTT		
GAM137 RBBP5		GAGATAGGAAATGACATGTCAAATG 1915	T CATA	AATGCTII
		GA GAATGACATGT		
		CT TTTACTGTACA		
		T ATCC GTTTTACT		
GAM137 WBSCR5		TGAAATAAACT-ACATGTAATGCT 1921	C ATG	I
		TGA ATAGA ACATGTAATGCT		
		ACT TATTT TGTACATTACGA		
		T GA_ I		
GAM137 WBSCR5		TGAAATAAACT-ACATGTAATGCT 1921_	C ATG	I
		GA ATAGA ACATGTAATGC		
		CT TATTT TGTACATTACG		
		A T GA_ I		
GAM137 WDR1		GAAATAGAGAAATGACATGT 1916	C _	III
		GA ATAGA ATGACATG		

	CT TATCT TACTGTAC			
	T CTT AII			
GAM137 WDR1	GAAATAGAGAAATGACATGT	1916	TGAC ____	AATGC
	ATAGA ATGACATGT			
	TATCT TACTGTACA			
	TT__ CTT AIIIT			
GAM138 ADAMTS13	TCAGGAGAGCCAGCCCGAGGAGT	1941	GA ____	TCTAI
	TCAGGAG CC CCGAGGAGT			
	AGTCCTC GG GGCTCCTCA			
	TC TCG IIIAT			
GAM138 ADAMTS13	TCAGGAGAGCCAGCCCGAGGAGT	1941	CA GAC_	I
	GGAG CCCGAGGAG			
	TCTC GGGCTCCTC			
	C_ GGTC I			
GAM138 ATP2B4	TCAGGAGGAGGAAGAGGAG	1945	CCCC	TTCT
	TCAGGAGGA GAGGAG			
	AGTCCTCCT CTCCTC			
	CCTT IIIA			
GAM138 ATP2B4	TCAGGAGGAGGAAGAGGAG	1945	CCCC	II
	TCAGGAGGA GAGGA			
	AGTCCTCCT CTCCT			
	CCTT CI			
GAM138 BAZ2A	CAGTAGTTGTCCCTGAGGAGTTC	1931	AGGAGGA C	I
	CCC GAGGAGTT			
	GGG CTCCTCAA			
	ATCAACA A I			
GAM138 BAZ2A	CAGTAGTTGTCCCTGAGGAGTTC	1931	TCAGGAGGA C	AI
	CCC GAGGAGTTCT			
	GGG CTCCTCAAGG			
	TCATCAACA A II			
GAM138 CXCL16	AGGACGACGGCCCGAGGAG	1926	G ____	III
	AGGA GAC CCCGAGGA			
	TCCT CTG GGGCTCCT			
	G CC CII			
GAM138 CXCL16	AGGACGACGGCCCGAGGAG	1926	TCAG G ____	CT
	GA GAC CCCGAGGAGTT			
	CT CTG GGGCTCCTCGG			
	____ G CC II			
GAM138 CYP3A43	TCAGGAGGA-CTTGAGG-GTACTA	1946	CCC A T	
	TCAGGAGGAC GAGG GT CTA			

	AGTCCTCCTG CTCC CA GAT		
	AA_ _ T		
GAM138 CYP3A43	TCAGGAGGA-CTTGAGG-GTACTA 1946	CCC	A TCI
	TCAGGAGGAC GAGG GT		
	AGTCCTCCTG CTCC CA		
	AA_ _ TGA		
GAM138 FMNL	TCAGGAGGACCTCCG-GGAG 1943	_ A	TTCT
	TCAGGAGGACC CCG GGAG		
	AGTCCTCCTGG GGC CCTC		
	A _ IIIA		
GAM138 FMNL	TCAGGAGGACCTCCG-GGAG 1943	_ A	II
	TCAGGAGGACC CCG GGA		
	AGTCCTCCTGG GGC CCT		
	A _ CI		
GAM138 GCH1	TCGGGAAGGACCCCGGGGCGCTTC 1940	A _	A A CTAI
	TC GGA GGACCCCG GG GTT		
	AG CCT CCTGGGGC CC CGA		
	C T C G AGII		
GAM138 GCH1	TCGGGAAGGACCCCGGGGCGCTTC 1940	A	A A I
	GGAGGACCCCG GG GTT		
	CTTCCTGGGGC CC CGA		
	C C G I		
GAM138 IGFBP4	GGAGGACCCGACCCGGAG 1936	C _	III
	GGAGGACCC GA GGA		
	CCTCCTGGG CT CCT		
	C GGG CII		
GAM138 IGFBP4	GGAGGACCCGACCCGGAG 1936	TCA _	C AGTTCT
	GGA GGACCC GAGG		
	CCT CCTGGG CTCC		
	_ GGG C GGIIIA		
GAM138 LTB4R	CAGGAGGACTCCTTAGAGG 1932	_ C_	III
	CAGGAGGAC CC GAG		
	GTCCTCCTG GG CTC		
	A AAT CII		
GAM138 LTB4R	CAGGAGGACTCCTTAGAGG 1932	TC	C GA TTCT
	AGGAGGAC CC GGAG		
	TCCTCCTG GG TCTC		
	_ A AA CAII		
GAM138 MCM7	CAAGAGGACCCC-AGG-GTT 1934	G	AGI
	CAGGAGGACCCC AGG		

	GTTCTCCTGGGG TCC		
	— CAA		
GAM138 MCM7	CAAGAGGACCCC-AGG-GTT 1934 TC	G A C	
	AGGAGGACCCC AGG GTT		
	TTCTCCTGGGG TCC CAA		
	— — — C		
GAM138 MRPS12	GGAGGACCCC-AGGA-TTC 1937	G GTTI	
	GGAGGACCCC AGGA		
	CCTCCTGGGG TCCT		
	— AAGI		
GAM138 MRPS12	GGAGGACCCC-AGGA-TTC 1937 TCAGGA	G G	
	GGACCCC AGGA TTC		
	CCTGGGG TCCT AAG		
	— — —		
GAM138 MUC4	TCAGGAGGACTCCGGTGGCGTT 1942	C A_ A CTA	
	TCAGGAGGAC CCG GG GTT		
	AGTCCTCCTG GGC CC CAA		
	A CA G		
GAM138 MUC4	TCAGGAGGACTCCGGTGGCGTT 1942 C	C A_ A I	
	AGGAGGAC CCG GG GT		
	TCCTCCTG GGC CC CA		
	— A CA G I		
GAM138 MYCL1	AGGAGGGCCT---GGAGTTCTA 1929 _ A CCGA		
	GGAGG CC GGAGTTCT		
	CCTCC GG CCTCAAGA		
	T C A_		
GAM138 MYCL1	AGGAGGGCCT---GGAGTTCTA 1929 TCAG A CCGA		
	GAGG CC GGAGTTCT		
	CTCC GG CCTCAAGA		
	— C A_		
GAM138 PKDREJ	CAGTGAGG---CCGAGGAGTT 1930 _ ACC I		
	CAG GAGG CCGAGGAG		
	GTC CTCC GGCTCCTC		
	A _ A		
GAM138 PKDREJ	CAGTGAGG---CCGAGGAGTT 1930 TCAG ACC C		
	GAGG CCGAGGAGTT		
	CTCC GGCTCCTCAA		
	TCA_ _ A		
GAM138 PTGS2	AGGAGGCGCTGCTGAGGAGTTC 1927 TCAG ACCCC_ A		
	GAGG GAGGAGTTCT		

	CTCC CTCCTCAAGG		
	____ GCGACGA A		
GAM138 PTK7	GGAGCCCGACCCCGAGGCGT 1935 ____	AGIII	
	GGAG GACCCCGAGG		
	CCTC CTGGGGCTCC		
	GGG GCAII		
GAM138 PTK7	GGAGCCCGACCCCGAGGCGT 1935 TCAGGAG	A	
	GACCCCGAGG GTTCT		
	CTGGGGCTCC CAGGG		
	CGGG____ G		
GAM138 RAD50	TCAGGAGGATCCGGGCGGGGAG 1944	_ C_ A TTCTA	
	TCAGGAGGA CC CG GGAG		
	AGTCCTCCT GG GC CCTC		
	A CCC C IIIAT		
GAM138 RAD50	TCAGGAGGATCCGGGCGGGGAG 1944	CC A AIII	
	TCAGGAGGA CCG GG		
	AGTCCTCCT GGC CC		
	A_ _ GCCC		
GAM138 RFC1	GGAGGA-CCCAAGCAGTCCTA 1938 _	C G I	
	GAGGACCC GAG AGTTCT		
	CTCCTGGG TTC TCAGGA		
	C _ G I		
GAM138 RFC1	GGAGGA-CCCAAGCAGTCCTA 1938 TCAGGA	C G	
	GGACCC GAG AGTTCT		
	CCTGGG TTC TCAGGA		
	____ _ G		
GAM138 S100A6	TCAGAGAGGACCCCCAGAGGTGT 1939 _	G GA TCTAI	
	TCAG GAGGACCCC AG GT		
	AGTC CTCCTGGGG TC CA		
	T G TC CAIII		
GAM138 S100A6	TCAGAGAGGACCCCCAGAGGTGT 1939 CA	__ AGI	
	GGAGGACCCC GAGG		
	TCTCCTGGGG CTCC		
	____ GT ACI		
GAM138 SAS	AGGACCCCGA-CAGCTTCT 1924	GG CII	
	AGGACCCCGA AGTT		
	TCCTGGGGCT TCGA		
	G_ AGA		
GAM138 TBL1X	CAGGAGGACCGCCAGGGGT 1933	_ G AGII	
	CAGGAGGACC CC AGG		

	GTCCTCCTGG GG TCC	
	C _ CCAI	
GAM138 TBL1X	CAGGAGGACCGCCAGGGGT 1933 TC	_ G A CT
	AGGAGGACC CC AGG GTT	
	TCCTCCTGG GG TCC CAG	
	_ C _ C II	
GAM138 TCF21	AGAAGGAACCCCGAGGACTTCT 1925 G	_ G I
	GAGGA CCCCAGGGA TTC	
	TTCCT GGGGCTCCT AAG	
	_ T G I	
GAM138 TCF21	AGAAGGAACCCCGAGGACTTCT 1925 TCAG	_ G A
	GAGGA CCCCAGGGA TTCT	
	TTCCT GGGGCTCCT AAGA	
	_ T G C	
GAM138 VAMP8	AGGAGGA--CCGAGCAGCATTCT 1928	CC G TCI
	GGAGGACC GAG AGT	
	CCTCCTGG CTC TCG	
	_ G TAA	
GAM138 VAMP8	AGGAGGA--CCGAGCAGCATTCT 1928 TCAG	CC G _ A
	GAGGACC GAG AGT TCT	
	CTCCTGG CTC TCG AGA	
	_ _ G TA G	
GAM139 BCAT1	ACTGCTC-ACTCCCGGGGTGC 1951 AACA	T CG C
	GCTT AC CCGGGGTGC	
	CGAG TG GGCCCCACG	
	GA_ _ AG T	
GAM139 BRCA1	CAGCTTTACCCAGAGCAGAGGGTG 1952 AACA	_ C _ CCTI
	GCTTTACC GC G GGGTG	
	CGAAATGG CG C CCCAC	
	_ GTCT T T TTII	
GAM139 KIAA0442	ACAGCTTTAGCCGACTGTGT 1950 AA	CC G_ CC
	CAGCTTTA GCCGG GTG	
	GTCGAAAT CGGCT CAC	
	_ _ GA AA	
GAM139 LCP1	AACAGCTTTGTCAAGCCTGGGTG 1949	ACC_ G CCTI
	AACAGCTTT GCC GGGTG	
	TTGTCGAAA CGG CCCAC	
	CAGTT A IIIT	
GAM139 P2RY2	GCTTCTCCTCTCGGGGTGCCT 1953 AACAGCTTTA	GC_
	CC CGGGGTGCCT	

	GG GCCCCACGGA	
	GA_____AGA	
GAM140 ADAR	TGGCA--CTGGGAACTGCAGTTTT 1965	AT TGTAG
	TGGC ACTG TGCAGTTTT	
	ACCG TGAC ACGTCAAAA	
	__ CCTTG	
GAM140 APPBP2	TGGCATG-TGTTCACTGCAGTTTT 1966	AC G G I
	TGGCAT TGT TA TGCAGTTTT	
	ACCGTA ACA GT ACGTCAAAA	
	C_ A G I	
GAM140 CAPN2	TGGCATACTG----GTTTCAGTT 1964	T AGTG
	TGGCATACTG GT CAGTT	
	ACCGTATGAC CA GTCAA	
	_ A_	
GAM140 CENTD1	CATAAACTGTCCTGCAGTTTT 1957	TGGCAT GTAG
	ACTGT TGCAGTTTT	
	TGACA ACGTCAAAA	
	TT___ GG_	
GAM140 CYP3A4	GCCTCCTGTGTAGTG-AGATT 1960	TGGCATA C TTT
	CTGTGTAGTG AG	
	GACACATCAC TC	
	GAG___ _ TAA	
GAM140 DAAM2	GCATACACCTG-GTAGTGCAG 1958	TG A T TT
	GCAT CTG GTAGTGCAGT	
	TGTG GAC CATCACGTCG	
	TA _ _ TI	
GAM140 FBXL7	GCCTACAGTAGGAGTGCAGTT 1959	TGGCA T T_ TT
	TAC GTG AGTGCAGTT	
	ATG CAT TCACGTCAA	
	G___ T CC CA	
GAM140 IL7R	GCAGACTGTGTAGTGGGGTTTT 1961	TGGCAT CA
	ACTGTGTAGTG GTTTT	
	TGACACATCAC CAAAA	
	TC___ CC	
GAM140 PEA15	GGCAGACATG-GCAGTGCAGTTTT 1962	TG T _ T I
	GCA AC TG GTAGTGCAGTTTT	
	CGT TG AC CGTCACGTCAAAA	
	_ C T _ T	
GAM140 RANBP9	TGCCATGACCTTTGTAGTGCA 1963	G _ G_ GTTTT
	TG CAT ACT TGTAGTGCA	

	AC GTA TGG ACATCACGT	
	G C AA I I I T T	
GAM140 SLC4A5	CATACTGTGATGGTGTCTAG 1956 TGGCAT TA_ _ TT	
	ACTGTG GTG CAGT	
	TGACAC CAC GTCG	
	_____ TAC A TG	
GAM141 CD34	ACACTACTCGGCTTGGCCAGG 1973 TGACACAG T T	
	TTC G CTTGGCCAGG	
	GAG C GAACCGGTCC	
	AT_____ C _	
GAM141 CIAS1	ACAGAGCTGTGGTCTTGGCCTGG 1971 TGACAC CT_ A I	
	AGTT GTCTTGGCC GG	
	TCGA CAGAACCGG CC	
	TC_____ CAC A T	
GAM141 DCLRE1C	GACACATTTCACTGTGTTGGCCAGG 1978 TG GTT_ C II	
	ACACA CTGT TTGGCCAGG	
	TGTGT GACA AACCGGTCC	
	_ AAAGT C GI	
GAM141 DGCR2	ACACAGTTCTGAGGCCTGG-CAGG 1970 TGAC T_ C I	
	ACAGTTCTG CTTGGC AGG	
	TGTCAAGAC GGACCG TCC	
	_____ TCC _ T	
GAM141 DPYSL2	TGGCCCATTCCTGCACTTGGCCAGG 1981 TGACA G _ II	
	CA TTCTGT CTTGGCCAGG	
	GT AGGACG GAACCGGTCC	
	ACCGG A T II	
GAM141 EIF4EBP2	ACAGGTTTCTTTCTTGGCCA 1972 TGACACAG G	
	TTCT TCTTGGCCAG	
	AAGA AGAACCGGTT	
	CA_____ A	
GAM141 GPR48	CACAGTTCTAGCTGGGACAG 1975 TGACAC T T C	
	AGTTCTG CT GG CAG	
	TCAAGAT GA CC GTC	
	_____ C C T	
GAM141 IL2RB	ACACAGTTCTGCTCGGGCAG 1969 TGAC GT_ C G	
	ACAGTTCT CTTGG CAG	
	TGTCAAGG GAGCC GTC	
	_____ ACC C G	
GAM141 IL8RA	GACAAAGGGATCTTCCTTGGCCAGG 1977 TG C T_ GT II	
	ACA AG TCT CTTGGCCAGG	

		TGT TC AGA GAACCGGTCC		
		__ T CCT AG CI		
GAM141 MAP3K14		GACAAAGG-CTGTCTTGGCAAG	1979	TG C TT C
		ACA AG CTGTCTTGGC AGG		
		TGT TC GACAGAACCG TCT		
		__ T C_ T		
GAM141 MEN1		TGAAACAGG-CTGTCTTGGCCA	1982	C TT GG
		TGA ACAG CTGTCTTGGCCA		
		ACT TGTC GACAGAACCGGT		
		T C_ II		
GAM141 RIG		ACAGTTCTGTCTTCTCAGG	1974	TGACACAG GGC
		TTCTGTCTT CAG		
		AAGACAGGA GTC		
		_____ AGA		
GAM141 STIM1		CAGTAATGCCTTCTTGGCCAGG	1976	TGACACA T G
		GT CT TCTTGGCCAGG		
		CG GA AGAACCGGTCC		
		TA_____ _ _		
GAM141 VNN3		GATAGAGTTGTC-CTTGGCCAGG	1980	TGACAC CTG
		AGTT TCTTGGCCAGG		
		TCAA GGAACCGGTCC		
		TATC__ CA_		
GAM142 CYP17		TGGAGTAGA--AGAGCTGTG	1990	TTAC _ TTG
		TGGAGTAGA AGC GTG		
		ACCTCATCT TCG CAC		
		TC__ A		
GAM142 CYP17		TGGAGTAGA--AGAGCTGTG	1990	TTAC GTI
		TGGAGTAGA AGC		
		ACCTCATCT TCG		
		TC__ ACA		
GAM142 CYP3A4		TGTAGTGAGATTACAGGCGAGT	1989	G _ _ T TGGA
		TG AGT AGATTACAG CG GT		
		AC TCA TCTAATGTC GC CA		
		A C C T A		
GAM142 CYP3A4		TGTAGTGAGATTACAGGCGAGT	1989	GG _ C I
		AGT AGATTACAG GTG		
		TCA TCTAATGTC CGC		
		__ C _ T		
GAM142 KRTHA4		TGGAGCTCAGATTACAGGGAGCTG	1988	__ CGT GAI
		TGGAGT AGATTACAG GTTG		

	ACCTCG TCTAATGTC CGAC		
	AG CCT III		
GAM142 KRTHA4	TGGAGCTCAGATTACAGGGAGCTG 1988	AG	CGT I
	GG TAGATTACAG GTT		
	II IIIIIIIII III		
	TC GTCTAATGTC CGA		
	GA CCT I		
GAM142 MPP5	AGTAGATTAGAGTGTGTTG 1985	C C	II
	AGTAGATTA AG GTGTT		
	IIIIIIII II IIIII		
	TCATCTAAT TC CACAA		
	C A CI		
GAM142 MPP5	AGTAGATTAGAGTGTGTTG 1985	TGGAGT	C C
	AGATTA AG GTGTTGG		
	IIIIII II IIIIIII		
	TCTAAT TC CACAAC		
	_____ C A		
GAM142 SNX6	GGAGTAGATTTATTACAGC 1986	_____	IIIG
	GGAGTAGAT TACAG		
	IIIIIIII IIIII		
	CCTCATCTA ATGTC		
	AATA GIII		
GAM142 SNX6	GGAGTAGATTTATTACAGC 1986	TG _____	GTGTTGG
	GAGTAGAT TACAGC		
	IIIIIIII IIIII		
	CTCATCTA ATGTCG		
	_____ AATA AIIIIAGG		
GAM142 USP18	TGGA--AAATGACAGCGTGT 1991	TA T	TG
	TGGAG GAT ACAGCGTGT		
	IIIIII III IIIIIIIII		
	ACCTT TTA TGTCGCACA		
	_____ C II		
GAM142 USP18	TGGA--AAATGACAGCGTGT 1991	_ TA T	I
	GGAG GAT ACAGCGTG		
	IIII III IIIIIIIII		
	CCTT TTA TGTCGCAC		
	A _ C I		
GAM142 VCL	GGAGTAGA-TGCAGAGAGCTTGG 1987	TG _ C C G A	
	GAGTAGAT TA AG GT TTGG		
	IIIIIIII II II IIIII		
	CTCATCTA GT TC CG AACC		
	_____ C C T _ A		
GAM142 VCL	GGAGTAGA-TGCAGAGAGCTTGG 1987	TA CGT	GI
	GAGTAGAT CAG GTT		
	IIIIIIII III III		
	CTCATCTA GTC CGA		
	C_ TCT AC		
GAM143 ACATN	TCTCAGCA---AATT-CCACAT 2006	ACA A	
	TCTCAGCAA ATT CCACAT		
	IIIIIIII III IIIIIII		

AGAGTCGTT TAA GGTGTA

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GAM143 ADCY1      TCAGCAAACAGGATGCTCACATT 2003 TCTC  ATTAC__ TI
                   AGCAAACA  CACATT
                   |||||  |||||
                   TCGTTTGT  GTGTAA
                   ____ CCTACGA  CA
GAM143 BAZ2B      TCTGCAAACAATATATACACAT 2004 TCTCA  TAC__ TT
                   GCAAACAAT  CACAT
                   |||||  |||||
                   CGTTTGTTA  GTGTA
                   A____ TATAT  TT
GAM143 COX6B      CTCAGCAAAGA--CACCACA 2002 TC  CAAT  T
                   TCAGCAAA  TACCACA
                   |||||  |||||
                   AGTCGTTT  GTGGTGT
                   ____ CT__  C
GAM143 CUL4B      CTCAAGCAAACAATCAACA 1997 TC  _  C CATT
                   TCA GCAAACAATTA CA
                   || ||||| ||
                   AGT CGTTTGTTAGT GT
                   ____ T  T C||
GAM143 CX3CR1     CAGCAATTTAACAGTTACCACAT 1995 TCTCAGCA  A  I
                   AACA TTACCACATTT
                   ||| |||||
                   TTGT AATGGTGTAGA
                   GTTAAA__ C  C
GAM143 HUNK       CTCAGCA---AATCACCACA 2001 TC  ACA  T
                   TCAGCAA  ATTACCACA
                   |||||  |||||
                   AGTCGTT  TAGTGGTGT
                   ____ C
GAM143 ITGA1      CTCAGCAAAGATAAATTCAGCATTT 1999 TC  C__ AC _  ||
                   TCAGCAAA  AATT CA CATTT
                   |||||  ||| || |||||
                   AGTCGTTT  TTAA GT GTAAA
                   ____ CTA  A_ C  GI
GAM143 MEN1       TCAG-AAATGCTTACCACATT 2005 TCTCAGCAAACAA
                   TTACCACATT
                   |||||
                   AATGGTGTAA
                   TCTTTACG____
GAM143 NOTCH2     TCTCAGCAAATTATGACATCAT 2007  ACA  CC  T
                   TCTCAGCAA  ATTA ACATT
                   |||||  ||| |||||
                   AGAGTCGTT  TAAT TGTA
                   ____ AC  T
GAM143 PLS1       CACCAAAAAAATCAAACCACATTT 1996 TCTCAGCAAA  TT  I
                   CAA ACCACATTT
                   ||| |||||
```

	GTT TGGTGTAAA	
	GTTTTTTTA_ _ G	
GAM143 RNTRE	CTGAGTAATAAATTACCAC	2000 TCTCAGCAAAC ATT
	AATTACCAC	
	TTAATGGTG	
	ACTCATTAT_ _ AII	
GAM143 SLC25A14	CTAACCAATTACATTTAACCACATTT	1998 TC_ CAA A _ II
	TCAG ACA TTA CCACATTT	
	GGTT TGT AAT GGTGTAAA	
	ATT AA_ A T CI	
GAM143 THBD	AGCAA-CAATTACCATTTTT	1994 TCTCAGCAA CATT
	ACAATTACCA	
	TGTTAATGGT	
	_____ AAAA	
GAM144 CNN1	TGAGTTCTA---CAGGGGCTGG	2018 ACC C G
	TGAGTTCT GCAG GGCTGG	
	ACTCAAGA TGTC CCGACC	
	_ _ C I	
GAM144 CYFIP2	TGAGG-CTACCGCAG-GGC	2015 TT C TGG
	TGAG CTACCGCAG GGC	
	ACTC GATGGCGTC CCG	
	C_ _ III	
GAM144 FGF1	TTCTGCCTTCCTGCGGCTGGGC	2019 TGAGT A GCA
	TCT CC GCGGCTGGGC	
	GGA GG CGCCGACCCG	
	C_ _ A A_	
GAM144 GRAF	TGTGGTCGGCCGCAGCGGCT	2016_ _ A CTA GGG
	TG GTT CCGCAGCGGCT	
	AC CAG GCGTCGCCGA	
	AC _ CC_ III	
GAM144 INHBB	GTTCGGCCG--GCGGCTGGG	2011 TGAGTTCTA CA
	CCG GCGGCTGG	
	GGC CGCCGACC	
	GCC_____ _	
GAM144 INSRR	TGGGTTTCGGCTGCCAGCAGCGGCT	2012 A TA_ _ GGGCI
	TG GTTC CC GCAGCGGCT	
	AC CAAG GG CGTCGCCGA	
	C CCGAC T IIICG	
GAM144 LETM1	TGAGTGTGACA-CAGCCGGCTGGGC	2013 TCTAC _ I
	TGAGT CGCAGC GGCTGGGC	

	ACTCA GTGTCTCG CCGACCCG	
	CACT_ G I	
GAM144 PKM2	TGAGTTCTAC--AAGCGTTGCTGG 2014 CGC _ GC	
	TGAGTTCTAC AGCG GCTGG	
	ACTCAAGATG TCGC CGACC	
	T_ AA II	
GAM144 RAI14	TGAGAACAAATGGCAGCGGCTG 2017 TTCTACC GGC	
	TGAG GCAGCGGCTG	
	ACTC CGTCGCCGAC	
	TTGTTAC III	
GAM144 WRN	AGTCTCTTC-GCAGGTGCGGCTGGGC 2010 TGAG AC _ II	
	TTCT CGCA GCGGCTGGGC	
	GAGA GCGT CGCCGACCCG	
	A_ A_ CCA TC	
GAM145 AQP8	AAGTGGCCAGGCCCCCAACA 2029 AC AGAA I	
	TGG GCCCCCAAC	
	ACC CGGGGGTTG	
	TC GGTC I	
GAM145 AQP8	AAGTGGCCAGGCCCCCAACA 2029 TCTAAACT AGAA	
	GG GCCCCCAAC	
	CC CGGGGGTTG	
	_____ GGTC	
GAM145 ARCN1	TCTAAACTGGAAGGACAGGCC 2038 AA C_ AACA	
	TCTAAACTGGAG GC CCC	
	AGATTGACCTT TG GGG	
	CC TCC IIIA	
GAM145 ARCN1	TCTAAACTGGAAGGACAGGCC 2038 _ A_ III	
	TCTAAACTGGA GA GCCC	
	AGATTGACCT CT CGGG	
	TC GTC III	
GAM145 ATP10C	ACTGGCTGAAGCCCCCACCA 2031 A_ ACII	
	ACTGG GAAGCCCCCA	
	TGACC CTTCGGGGGT	
	GA GGTI	
GAM145 ATP10C	ACTGGCTGAAGCCCCCACCA 2031 TCTAAACTGGA AC	
	GAAGCCCCCA	
	CTTCGGGGGT	
	GA_____ GG	
GAM145 BAZ2A	AAAAAGCAGA-GCCCCCAAC 2023 AACTGG_ A I	
	AGA GCCCCCA	

	TCT CGGGGGTT	
	TTTTTCG _ I	
GAM145 BAZ2A	AAAAAGCAGA-GCCCCCAAC	2023 TCTAAACTGG A
	AGA GCCCCCAAC	
	TCT CGGGGGTTG	
	TTCG_____ _	
GAM145 CRY2	AACAGG-GAAGCCCCCAAC	2027 T A I
	AAC GG GAAGCCCCCA	
	TTG CC CTTCGGGGTT	
	T _ G	
GAM145 CRY2	AACAGG-GAAGCCCCCAAC	2027 TCTAAACT A
	GG GAAGCCCCCA	
	CC CTTCGGGGTT	
	_____ _	
GAM145 EFNB1	ACTGGGCAGCCGCCCAAC	2030 _ AA
	ACTGG AG GCCCCCA	
	TGACC TC CGGGGGTT	
	CG GG GII	
GAM145 EFNB1	ACTGGGCAGCCGCCCAAC	2030 TCTAAACT G AA
	G AG GCCCCCAAC	
	C TC CGGGGGTTG	
	_____ G GG	
GAM145 FGF1	AACTGCAGAACTCTGCCCAAC	2026 G _ IG
	AACTG AGAA GCCCCCA	
	TTGAC TCTT CGGGGGTT	
	G TGAGA GIII	
GAM145 FGF1	AACTGCAGAACTCTGCCCAAC	2026 TCTAAACT A_ AI
	GGAGA GCCCCCAAC	
	TCTTT CGGGGGTTG	
	CG_____ GAGA GG	
GAM145 GAB2	AAACTGGAGACAGCAGCCA	2022 _ CCCII
	AAACTGGAGA AGCC	
	TTTGACCTCT TCGG	
	GTCG TIIIC	
GAM145 GAB2	AAACTGGAGACAGCAGCCA	2022 TCTAAA _ CC AC
	CTGGAGA AGC CCA	
	GACCTCT TCG GGT	
	_____ G TC AA	
GAM145 HD	AAACAGGAG---CCCCCAAC	2024 T GAA I
	AAAC GGA GCCCCCA	

	TTTG CCT CGGGGGT			
	T _ _ T			
GAM145 HD	AAACAGGAG---CCCCCAAC	2024	TCTAAACTGG A	
	AG AGCCCCCAA			
	TC TCGGGGGTT			
	G _ _ _ C			
GAM145 IHPK1	TAAGACTGGA-AAGCCCCCAA	2034	AA_ A I	
	ACTGGAGA GCCCCCA			
	TGACCTTT CGGGGGT			
	TTC _ _ I			
GAM145 IHPK1	TAAGACTGGA-AAGCCCCCAA	2034	TCTAA A C	
	ACTGGAGA GCCCCCAA			
	TGACCTTT CGGGGGT			
	TC _ _ C			
GAM145 M17S2	CTAAACTGGAGA--CCTCCA	2032	AG_ CCI	
	CTAAACTGGAGA CC			
	GATTTGACCTCT GG			
	GGA TII			
GAM145 M17S2	CTAAACTGGAGA--CCTCCA	2032	TC AA C A	
	TAAACTGGAG GCC CCA			
	ATTTGACCTC TGG GGT			
	_ _ A A			
GAM145 MMP14	AAGTGCAGA-GCCCCCAACA	2028	AC_ G A I	
	TG AGA GCCCCCAAC			
	AC TCT CGGGGGTTG			
	TTC G _ I			
GAM145 MMP14	AAGTGCAGA-GCCCCCAACA	2028	TCTAAACT G A	
	G AGA GCCCCCAAC			
	C TCT CGGGGGTTG			
	_ _ G _			
GAM145 NKTR	TCTGTA CTTGAGAGAAGCCCCC	2037	AA _ AACA	
	TCT ACT GGAGAAGCCCCC			
	AGA TGA TCTCTTCGGGGG			
	CA AC IIIA			
GAM145 NKTR	TCTGTA CTTGAGAGAAGCCCCC	2037	CTAA _ I	
	ACT GGAGAAGCCCCC			
	TGA TCTCTTCGGGGG			
	CA _ AC I			
GAM145 OAS3	CTAGACCGG-GAAGCCCCCAA	2033	_ A A I	
	TA ACTGG GAAGCCCCCA			

	AT TGGCC CTTCGGGGGT		
	G C _ I		
GAM145 OAS3	CTAGACCGG-GAAGCCCCCAA 2033 TCTAA A C		
	ACTGG GAAGCCCCCAA		
	TGGCC CTTCGGGGGT		
	ATC_ _ T		
GAM145 PDGFB	TAAAA-GGA-AAGCCCCCAA 2036 AAAC T A I		
	GGAGA GCCCCCA		
	CCTTT CGGGGT		
	ATTTT _ I		
GAM145 PDGFB	TAAAA-GGA-AAGCCCCCAA 2036 TCTAACT A		
	GGAGA GCCCCCAA		
	CCTTT CGGGGT		
	TTT_ _		
GAM145 RAB3A	TCCACACAGG-GAAACCCCCAACA 2039 A T A I		
	TCTA AC GG GAAGCCCCCAACA		
	AGGT TG CC CTTTGGGGGTTGT		
	G T _ I		
GAM145 RAB3A	TCCACACAGG-GAAACCCCCAACA 2039 _ A T A I		
	CTA AC GG GAAGCCCCCAAC		
	GGT TG CC CTTTGGGGGTTG		
	A G T _ I		
GAM145 TRPM8	AACTGGAGATAGCCTTCAA 2025 _ CCCAI		
	AACTGGAGA AGCC		
	TTGACCTCT TCGG		
	A AAGTTI		
GAM145 TRPM8	AACTGGAGATAGCCTTCAA 2025 TCTAACT _ CC C		
	GGAGA AGCC CAA		
	CCTCT TCGG GTT		
	_ _ A AA A		
GAM145 WARS	TAAACTGGA-AAGTTTCACCCCCAA 2035 AAAC A_ I		
	TGGAGA GCCCCCA		
	ACCTTT TGGGGGT		
	_ _ CAAAG I		
GAM145 WARS	TAAACTGGA-AAGTTTCACCCCCAA 2035 TCTA A_ CAI		
	AACTGGAGA GCCCCCAA		
	TTGACCTTT TGGGGGT		
	_ _ CAAAG CAI		
GAM146 ABCF1	GGGGCAGCTGGGCCTGAAG 2089 _ A GA II		
	GG GCAGCTGGG TGAA		

	CC CGTCGACCC ACTT		
	C _ GG CI		
GAM146 ABCF1	GGGGCAGCTGGGCCTGAAG 2089 TAGGA GA GG		
	GCAGCTGGG TGAAG		
	CGTCGACCC ACTTC		
	C _ GG GA		
GAM146 ACAD8	TAGAACCAGAGGTGGATGAAGG 2095 G CT _ GG		
	TAGGA CAG GG GGATGAAGG		
	ATCTT GTC CC CCTACTTCC		
	G T_ A II		
GAM146 ACAD8	TAGAACCAGAGGTGGATGAAGG 2095 G CT _ I		
	AGGA CAG GG GGATGAAG		
	TCTT GTC CC CCTACTTC		
	G T_ A I		
GAM146 ADAT1	AGGAAGGCAGTTCAGGATGAAGGG 2047 _ A CTG I		
	GG GCAG GGGATGAAGG		
	TC CGTC TCCTACTTCC		
	T _ AAG I		
GAM146 ADAT1	AGGAAGGCAGTTCAGGATGAAGGG 2047 TA _ CTG GI		
	GGA GCAG GGGATGAAGGG		
	CCT CGTC TCCTACTTCCC		
	_ TC AAG AI		
GAM146 ADCY6	AGGACCAGTGCTGGGGATGCAGG 2051 AGGAGCA AI		
	GCTGGGGATG		
	CGACCCCTAC		
	GTCA _ GT		
GAM146 ADCY6	AGGACCAGTGCTGGGGATGCAGG 2051 TA G _ A GGI		
	GGA CA GCTGGGGATG AGG		
	CCT GT CGACCCCTAC TCC		
	_ G CA G AII		
GAM146 ANXA6	CCCCTCCCCCACC--CCTGCCC 2072 T A GC		
	CCC TCCCCCACC CTGCCC		
	GGG AGGGGGGTGGG GACGGG		
	_ _ _		
GAM146 APOC3	GGAGCAGCTGCCTCTAGGGATGAA 2085 _ IIT		
	GGAGCAGCTG GGGATGA T		
	CCTCGTCGAC CCCTACT A		
	GGAGAT TIII		
GAM146 ASIC4	TCCCCTCCCCCACC CGGCT 2103 A C GCC		
	TCCC TCCCCCACC CG CT		

	AGGG AGGGGGGTGGGC GA	
	G C III	
GAM146 ATF5	TAGAGGCAG--GGGGATGAAGG 2096 GA CT G	
	TAG GCAG GGGGATGAAGG	
	ATC CGTC CCCCTACTTCC	
	TC _ I	
GAM146 ATF5	TAGAGGCAG--GGGGATGAAGG 2096_ GA CT I	
	AG GCAG GGGGATGAAG	
	TC CGTC CCCCTACTTC	
	A TC _ I	
GAM146 ATP8B2	TCCCATTCCTGCCCACCCGCC 2098 _ _ TGCCC	
	TCCCAT CCC CCCACCCGCC	
	AGGGTA GGG GGGTGGGCGG	
	A AC CC	
GAM146 BGLAP	GCAGCT-GGGATGATGGGG 2081 G A I	
	GCAGCTGGG ATGA GGG	
	CGTCGACCC TACT CCC	
	_ A C	
GAM146 BHMT2	AGG-GCATGGTGAGGATGAAGG 2050 A GC_ I	
	GG GCA TGGGGATGAAG	
	CC CGT ACTCCTACTTC	
	_ ACC I	
GAM146 BHMT2	AGG-GCATGGTGAGGATGAAGG 2050 TA A GC_ GG	
	GG GCA TGGGGATGAAGG	
	CC CGT ACTCCTACTTCC	
	_ _ ACC AI	
GAM146 BHMT2	AGCAGCTGGAGATAGCAGGG 2043 A_ II	
	AGCAGCTGGGGATG AGG	
	TCGTCGACCTCTAT TCC	
	CG CI	
GAM146 BHMT2	AGCAGCTGGAGATAGCAGGG 2043 TAGGAGCA A_	
	GCTGGGGATG AGGG	
	CGACCTCTAT TCCC	
	CG	
GAM146 CDKN2D	TCCCCCACCACCCCATGCC 2110 TC T CCC CC	
	CCA CCCCCA GCCTG	
	GGT GGGGGGT CGGAC	
	_ _ A_ TT	
GAM146 CHGA	GAGCAGCTGGCGGTGTGGGG 2077 _ A AA I	
	AGCAGCTGG GG TG GG	

	TCGTCGACC CC AC CC		
	G _ AC I		
GAM146 CHGA	GAGCAGCTGGCGGTGTGGGG	2077 TAGGAG	_ A AA
	CAGCTGG GG TG GGG		
	GTCGACC CC AC CCC		
	_____ G _ A_		
GAM146 CHI3L1	GAGCAGCTGTGGAATTAGGAAGGGG	2073 AGCA	_ _ _ I
	GCTG GGGAT GAAGGG		
	CGAC CCTTA CTTCCC		
	_____ A ATC I		
GAM146 CSNK2A1	AGAAGCAGCTGGGGGT-AAG	2057 _	ATGAAI
	GGAGCAGCTGGGG		
	CTTCGTCGACCCC		
	T CATTII		
GAM146 CSNK2A1	AGAAGCAGCTGGGGGT-AAG	2057 TA	ATG G
	GGAGCAGCTGGGG AAGG		
	CTTCGTCGACCCC TTCT		
	_____ CA_ I		
GAM146 CYP2B6	TAGGAAGAGGCAGCTGGGAATGA	2093	_____ AGGGGI
	TAGGA GCAGCTGGGGATGA		
	ATCCT CGTCGACCCTTACT		
	TCTC IIIGGG		
GAM146 CYP2B6	TAGGAAGAGGCAGCTGGGAATGA	2093	_____ IIIT
	TAGGA GCAGCTGGGGATG		
	ATCCT CGTCGACCCTTAC		
	TCTC TIII		
GAM146 DNMT3B	GGAGCAGCTGCTGCGAGGAAGCGG	2086 A	GG_ T GGI
	GCAGCTG GA GAAG		
	CGTCGAC CT CTTC		
	_ GACG C GII		
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	AGCAGCTG GA GAAG GG		
	TCGTCGAC CT CTTC CC		
	_____ GACG C G G		
GAM146 DUSP4	TCCCA---CCCAACCCGCCTGC	2104	CCCC C
	TCCCATCC ACCCGCCTGC		
	AGGGTGGG TGGGCGGACG		
	T_____ I		
GAM146 EEF2	TCCCATCCCGCCTCCC-CCTCCCC	2109	C A G G I
	TCCCATCCC CC CCC CCT CCC		

	AGGGTAGGG GG GGG GGA GGG	
	C A _ G I	
GAM146 EGR3	AGGA-CAGCTGGGGAAGAGGGG 2060 _ G	T A I
	GGA CAGCTGGGGA GA GG	
	CCT GTCGACCCCT CT CC	
	T _ T C I	
GAM146 EGR3	AGGA-CAGCTGGGGAAGAGGGG 2060 TA G	T A
	GGA CAGCTGGGGA GA GGGG	
	CCT GTCGACCCCT CT CCCC	
	_ _ T _	
GAM146 EPB49	GAGCAGCTGGGAGTGTGGGGG 2079	GA AA I
	AGCAGCTGGG TG GGG	
	TCGTCGACCC AC CCC	
	TC AC I	
GAM146 EPB49	GAGCAGCTGGGAGTGTGGGGG 2079 TAGGAG	GA AA
	CAGCTGGG TG GGGG	
	GTCGACCC AC CCCC	
	_____ TC AC	
GAM146 EPHB4	AGGCAGCAGCTGGGG--GAGGGG 2046 _ _	AT A I
	GG AGCAGCTGGGG GA GG	
	CC TCGTCGACCCC CT CC	
	T G _ C I	
GAM146 EPHB4	AGGCAGCAGCTGGGG--GAGGGG 2046 TA _	ATGA
	GG AGCAGCTGGGG AGGGG	
	CC TCGTCGACCCC TCCCC	
	_ G C _	
GAM146 ETF1	TCCCATCCCTTCCCACCCGCC 2100 _	TGCCC
	TCCCATCCC CCCACCCGCC	
	AGGGTAGGG GGGTGGGCGG	
	AA IIIC	
GAM146 ETS2	GGAGCAGCTGGTCAGGATGGG 2090 _	AAGGI
	GAGCAGCTGG GGATG	
	CTCGTCGACC CCTAC	
	AGT CIIG	
GAM146 ETS2	GGAGCAGCTGGTCAGGATGGG 2090 TAGG	GGAT A G
	AGCAGCTGG GA GGG	
	TCGTCGACC CT CCC	
	_____ AGTC A G	
GAM146 FLRT1	AGG-GCAGCTGGGGCTGAGGCGG 2062 _ A	A A GI
	GG GCAGCTGGGG TGA GG	

	CC CGTCGACCCC ACT CC		
	T _ G _ GC		
GAM146 FLRT1	AGG-GCAGCTGGGGCTGAGGCGG	2062 TA A	A A _
	GG GCAGCTGGGG TGA GG GG		
	CC CGTCGACCCC ACT CC CC		
	_ _ G _ G		
GAM146 FRDA	AGCAGCTGGNTATGTGGGG	2044 C	T A I
	AG AGCTGGGGA GA GG		
	TC TCGACCCCT CT CC		
	C _ C C		
GAM146 FXYD6	TAGGAGCAGAAGGTGATGGAGGG	2097	CT _ A GI
	TAGGAGCAG GGG GATG AGGG		
	ATCCTCGTC TCC CTAC TCCC		
	T_ A C		
GAM146 FXYD6	TAGGAGCAGAAGGTGATGGAGGG	2097	CT _ A I
	AGGAGCAG GGG GATG AGG		
	TCCTCGTC TCC CTAC TCC		
	T_ A C I		
GAM146 FY	AGG-GCAGCTGGGGCTGGAGG	2058 _ A	A AAGI
	GG GCAGCTGGGG TG		
	CC CGTCGACCCC AC		
	T _ G CTCT		
GAM146 FY	AGG-GCAGCTGGGGCTGGAGG	2058 TA A	A A
	GG GCAGCTGGGG TG AGGG		
	CC CGTCGACCCC AC TCCT		
	_ _ G C		
GAM146 GA	AGGAGC-GTTGGGGATGAAGG	2059 _ AGC	I
	GGAGC TGGGGATGAAG		
	CCTCG ACCCCTACTTC		
	T CA_ I		
GAM146 GA	AGGAGC-GTTGGGGATGAAGG	2059 TA AGC	
	GGAGC TGGGGATGAAGG		
	CCTCG ACCCCTACTTCCT		
	_ CA_		
GAM146 GAS7	AGGAAGCAGCTGGGG--GAAGG	2048 _	AT I
	GGAGCAGCTGGGG GAAG		
	CTTCGTCGACCCC CTTC		
	TC _ I		
GAM146 GAS7	AGGAAGCAGCTGGGG--GAAGG	2048 TA	AT
	GGAGCAGCTGGGG GAAGG		

	CTTCGTCGACCCC CTTCCT		
	C_ _		
GAM146 GFAP	GGAGCAGCTGGGG-TGGTGGGG 2092_	A AA I	
	GAGCAGCTGGGG TG GGG		
	CTCGTCGACCCC AC CCC		
	C _ CA I		
GAM146 GFAP	GGAGCAGCTGGGG-TGGTGGGG 2092 TAGG	A AA	
	AGCAGCTGGGG TG GGGG		
	TCGTCGACCCC AC CCCC		
	_ _ CA		
GAM146 GGA3	CCCA-CCCCCACCACCCACCCC 2069 TC T	G TG	
	CCA CCCCCACCC CC CCC		
	GGT GGGGGGTGGG GG GGG		
	_ _ _ GT		
GAM146 GNA15	TCCCA-CCTCCCACCCGCCGCC 2106 T C	C	
	TCCCA CC CCCACCCGCCTGCC		
	AGGGT GG GGGTGGCGGGCGG		
	_ A I		
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	GAGCAGCTG GGG		
	CTCGTCGAC TCC		
	ACACG GAAG		
GAM146 GNAZ	GAGCAGCTGTG--TGCAGG 2076 TAGGAG	GGGA A	
	CAGCTG TG AGG		
	GTCGAC AC TCC		
	_ AC_ G		
GAM146 HMGCS1	TCCCATACCCCCACCC-CATGCC 2108 C	GCC I	
	TCCCAT CCCCCACCC TGCCC		
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	T GT_ I		
GAM146 HRMT1L2	CCCATCCCCCAGCC-CAGGCC 2071 TC	_ CCT	
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	GGTAGGGGGGT GGGT CGGG		
	_ C C_		
GAM146 HUS1	AGGAGCAGC-GGGG-TGAA 2056 T A I		
	AGGAGCAGC GGGG TGA		
	TCCTCGTCG CCCC ACT		
	_ _ T		
GAM146 HUS1	AGGAGCAGC-GGGG-TGAA 2056 TA T A GG		
	GGAGCAGC GGGG TGAA		

	CCTCGTCG CCCC ACTT		
	— — — GI		
GAM146 ICMT	AGGAGCAGCTCG---TGAAGGGG 2063 _	GGGGA	
	GGAGCAGCT TGAAGGG		
	CCTCGTCGA ACTTCCC		
	T GC__		
GAM146 ICMT	AGGAGCAGCTCG---TGAAGGGG 2063 TA	GGGGA	
	GGAGCAGCT TGAAGGG		
	CCTCGTCGA ACTTCCC		
	— GC__		
GAM146 ICOS	TAGGAGCAGATGTGGA-GACAGGG 2094	C__ GA GI	
	TAGGAGCAG TGGGGAT AGGG		
	ATCCTCGTC ACCTCTG TCCC		
	TAC — II		
GAM146 ICOS	TAGGAGCAGATGTGGA-GACAGGG 2094	C__ GA I	
	AGGAGCAG TGGGGAT AGG		
	TCCTCGTC ACCTCTG TCC		
	TAC — I		
GAM146 IVD	GAGCAGCTGGGCAGGAGGG 2075	GATGAAGII	
	GAGCAGCTGGG		
	CTCGTCGACCC		
	GTCCTCCCI		
GAM146 IVD	GAGCAGCTGGGCAGGAGGG 2075 TAGGAG	GAT A	
	CAGCTGGG GA GGG		
	GTCGACCC CT CCC		
	GTC —		
GAM146 KCNK3	GGAGACACAGCTGGGGATGAGGAAGGGG2082 GAG	— I	
	CAGCTGGGGATGA AGGG		
	GTCGACCCCTACT TCCC		
	— CCT I		
GAM146 KCNK3	GGAGACACAGCTGGGGATGAGGAAGGGG2082 T GA	— III	
	AG GCAGCTGGGGATGA AGGGG		
	TC TGTGACCCCTACT TCCCC		
	_ TG CCT TCI		
GAM146 KCNK4	TCCCTGCACCCACCCGCC 2102 ATCC	TGCC	
	TCCC CCCCACCCGCC		
	AGGG GGGGTGGGCGG		
	ACGT IIIC		
GAM146 KCNK7	AGCAGCT-GGGATGGTGGGG 2045 _	G AA I	
	GCAGCTGGG ATG GGG		

	CGTCGACCC TAC CCC		
	T _ CA I		
GAM146 MAG	AGGGGCAGCTGGGAAGGAGGGGG 2064 _ A	T A I	
	GG GCAGCTGGGGA GA GGG		
	II IIIIIIIII II III		
	CC CGTCGACCCTT CT CCC		
	C _ C C I		
GAM146 MAG	AGGGGCAGCTGGGAAGGAGGGGG 2064 TA A	T A I	
	GG GCAGCTGGGGA GA GGGG		
	II IIIIIIIII II IIII		
	CC CGTCGACCCTT CT CCCC		
	C _ C C T		
GAM146 MAP3K12	CCCCTCCCCCACCC-CCT 2067 T A	G C	
	CCC TCCCCCACCC CCTG		
	III IIIIIIIII IIII		
	GGG AGGGGGGTGGG GGAT		
	_ _ _ I		
GAM146 MT3	AGCAGCAGCTGGAGGCGGTGAACGGG 2052 GGA	A__ G I	
	GCAGCTGGGG TGAA GG		
	IIIIIIII IIII II		
	CGTCGACCTC ACTT CC		
	_ CGCC G I		
GAM146 MT3	AGCAGCAGCTGGAGGCGGTGAACGGG 2052 TA G	A__ G II	
	G AGCAGCTGGGG TGAA GGG		
	I IIIIIIIII IIII III		
	C TCGTCGACCTC ACTT CCC		
	_ G CGCC G GI		
GAM146 MTMR2	GGTGAAGCGGGAGGGATGAAGG 2087 _ AGCT	I	
	GAGC GGGGATGAAG		
	IIII IIIIIIIII		
	TTCG TCCCTACTTC		
	C CCC_ I		
GAM146 MTMR2	GGTGAAGCGGGAGGGATGAAGG 2087 TA AGCT	G	
	GGAGC GGGGATGAAGGG		
	IIII IIIIIIIII		
	CTTCG TCCCTACTTCCT		
	A_ CCC_ G		
GAM146 MUC3B	AGCAGCTGGGGTATTTAGGG 2042 _ GA II		
	AGCAGCTGGGG AT AGG		
	IIIIIIII II III		
	TCGTCGACCCC TA TCC		
	A AA CI		
GAM146 MUC3B	AGCAGCTGGGGTATTTAGGG 2042 TAGGAGCA _ GA		
	GCTGGGG AT AGGG		
	IIIIII II IIII		
	CGACCCC TA TCCC		
	_ A AA		
GAM146 NAP1L3	GGAGCTGGAGCTGGGGATGCAGAGG 2083 GAGC	A I	
	AGCTGGGGATG AGGG		
	IIIIIIII IIII		

	TCGACCCCTAC TCTC			
	GACC G I			
GAM146 NAP1L3	GGAGCTGGAGCTGGGGATGCAGAGG	2083	TA__ AGC	A II
	GGAGC TGGGGATG AGGGG			
	CCTCG ACCCCTAC TCTCC			
	TCGA __ G GG			
GAM146 NDST1	AGGAGCAGCTGGGAACGGAATGG	2053		AAGGI
	GAGCAGCTGGGGATG			
	CTCGTCGACCCTTGC			
	CTTAI			
GAM146 NDST1	AGGAGCAGCTGGGAACGGAATGG	2053	TA _ G I	
	GGAGCAGCTGGGGATG AA GGG			
	CCTCGTCGACCCTTGC TT CCT			
	_ C A I			
GAM146 NGB	GGAGCGGGTTGGTGTATGAAGGG	2088	G AGC_ G I	
	AGC TGG GATGAAGG			
	TCG ACC CTACTTCC			
	_ CCCA A I			
GAM146 NGB	GGAGCGGGTTGGTGTATGAAGGG	2088	TAGG AGC_ G G	
	AGC TGG GATGAAGGG			
	TCG ACC CTACTTCCC			
	_ CCCA A G			
GAM146 NRXN2	GGAGCGGGGTAGGGATGAAGCGG	2084	AGC_ GGI	
	AGC TGGGGATGAAG			
	TCG ATCCCTACTTC			
	CCCC GII			
GAM146 NRXN2	GGAGCGGGGTAGGGATGAAGCGG	2084	TAGG AGC_ G I	
	AGC TGGGGATGAAG GG			
	TCG ATCCCTACTTC CC			
	_ CCCC G T			
GAM146 NRXN2	TCCCA-CCCCCACC--CCTGC	2105	T GC C	
	TCCCA CCCCCACCC CTGC			
	AGGGT GGGGGGTGGG GACG			
	_ _ I			
GAM146 OTP	GGCGCAGCTGGGTGGGAAGGG	2091	GA GAT I	
	GCAGCTGGG GAAGG			
	CGTCGACCC CTTCC			
	CG ACC I			
GAM146 OTP	GGCGCAGCTGGGTGGGAAGGG	2091	TAGGA GAT	
	GCAGCTGGG GAAGGGG			

	CGTCGACCC CTTCCCT		
	G_____ ACC		
GAM146 PAFAH1B1	CCCTCCCCCACCCTACTG	2065 TCCCA	GC CC
	TCCCCCACCCT CTG		
	AGGGGGGTGGG GAC		
	G_____ GT CT		
GAM146 PCSK2	AGGCGGAGCTGGGGAGGGAGGG	2061 AGC	TGA I
	GG AGCTGGGGA AGG		
	CC TCGACCCCT TCC		
	GCC CCC I		
GAM146 PCSK2	AGGCGGAGCTGGGGAGGGAGGG	2061 TA AGC	TGA G
	GG AGCTGGGGA AGGG		
	CC TCGACCCCT TCCC		
	___ GCC CCC G		
GAM146 PKD2	TCCCCCACCCTACTCCCC	2111 TC	CCCA C CC
	CCATCCC CCGC TG		
	GGTGGGG GGGTG AC		
	___ TGAG C II		
GAM146 PRKACG	TCCCATCCCCCAAACCACC	2101	CAC TGCC
	TCCCATCCCCC CCGCC		
	AGGGTAGGGGG GGTGG		
	TTT IIIC		
GAM146 PRX	TCCCATCCCAGCCCCAGCC-CTTGCCC2099	___ _ GCC	II
	TCCCATCCC CCA CCC TGCCC		
	AGGGTAGGG GGGT GGG ACGGG		
	TCG C A___ II		
GAM146 RASGRP2	CCCAT--CCCCAGCCTCCTGCCC	2070 TC	CCAC G
	CCATCCCC CC CCTGCCC		
	GGTAGGGG GG GGACGGG		
	___ TC___ A		
GAM146 SLC16A2	GAGCAGGGTGGGATGAAGGGG	2080 CTG	I
	AGCAG GGGATGAAGGG		
	TCGTC CCCTACTTCCC		
	CCA I		
GAM146 SLC16A2	GAGCAGGGTGGGATGAAGGGG	2080 TAGGAG	CTG
	CAG GGGATGAAGGGG		
	GTC CCCTACTTCCCC		
	___ CCA		
GAM146 SLC23A1	GAGCAGCTGGAAGTGAAGG	2074	GA II
	GAGCAGCTGGG TGAAG		

	CTCGTCGACCT ACTTC			
	TC CI			
GAM146 SLC23A1	GAGCAGCTGGAAGTGAAGG	2074	TAGGAG	GA G
	CAGCTGGG TGAAGG			
	GTCGACCT ACTTCC			
	_____ TC G			
GAM146 SORCS3	CCCCTCCCCCACCCT	2068	T A	G GCC
	CCC TCCCCCACCCT			
	GGG AGGGGGGTGGG GGA			
	— — G All			
GAM146 SPTBN2	GAGCAGCTGGAGATGGAGTGG	2078		A GGI
	AGCAGCTGGGGATG AG			
	TCGTCGACCTCTAC TC			
	C ACI			
GAM146 SPTBN2	GAGCAGCTGGAGATGGAGTGG	2078	TAGGAG	A _ G
	CAGCTGGGGATG AG GG			
	GTCGACCTCTAC TC CC			
	_____ C A G			
GAM146 SYNGR1	AGG-GCAGCT-GGGAGGAA	2054	A	ATGAI
	AGG GCAGCTGGGG			
	TCC CGTCGACCCT			
	— CCTTI			
GAM146 SYNGR1	AGG-GCAGCT-GGGAGGAA	2054	TA A	AT G
	GG GCAGCTGGGG GAAG			
	CC CGTCGACCCT CTTT			
	— — C_ I			
GAM146 SYNGR1	AGGAACAGCTGGGGCAGAA	2055		ATGAI
	AGGAGCAGCTGGGG			
	TCCTTGTCGACCCC			
	GTCTTI			
GAM146 SYNGR1	AGGAACAGCTGGGGCAGAA	2055	TA	AT GGG
	GGAGCAGCTGGGG GAA			
	CCTTGTCGACCCC CTT			
	_____ GT GII			
GAM146 TBXAS1	CCCTCCCCCACC CGGCAGCC	2066	TCCCA	CCT C
	TCCCCCACC CGC			
	AGGGGGGTGGGC CGG			
	G_____ CGT A			
GAM146 TGFB1	AGGAGACAGGCCGGGATGAAGG	2049	G _	I
	GGA CAG CTGGGGATGAAG			

	TCT GTC GGCCCCTACTTC		
	_ C I		
GAM146 TGFB1	AGGAGACAGGCCGGGGATGAAGG	2049 TA	_ _ GGI
	GGAG CAG CTGGGGATGAAGG		
	CCTC GTC GGCCCCTACTTCC		
	_ T C GII		
GAM146 TMEM1	TCCC-TCCCCC-ACCCGCCTCCCC	2107 ATC	G
	TCCC CCCCCACCCGCCT CCC		
	AGGG GGGGGTGGGCGGA GGG		
	A_ G		
GAM147 ADRA1A	CAGGTGGGTTTGGCTGGGGGTGA	2115 CT_	___ AGGGI
	CAG GGTTT TGGGGGTGA		
	GTC CAAA ACCCCCACT		
	CAC CCG IIIGG		
GAM147 ATP11B	CTGGTTTTGGCAGATAAGGG	2122 CAGCTG	G TG
	GTTTTGG GG AAGGG		
	CAAAACC TC TTCCC		
	G TA		
GAM147 ATP8A2	CAGCAGGTGT-GGGGGTGAGGGG	2121 T TT	A I
	CAGC GGT TGGGGGTGA GGG		
	GTCG CCA ACCCCCACT CCC		
	T C_ C I		
GAM147 G6PC	CAGCTTTTTTTGGGGG-GTAGG	2120 GG	TGA G
	CAGCT TTTTGGGGG AGG		
	GTCGA AAAACCCCC TCC		
	AA CA_ I		
GAM147 NCYM	CAGCTGGTTCTCAGAGTGCAG	2119 G	A GG
	CAGCTGGTTTT GGGGTG AG		
	GTCGACCAAGA TCTCAC TC		
	G G II		
GAM147 OTC	AGCTA-TTTTGGGGGTGCAAG	2114 CA G	_ G
	GCTG TTTTGGGGGTG AAGG		
	CGAT AAAACCCCCAC TTCT		
	_ _ G I		
GAM147 PIN1	GGTTTAATTGGGGGTGAAAGG	2124 CAGCTGGTT	
	TTGGGGGTGAAGGG		
	AACCCCACTTTCC		
	TT_____		
GAM147 RNASE2	CAGCTGGTTGTTCTGGGGTTCAGGG	2116 TTG_	GA II
	CAGCTGGTT GGGGT AGGG		

	GTCGACCAA	CCCCA	TCCC	
	CAAGA	AG	II	
GAM147 SLC22A12	GCTGGGTTTGGGGGT	TAAAG	2123	CAGC T G G
	TGG	TTTGGGGGT	AAG	
	ACC	AAACCCCCA	TTC	
	___	C A A		
GAM147 SOX12	CAGCTGGTTTGGGGG	CGTG	2117	T AAGG
	CAGCTGGTTT	GGGGGTG		
	GTCGACCAAA	CCCCCGC		
	—	ACII		
GAM147 TIMP3	CAGCAGGACTTGGG	GTGAAG	2118	T TTTTG GG
	CAGC	GG GGGGTGAAG		
	GTCG	CC CCCCACTTC		
	T	TGAA_ II		
GAM148 ADAMTS13	TGGAATGGGA--CAGGC--	CTGC	2131	TCAC GA
	TGGAATGGGAT	GC CTGC		
	ACCTTACCCTG	CG GACG		
	TC_ _			
GAM148 GRIN2A	GAATGGGATAATGCAGG	CGACT	2128	TGGA T_ C GCA
	ATGGGAT	CA GCGACT		
	TACCCTA	GT CGCTGA		
	___	TTAC C GTI		
GAM148 KCNJ15	ATGGGATTC-TGCTACTGC		2127	TGGAATGG AC G
	GATTC	GC ACTG		
	CTAAG	CG TGAC		
	___	A_ A		
GAM148 MFGE8	TGGAATGGG---CACGCTGGG	CTGC	2130	ATT GA_ A
	TGGAATGGG	CACGC CTGC		
	ACCTTACCC	GTGCG GACG		
	___	ACCC I		
GAM148 VBP1	GGGATGCGAG-CGCGC	GACTGC	2129	T A G TTCA A
	GGA	TG GA CGCGACTGC		
	CCT	AC CT GCGCTGACG		
	_ _	G CGC_ G		
GAM149 CASP8	TCATCGTGGGGCTTGATCTCAA		2139	TATC AG_ G
	ATCGTGGGGC	CTCAAGA		
	TAGCACCCCG	GAGTTTT		
	___	AACTA I		
GAM149 GRAP2	TCTTGTGGGCAGCTCCAGA		2140	TATCATCGTG A
	GGGCAGCTC	AGA		

	CCCGTCGAG TCT	
	A _____ G	
GAM149 MAP3K14	CAT-GTGGG-CAGCTCAAGA 2135 TATCATCGTG	
	GGGCAGCTCAAG	
	CCTGTCGAGTTC	
	CA _____	
GAM149 NESH	TATC-TCTGTGGGGCAG-TCA 2136 A _ C AGA	
	TATC TC GTGGGGCAG TCA	
	ATAG AG CACCCCGTC AGT	
	_ A _	
GAM149 PACSIN1	CATCGTGGGTGCAG-GCAGGAG 2134 TATCAT _ CT A	
	CGTGGG GCAG CA GAG	
	GCACCC CGTC GT CTC	
	_____ A C_ C	
GAM149 PROX1	TCAGC-TGGGCACAGCTCAAGA 2138 TATCATCG _	
	TGGG GCAGCTCAAGAG	
	ACCC TGTCGAGTTCTT	
	TCG_____ G	
GAM149 ZNF148	TATCATCGTATATCAGCTTAA 2137 GGG CAAGAG	
	TATCATCGTG CAGCT	
	ATAGTAGCAT GTCGA	
	ATA ATT	
GAM150 ACRV1	TGAGAG--AA--AGAGTTGGAG 2154 TTAA	
	TGAGAG GGAGAGTTGGAG	
	ACTCTC TTTCTCAACCTC	

GAM150 ACRV1	TGAGAG--AA--AGAGTTGGAG 2154_ TTAA	
	GAGAG GGAGAGTTGGA	
	CTCTC TTTCTCAACCT	
	A _____	
GAM150 BTG2	GAGGGTTAGAGGAGAGTTG 2146 A _	
	GAG GTTA AGGAGAGTT	
	CTC CAAT TCCTCTCAA	
	C C CI	
GAM150 BTG2	GAGGGTTAGAGGAGAGTTG 2146 TG A _ GAGG	
	AG GTTA AGGAGAGTTG	
	TC CAAT TCCTCTCAAC	
	_ C C A	
GAM150 F8	AGAGTTAAGTTAAATTGGATGC 2144 GA GGI	
	GAGTTAAG GAGTTGGA	

	CTCAATTC TTTAACCT			
	AA ACI			
GAM150 F8	AGAGTTAAGTTAAATTGGATGC 2144 TGAG GA G			
	AGTTAAG GAGTTGGA GC			
	TCAATTC TTTAACCT CG			
	____ AA A			
GAM150 FGR	TGAGATAAAAGGAGAGTAGGA 2153 GTT T GGC			
	TGAGA AAGGAGAGT GGA			
	ACTCT TTCCTCTCA CCT			
	ATT T III			
GAM150 FGR	TGAGATAAAAGGAGAGTAGGA 2153 GTT T I			
	GAGA AAGGAGAGT GG			
	CTCT TTCCTCTCA CC			
	ATT T I			
GAM150 GPR4	TGAGAGGGAA--A-AGTTGGAGG 2156 TTAA			
	TGAGAG GGAGAGTTGGAGG			
	ACTCTC CTTTTCAACCTCC			
	C____			
GAM150 GPR4	TGAGAGGGAA--A-AGTTGGAGG 2156_ TTAA			
	GAGAG GGAGAGTTGGAG			
	CTCTC CTTTTCAACCTC			
	A C____			
GAM150 HOXC6	TGTGA-TTAGGGGAGAGTTGGTGG 2151 A GTTAA AI			
	GA GGAGAGTTGG			
	CT CCTCTCAACC			
	A AATCC AI			
GAM150 HOXC6	TGTGA-TTAGGGGAGAGTTGGTGG 2151 TGA GTTAA A CI			
	GA GGAGAGTTGG GG			
	CT CCTCTCAACC CC			
	ACA AATCC A II			
GAM150 KPNA3	TGAGATTGTTAAGGAGAGTT 2150 ____ GGAGG			
	TGAGA GTTAAGGAGAGTT			
	ACTCT CAATTCCTCTCAA			
	AA IIICG			
GAM150 KPNA3	TGAGATTGTTAAGGAGAGTT 2150 ____ III			
	TGAGA GTTAAGGAGAGT			
	ACTCT CAATTCCTCTCA			
	AA AII			
GAM150 MAML1	AGAGTTAAGGGCAGTAGAAG 2143 AG T I			
	GAGTTAAGG AGT GGA			

	CTCAATTCC TCA CTT		
	CG T I		
GAM150 MAML1	AGAGTTAAGGGCAGTAGAAG	2143 TGAG	AG T
	AGTTAAGG AGT GGAGG		
	TCAATTCC TCA CTTCT		
	_____ CG T		
GAM150 MAPK10	GAGGATGAAGAAGAGTTGGAGG	2148 AG T	I
	AG T AAGGAGAGTTGGAG		
	TC A TTCTTCTCAACCTC		
	CT C I		
GAM150 MAPK10	GAGGATGAAGAAGAGTTGGAGG	2148 TG AG T	C
	AG T AAGGAGAGTTGGAGG		
	TC A TTCTTCTCAACCTCC		
	___ CT C T		
GAM150 MME	TGGGA-TTCGGGAGAAGTTGGAGGC	2152 A GTTAA	_ I
	TG GA GGAGA GTTGGAGGC		
	AC CT CCTCT CAACCTCCG		
	C AAGC_ T I		
GAM150 MME	TGGGA-TTCGGGAGAAGTTGGAGGC	2152 GAGA AA	_ I
	GTT GGAGA GTTGGAGG		
	TAA CCTCT CAACCTCC		
	CCC_ GC T I		
GAM150 MYEOV	GAGAGGGTAGGAGAGTTGG	2147 TTA	II
	GAGAG AGGAGAGTTG		
	CTCTC TCCTCTCAAC		
	CCA CI		
GAM150 MYEOV	GAGAGGGTAGGAGAGTTGG	2147 T A TA	AGG
	GAG GT AGGAGAGTTGG		
	CTC CA TCCTCTCAACC		
	T C _ CII		
GAM150 PDE4B	AGTTAAAAGTACTGTTGGAGGC	2145 GTTAAGGAGA	I
	GTTGGAGG		
	CAACCTCC		
	ATTTTCATGA I		
GAM150 PDE4B	AGTTAAAAGTACTGTTGGAGGC	2145 T TAAGGAGA	
	GAGAGT GTTGGAGGC		
	TTTTCA CAACCTCCG		
	_ TGA_____		
GAM150 STK38	GTTATGGGAAGTTGGAGGC	2149 A AG	II
	GTTA GG AGTTGGAGG		

	CAAT CC TCAACCTCC	
	A CT GI	
GAM150 TEM7	TGAGAGACAAGG--AGTTGGAG 2155 TTA A G	
	TGAGAG AGG GAGTTGGAG	
	ACTCTC TTC CTCAACCTC	
	TG_ _ I	
GAM150 TEM7	TGAGAGACAAGG--AGTTGGAG 2155_ TTA A I	
	GAGAG AGG GAGTTGGA	
	CTCTC TTC CTCAACCT	
	A TG_ _ I	
GAM151 ATP5G2	CCAACTGTGGAAAAGAAATAT 2168 TACC CTT C	
	AACTGTGGA GGAATAT	
	TTGACACCT CTTTATA	
	____ TTT T	
GAM151 CNGB3	ACCATCTTTGGGGGACTTGGAA 2161 TA A GT____ TATC	
	CCA CT GGACTTGGAA	
	GGT GA CCTGAACCTT	
	_ A AACCC T	
GAM151 ENO2	CAACTGTGGAACGTGGCAT 2165 TACCAA _T AATAT	
	CTGTGGA C TGG	
	GACACCT G ACC	
	____ T C GTACC	
GAM151 FZD4	ACCACCTGTAAGTACTGACTTGGAA 2160 TA A ____ TATC	
	CCA CTGTG GACTTGGAA	
	GGT GACAT CTGAACCTT	
	_ G TGA C	
GAM151 GAS1	ACCAA--GTTGACTTGGAA 2162 TA CT G TA	
	CCAA GT GACTTGGAA	
	GGTT CA CTGAACCTT	
	_ _ A TI	
GAM151 PIM1	CAGCTATGGAAGCTTGGAAATA 2166 TACCAA ____ TC	
	CTGTGGA CTTGGAATA	
	GATACCT GAACCTTAT	
	____ TC CC	
GAM151 PLGL	ACCAACTGTGGA--TGGAA 2163 TA CT TA	
	CCAACTGTGGA TGGAA	
	GGTTGACACCT ACCTT	
	_ _ TI	
GAM151 PTPN2	ACCAACTGTTTACCT-GACTATC 2164 TA GG AA	
	CCAACTGT ACTTGG TATC	

	GGTTGACA TGGACT ATAG	
	___ AA G_	
GAM151 RNH	TACCAACTG-GGA---GGAA 2169 T CTT T	
	TACCAACTG GGA GGAA	
	ATGGTTGAC CCT CCTT	
	___ I	
GAM151 TIMP3	AAATGTCAACTTGGAATGTC 2159 TACCAACT G AT	
	GT GACTTGGAAT	
	CA TTGAACCTTA	
	___ G CA	
GAM151 ZNF80	CCAACTGTGTCC--GGAAT 2167 TACC GACT A	
	AACTGTG TGGAAT	
	TTGACAC GCCTTA	
	___ AG_ A	
GAM152 ABCB8	TGGCAGCGACCACACCTCA 2180 ACT TTGC	
	TGGCAG TCACACCTCA	
	ACCGTC GGTGTGGAGT	
	GCT IIIT	
GAM152 CDC23	TGGCAGACTT---TCCTCCTTTCT 2181 CACA ATTG	
	TGGCAGACTT CCTC CT	
	ACCGTCTGAA GGAG GA	
	A___ GAAA	
GAM152 CDKN1A	GGCAG-CTGCTCACACCTCA 2175 TG AC_ TTGC	
	GCAG TTCACACCTCA	
	CGTC GAGTGTGGAGT	
	___ GAC CIII	
GAM152 CYP27B1	GCATACTTCACA---CATTG 2174 TGGCAG CTC	
	ACTTCACAC ATTG	
	TGAAGTGTG TAAC	
	TA___	
GAM152 DCTN1	GGCA-ACTTCACA-CACATAGC 2177 TG A CT T	
	GCAG CTTCACAC CAT GC	
	CGTT GAAGTGTG GTA CG	
	___ _ T_ T	
GAM152 FLNB	GGCAAATTCCTACACCTCATTTCT 2176 TG ___ TC GCTII	
	GCAGA CT ACACCTCATT	
	CGTTT GG TGTGGAGTAA	
	___ TAA GA AGACI	
GAM152 MMP15	TGGCAGACTCCACTCGCTCA 2179 AC_ TTGC	
	TGGCAGACTTCAC CTCA	

	ACCGTCTGAGGTG GAGT			
	AGC IIIT			
GAM152 PDGFRA	CAAAC TTCACACACCACTG	2172	TGGCAG	C C
	ACTTCACAC TCATTG			
	TGAAGTGTG GGTGAC			
	_____ T T			
GAM152 TARBP2	CAGGCT-C-CACCTCATTGC	2173	TGGCAGAC	A
	TTC CACCTCATTG			
	GAG GTGGAGTAAC			
	C_____ _			
GAM152 XK	TGGCT-ACTCCCACACCTCA	2178	AG _ TTGC	
	TGGC ACTTC ACACCTCA			
	ACCG TGAGG TGTGGAGT			
	A_ G IIIT			
GAM153 GAS1	GCCAACGGCGGGGGGCGCG	2190	CT	II
	GCC CGGCGGGGGGTGC			
	CGG GCCGCCCCCGCG			
	TT CI			
GAM153 GAS1	GCCAACGGCGGGGGGCGCG	2190	TGTCGCCCT	
	CGGCGGGGGGTGC			
	GCCGCCCCCGCGC			
	T_____			
GAM153 GRLF1	GCTCTCGCCTGGGGGGTGC	2189	C GC_ II	
	GC CTCG GGGGGGTG			
	CG GAGC CCCCCAC			
	A GGA GI			
GAM153 GRLF1	GCTCTCGCCTGGGGGGTGC	2189	TG CTCGGC G	
	TCGCC GGGGGGTGC			
	AGCGG CCCCCACG			
	_____ A_____ G			
GAM153 HPCA	TGTTGCCTCTGGGATTGGGGGGTGC	2193	C _ C C_ GGII	
	TGT GCC CT GG GGGGGGTGC			
	ACA CGG GA CC CCCCCACG			
	A A C TAA IIIG			
GAM153 HPCA	TGTTGCCTCTGGGATTGGGGGGTGC	2193	GTC _ C C_ I	
	GCC CT GG GGGGGGTG			
	CGG GA CC CCCCCAC			
	_____ A C TAA I			
GAM153 IFI35	CCTTGGCGGGGGGTGGGG	2186	C _ CGII	
	CCT GGCGGGGGG TG			

	GGA CCGCCCCC AC			
	A C CCCI			
GAM153 LBX1	CCCTCGGCGGTCCGGTCCGG	2184	GG_ G II	
	CCCTCGGCGG GGT CG			
	GGGAGCCGCC CCA GC			
	AGG G CI			
GAM153 LBX1	CCCTCGGCGGTCCGGTCCGG	2184	TGTC CC_ _ GCG	
	GC TCGG CGGGGGGT			
	CG GGCC GCCCTCCG			
	C_ CCA AG III			
GAM153 PTPRF	CCCACGGCGGGGGTGGCGG	2185	T GT II	
	CCC CGGCGGGGG GCG			
	GGG GCCGCCCCC CGC			
	T AC CI			
GAM153 SLC6A8	GCCCCCTG-GAGGGGTGCGG	2192_	GGC I	
	CCCTC GGGGGGTGCG			
	GGGGG CTCCCCACGC			
	C AC_ I			
GAM153 SUFU	GCCAGCGGCG--GGGTGCGG	2191	CCC _ I	
	TCGGCGG GGGGTGCG			
	GGTCGCC CCCCACGC			
	C_ G I			
GAM153 TEF	CGCCCG-GGCGGGGGGCACGG	2188_	TC TG I	
	GCCC GGCGGGGGG CG			
	CGGG CCGCCCCC GC			
	G C_ GT I			
GAM153 TEF	CGCCCG-GGCGGGGGGCACGG	2188 ____	T GGC	
	TG CGCCCTC			
	GC GTGGGGG			
	G _ GCG			
GAM153 VGF	CGCGCGCGGCGGGGGCGCGCGG	2187_	CCT _ I	
	GC CGGCGGGGG GTGCG			
	CG GCCGCCCCC CGCGC			
	G C_ G I			
GAM153 VGF	CGCGCGCGGCGGGGGCGCGCGG	2187	TGTC CCT _	
	GC CGGCGGGGG GTGCGG			
	CG GCCGCCCCC CGCGCC			
	_ C_ G			
GAM154 CRIM1	GGCTTCCTCACTGCCTACT	2202	TGCGGC GC A	
	TTCCTCG GTCTACT			

		AAGGAGT CGGATGA		
		_____ GA C		
GAM154 FZD4		GCCGCGTCCGTTCCGGCGTCT	2197 TGCG T	___ ACTA
		GC TCC TCGGCGTCT		
		CG AGG AGCCGCAGA		
		GG_ C CA GIII		
GAM154 HPS1		TGGGGCTTCCTCCCCATCT	2203 C	GG ACTA
		TG GGCTTCCTC CGTCT		
		AC CCGAAGGAG GTAGA		
		C GG IIIC		
GAM154 MNT		CGGCTTCCTC-CCG-CTAC	2196 TGCG	GG T T
		GCTTCCTC CG CTAC		
		CGAAGGAG GC GATG		
		_____ G_ _ T		
GAM154 MYO1D		GCTGCT-CCTCGGCGCCTTCT	2198 TGCG T	A A
		GCT CCTCGGCGTCT CT		
		CGA GGAGCCGCGGA GA		
		GA_ _ A G		
GAM154 NRXN3		GCGGCTTCCTCCGGATCT-CTA	2199 TG	_ C A C
		CGGCTTCCTC GG GTCT CTA		
		GCCGAAGGAG CC TAGA GAT		
		_____ G_ _ C		
GAM154 TGFB1		GGCTGCTCCTCGGCGACTCCT	2200 TGCG T	T A AC
		GCT CCTCGGCG CT CT		
		CGA GGAGCCGC GA GA		
		A_ _ T G AG		
GAM154 TNFSF7		GGCT-CCTGGGCGTCTACT	2201 TGCGGCT	C
		TCCT GGCGTCTACT		
		AGGA CCGCAGATGA		
		_____ C		
GAM155 ADCY7		CAGCATT-TGTGAGGGGGCGG	2209 TGGCAGCATCA	GA
		TG AGGGGGCG		
		AC TCCCCCGC		
		GTAA_____ AC		
GAM155 C18orf1		TGGGAGCATCAAGTGCAGGAGGGGGCGG	2219 C	T_____ A
		TGG AGCATCA GGA GGGGGCGG		
		ACC TCGTAGT CCT CCCCCGCC		
		C TCACGT _		
GAM155 CAV3		TGGGGGCATCATGGTGGGG	2224 CA	AA GCG
		TGG GCATCATGG GGGG		

	ACC CGTAGTACC CCCC		
	CC A_ III		
GAM155 CFL1	TGGCAGCATG--GGAAGGGGGAGG 2226	CAT	C
	TGGCAGCAT GGAAGGGGG GG		
	II		
	ACCGTCGTA CCTTCCCCC CC		
	C_ T		
GAM155 DAPP1	TGGCAACATCATGGAAGGG 2223	GGCG	
	TGGCAGCATCATGGAAGGG		
	ACCGTTGTAGTACCTTCCC		
	IIIG		
GAM155 DRIL1	GGCAGTGCAGGGTGGCAGGGGGCGG 2211 TG__	CATCA A	II
	GCAG TGG AGGGGGCGG		
	CGTC ACC TCCCCCGCC		
	CGTCA CC__ G CI		
GAM155 FOXF1	AGGAACATGGAAGGGGACGG 2207 TGGCAGCAT		
	CATGGAAGGGGGCG		
	GTACCTTCCCCTGC		
	T_____		
GAM155 HTR6	AGCCCCCTGGA-GGGGGCGG 2206 TGGCAGCATCA A		
	TGGA GGGGGCG		
	ACCT CCCCCG		
	GGG_____ -		
GAM155 IL1F5	TGGCAGGATTAAAGGGAAGGGGGTGG 2221	CATCAT__	C II
	TGGCAG GGAAGGGGG GG		
	II		
	ACCGTC CCTTCCCCC CC		
	CTAATTTC A II		
GAM155 MECP2	GGCAGAA--ATGGAAGGGG 2214 TG	CATC	C
	GCAG ATGGAAGGGGG		
	CGTC TACCTTCCCCT		
	_ TT_ I		
GAM155 MSF	TGGCAGCAT-GTCGAAGGGG 2225	CATG	GCG
	TGGCAGCAT GAAGGGG		
	ACCGTCGTA CTTCCCC		
	CAG_ III		
GAM155 NPEPPS	GGCGGCGAGCGAGGGAGGGGGCGG 2212 T_ _	ATCAT A	I
	GGC AGC GG AGGGGGCGG		
	CCG TCG CC TCCCCCGCC		
	CG C CT__ C G		
GAM155 NRXN2	GGCAGGA---GGAAGGGGGCG 2216 TG	CATCAT	
	GCAG GGAAGGGGGC		

	CGTC CCTTCCCCCG		
	___ CT___		
GAM155 PLIN	TGGCAGCATCATCAGGATGAGG 2220	___ A	GCGG
	TGGCAGCATCAT GGA GGGG		
	ACCGTCGTAGTA CCT CTCC		
	GT A G		
GAM155 PLOD3	GGGAGC-TCCGGAAGGGGGCG 2217	T C A A _	G
	GG AGC TC TGGAA GGGGGCG		
	CC TCG AG GCCTT CCCCCG		
	___ _ _ _ T G		
GAM155 POLH	TGGAAGGAAAATGGAAGGG 2222	C CATC	GGCG
	TGG AG ATGGAAGGG		
	ACC TC TACCTTCCC		
	T CTTT G		
GAM155 RAB2L	GCTGCACTCATGGAAGGTGG 2210	TGGCA _ _	CG
	GCA TCATGGAAGG GGG		
	CGT AGTACCTTCC CCC		
	A___ G A TI		
GAM155 SERPINH2	CAGCATCATGGTATCTGGGGC 2208	TGGCAG	AAG___ GG
	CATCATGG GGGGC		
	GTAGTACC CCCC		
	___ ATAGA GG		
GAM155 SOX4	GGAAGC-TCGTTGGAAGGGGGAGG 2213	TGGC A A_	C I
	AGC TC TGGAAAGGGG GG		
	TCG AG ACCTTCCCCC CC		
	CT___ _ CA T C		
GAM155 WNT3A	GGCAGCTGCAAAGAAGGGGGCG 2215	TG AT T	G
	GCAGC CA GGAAGGGGGCG		
	CGTCG GT TCTTCCCCCGC		
	___ AC T G		
GAM155 ZNF22	TGGCACCATCTCATGGAAG 2218	G ___	GGGGCG
	TGGCA CA TCATGGAAG		
	ACCGT GT AGTACCTTC		
	G AAG GGC		
GAM156 CASP8	TGGCACCATCGCAGTCTCCG 2238	GGA ___	TGA
	TGGCACCAT TGC CTTCG		
	ACCGTGGTA GCG GAGGC		
	___ TCA		
GAM156 CASP8	TGGCACCATCGCAGTCTCCG 2238	GGA ___	I
	GGCACCAT TGC CTTC		

	CCGTGGTA GCG GAGG			
	___ TCA I			
GAM156 CD83	CCATGCAACACTTCGTGAA 2234	GAT _	II	
	CCATG GC CTTCGTGA			
	GGTAC TG GAAGCACT			
	GT_ T TI			
GAM156 DISC1	GCACCA--GATGCCTTCTGGAA 2235	TG	GTGI	
	GCACCA GATGCCTTC			
	CGTGGT CTACGGAAG			
	___ ACCT			
GAM156 DISC1	GCACCA--GATGCCTTCTGGAA 2235	TGGC TG	G A	
	ACCA GATGCCTTC TG			
	TGGT CTACGGAAG AC			
	___ _ _ C			
GAM156 GCSH	ACCATGGATAATTTTCATGAA 2231	CC	I	
	CCATGGATG TTCGTGA			
	GGTACCTAT AAGTACT			
	TA I			
GAM156 HNRPF	ACCACGGATGCCTTCAGTG 2230		TII	
	ACCATGGATGCCTTCG			
	TGGTGCCTACGGAAGT			
	CAC			
GAM156 IFNGR2	CACCATGGATG--TACATGAA 2233	_ CCTT	I	
	ACCATGGATG CGTGA			
	TGGTACCTAC GTACT			
	G AT_ I			
GAM156 IFNGR2	CACCATGGATG--TACATGAA 2233	TGGCAC	CCTT	
	CATGGATG CGTGA			
	GTACCTAC GTACT			
	___ AT_			
GAM156 MTMR3	GGCACAAAACATGGATGCC 2236	___	IIIG	
	GGCAC CATGGATGC			
	CCGTG GTACCTACG			
	TTTT GIII			
GAM156 MTMR3	GGCACAAAACATGGATGCC 2236	TG	___	TTCGTGA
	GCAC CATGGATGCC			
	CGTG GTACCTACGG			
	___ TTTT TIIIAAG			
GAM156 PAICS	ACCATGGATAGGCTTCGGGA 2229	C_ TGII		
	ACCATGGATG CTTCG			

	TGGTACCTAT GAAGC			
	CC CCTI			
GAM156 SOX12	GGCACCATGGTGAATG-CTTC	2237	___	CTTIII
	GGCACCATGG ATGC			
	CCGTGGTACC TACG			
	ACT AAGIII			
GAM156 SOX12	GGCACCATGGTGAATG-CTTC	2237 TG	___	C GTGA
	GCACCATGG ATGC TTC			
	CGTGGTACC TACG AAG			
	___ ACT _ AIII			
GAM156 SQSTM1	CAACATTGCGGATGCCCTTCGTGA	2232 ACCA	_	I
	TGGATGCC TTCGTG			
	GCCTACGG AAGCAC			
	AAC_ G I			
GAM156 WNT6	TGGCGCCCTGG--GCCTTCGTG	2239	A A AT	A
	TGGC CC TGG GCCTTCGTG			
	ACCG GG ACC CGGAAGCAC			
	C G _ I			
GAM156 WNT6	TGGCGCCCTGG--GCCTTCGTG	2239 _	A A AT	I
	GGC CC TGG GCCTTCGT			
	CCG GG ACC CGGAAGCA			
	A C G _ I			
GAM157 CA14	GAGAGAGAGCGAG-CGAGCTC	2257 TGAA		AA
	AGAGAGCGAG GAGTTCT			
	TCTCTCGCTC CTCGAGG			
	TC_ G_			
GAM157 CCKAR	AAAGAGACCTTGAAGAGTTC	2245 TGAA		GCGA
	AGAGA GAAGAGTTCT			
	TCTCT CTTCTCAAGG			
	___ GGAA			
GAM157 COL2A1	GAAAGAGAGGGGAGAAAAGT	2250 TG	C_	CT
	AAAGAGAG GAGAAGAGTT			
	TTTCTCTC CTCTTTTCAG			
	_ CC II			
GAM157 EGR3	TGAAAGAGATGGGAGAAG-GTT	2260	GC_	A CTA
	TGAAAGAGA GAGAAG GTT			
	ACTTTCTCT CTCTTC CAA			
	ACC _ III			
GAM157 ELK4	GAGAGAGAGCGAG-AGAGT	2256 TGAA		A TC
	AGAGAGCGAGA GAGT			

	TCTCTCGCTCT CTCA			
	TC__ _ CI			
GAM157 EPHX1	GAAAGAGAGC-TGTGGAGCTCT 2258 TG	GAGAA	A	
	AAAGAGAGC GAGTTCT			
	TTTCTCTCG CTCGAGA			
	_ ACAC_ C			
GAM157 EYA3	GAAAGAGAGAGAGATAGAG 2254 TG	C _	TTCT	
	AAAGAGAG GAGA AGAG			
	TTTCTCTC CTCT TCTC			
	_ T A TIII			
GAM157 EYA3	GAAAGAGAGAAAGAGAGAG 2252 TG	C _	TTCT	
	AAAGAGAG GAGA AGAG			
	TTTCTCTC TTCT TCTC			
	_ T C TIII			
GAM157 FVT1	GAAAGAGAGAGAGAGAGAG 2253 TG	C _	TTCT	
	AAAGAGAG GAGA AGAG			
	TTTCTCTC CTCT TCTC			
	_ T C TIII			
GAM157 GM2A	TGAAAGAGAGAGAGTCATAAAGA-TTCT2262	C A__ _	AIII	
	TGAAAGAGAG GAG AGAG TTCT			
	ACTTTCTCTC CTC TTTC AAGA			
	T AGTA T IIIA			
GAM157 GRM7	TGAAAGAGAATGGAAAGAG 2263	CGA	TTCT	
	TGAAAGAGAG GAAGAG			
	ACTTTCTCTT TTTCTC			
	ACC IIIA			
GAM157 KLF8	AAACATATGGATAAGAGTTCTA 2247 TGAAAGAGAGC G			
	GA AAGAGTTCTA			
	CT TTCTCAAGAT			
	TGTATAC__ A			
GAM157 MFRP	GAGAGATGAGGGTGGAGAGTTCTA 2248 TGAA	GC A__	I	
	AGAGA GAG AGAGTTCTA			
	TCTCT CTC TCTCAAGAT			
	_ A_ CCACC C			
GAM157 MYO1E	GAAAGAGTT-GAGAAGAGT 2255 TG	AGC	C	
	AAAGAG GAGAAGAGTT			
	TTTCTC CTCTTCTCAG			
	_ AA_ I			
GAM157 NCOA6	AAAGTGTATGGCGTGAGAAGAGTTCTA 2242 TGAAA	GA _	II	
	GA GC GAGAAGAGTTCTA			

	CT CG CTCTTCTCAAGAT			
	TCA__ AC CA AG			
GAM157 OLR1	AAACAGAGTTGAGAAGAGTTC 2243 TGAAAG C_ TA			
	AGAG GAGAAGAGTTC			
	TCTC CTCTTCTCAAG			
	TG__ AA TA			
GAM157 RAD52	GAAAGAGAGCAAGTTGAAGAG 2251 TG _ TTCTA			
	AAAGAGAGCGA GAAGAG			
	TTTCTCTCGTT CTTCTC			
	_ CAA CIIIA			
GAM157 RBL1	AAAGAGAGCTA-AAAAGTT 2244 TGAA GA C			
	AGAGAGC GAAGAGTT			
	TCTCTCG TTTTCAA			
	_ A_ T			
GAM157 SLC13A3	TGAAAGAGAGAGA-AAGTATCCTA 2265 C A A I			
	TGAAAGAGAG GAGA G GTTCTA			
	I			
	ACTTTCTCTC CTTT C TAGGAT			
	T _A I			
GAM157 SLC29A2	GAAGGAGACGTCGAGAAGAG 2249 TGAAA G_ TTCT			
	GAGA CGAGAAGAG			
	CTCT GCTCTTCTC			
	TTC_ GCA CII			
GAM157 SLC38A3	TGAAGGGAGATGGGAGAAGAGT 2259 A_ GC_ TCTA			
	TGAA GAGA GAGAAGAGT			
	ACTT CTCT CTCTTCTCA			
	CC ACC IIIA			
GAM157 TNFSF15	TGAAAGAGAGAGACAGGAG 2264 C GAA TTCT			
	TGAAAGAGAG GA GAG			
	ACTTTCTCTC CT CTC			
	T GTC IIIA			
GAM157 TNFSF5	TGAAAGAGAGAGATGGAGAG 2261 C GA_ TTCT			
	TGAAAGAGAG GA AGAG			
	ACTTTCTCTC CT TCTC			
	T ACC IIIA			
GAM157 TR2	AAAGA-AG--AAAAGAGTTCT 2246 TGAAAG C			
	AGAG GAGAAGAGTTC			
	TCTT CTTTTCTCAAG			
	_____ -			
GAM158 CDKN2C	TGCCACCTCTCGCGGTCCCCGG 2275 _ _ III			
	TGCCACCTCTC CG CCCCCG			

	ACGGTGGAGAG GC GGGGCC			
	C CA III			
GAM158 CDKN2C	TGCCACCTCTCGCGGTCCCCGG 2275	_ _	III	
	TGCCACCTCTC CG CCCCCG			
	ACGGTGGAGAG GC GGGGC			
	C CA CII			
GAM158 CPT2	GCCATCGGCTCCGCCCCGG 2270	CCT_	II	
	GCCA CTCCGCCCCG			
	CGGT GAGGCGGGGC			
	AGCC CI			
GAM158 CPT2	GCCATCGGCTCCGCCCCGG 2270	TG CCT_	I	
	CCA CTCCGCCCCGG			
	GGT GAGGCGGGGCC			
	_ AGCC T			
GAM158 FMOD	TGCCACGGGGGCTCTCCGCCC 2272	_____	CGGII	
	TGCCAC CTCTCCGCCC			
	ACGGTG GAGAGGCGGG			
	CCCCC IIIG			
GAM158 FMOD	TGCCACGGGGGCTCTCCGCCC 2272	_____	IIIG	
	TGCCAC CTCTCCGCC			
	ACGGTG GAGAGGCGG			
	CCCCC GIII			
GAM158 GATA6	GCCCCGCTCTCCGCCCCGG 2268	AC_	II	
	GCC CTCTCCGCCCCG			
	CGG GAGAGGCGGGGC			
	GGC CI			
GAM158 GATA6	GCCCCGCTCTCCGCCCCGG 2268	TG AC	I	
	CC CTCTCCGCCCCG			
	GG GAGAGGCGGGGCC			
	G_ GC C			
GAM158 KCNF1	TGGCACCGTCCTCCGCCCCGG 2273	C _	II	
	TG CACC TCTCCGCCCCGG			
	AC GTGG GGAGGCGGGGCC			
	C CA II			
GAM158 KCNF1	TGGCACCGTCCTCCGCCCCGG 2273	C _	III	
	TG CACC TCTCCGCCCCG			
	AC GTGG GGAGGCGGGGC			
	C CA CII			
GAM158 MIC2	TGCGCCCGCCCCGCCCCGG 2276	CA T	I	
	TGC CC CTCCGCCCCG			

	ACG GG GGGGCGGGGCC			
	CG C I			
GAM158 MIC2	TGCGCCCGCCCCGCCCGG	2276	CA T	II
	TGC CC CTCCGCCCCG			
	ACG GG GGGGCGGGGC			
	CG C CI			
GAM158 MLF2	TGCCACCTCCGTACGCCCC	2274	C__	GGI
	TGCCACCTCT CGCCCC			
	ACGGTGGAGG GCGGGG			
	CAT III			
GAM158 MLF2	TGCCACCTCCGTACGCCCC	2274	C__	III
	TGCCACCTCT CGCCC			
	ACGGTGGAGG GCGGG			
	CAT GII			
GAM158 MTCP1	GCCACCGCCCTCCGCCCCG	2271	__	III
	GCCACC TCTCCGCCCC			
	CGGTGG GGAGGCGGGG			
	CG CII			
GAM158 MTCP1	GCCACCGCCCTCCGCCCCG	2271	T_ A T	I
	GCC CC CTCCGCCCCG			
	TGG GG GAGGCGGGGCT			
	GG C _ I			
GAM158 PRDM2	GCCCCCTTCCTGCCGCCCGG	2269	A _ _	III
	GCC CCT CT CCGCCCCG			
	CGG GGA GG GCGGGGC			
	G A AC CII			
GAM158 PRDM2	GCCCCCTTCCTGCCGCCCGG	2269	TG A _ _	II
	CC CCT CT CCGCCCCG			
	GG GGA GG GCGGGGCC			
	G_ _ A AC CI			
GAM159 CCKBR	GCCTCGGTCCTTAAGTGA	2287	TAACGCCT	AGC _
	CGGTC AAC GGAG			
	GCCAG TTG CCTT			
	_____ GAA A			
GAM159 CLU	ACGCCTCGGTCAGCGGCGGA	2282	TAAC	AA
	GCCTCGGTCAGC CGGAG			
	CGGAGCCAGTCG GCCTT			
	_____ CC			
GAM159 DPYSL3	AACGGC---GACAGCAACGG	2280	TAACGCCT	_
	CGGT CAGCAACGG			

GCGG GTCGTTGCC
 T_____ CT
 GAM159 GLS CGCC---GACAGCAACGGA 2286 TAACGCCT T
 CGG CAGCAACGG
 ||| |||||
 GCT GTCGTTGCC

_____ -
 GAM159 HAS3 CGCCTCGGTGCAGTGCCGGAG 2285 TAACGC _ CAA C
 CTCGGT CAG CGGAG
 ||||| ||| |||||
 GAGCCA GTC GCCTC
 _____ C ACG C
 GAM159 NXF1 CCTCGGTACAGTCACGGGGC 2283 TAACGCCT AGCA A
 CGGTC ACGG GC
 ||||| ||| ||
 GTCAG TGCC CG
 CAGT_____ C
 GAM159 SLC4A10 TAACGCCTCTGGAATAAGCA 2288 _ TC_ ACGGAG
 TAACGCCTC GG AGCA
 ||||| || |||||
 ATTGCGGAG CC TCGT
 A TTAT |||CGA
 GAM159 SNRPN AACGCCTCGGGTA-CAACTGA 2281 TA TCA G G
 ACGCCTCGG GCAAC GA
 ||||| ||||| ||
 TGCGGAGCC TGTTG CT
 _____ CA_ A G
 GAM159 SNX6 AACGCACTCAGCCAGCAACGGA 2279 TA _ C
 ACGC CTCGGTCAGCAACGGAG
 ||| ||||| ||||| |||||
 TGCG GAGTCGGTCGTTGCCTT
 _____ T I
 GAM159 STK6 CGCCTCGGTGCCAGGAGCGGA 2284 TAACGC CA AAC
 CTCGGT GC GGAGC
 ||||| || |||||
 GAGCCA CG CCTCG
 _____ GGT
 GAM159 TSSC3 TAAGGCGCCCGT--GCAACGGAGC 2289 TAA_ T GTCA
 CGCC CG GCAACGGAGC
 ||||| || ||||| |||||
 GCGG GC CGTTGCCTCG
 ATTCC _ A_
 GAM160 AANAT CCCGGG--CAGCC-TGTGGTGCT 2293 TC AGAA C
 CCG CAGCC TGTGGTG
 ||| ||||| ||||| |||||
 GGC GTCGG ACACCACG
 _____ CC_ _
 GAM160 GPR30 TCCCCAGGAGGAGCACCTGTGGTG 2294 G AAC_ _ CTI
 TCCC AG AGC CCTGTGGTG
 ||||| || ||| ||||| |||||

	AGGG TC TCG GGACACCAC	
	G CTCC T III	
GAM160 MATN1	CCCG-GCCCAGCCCTGTCCTGC 2292 TC AGAA GG T	
	CCG CAGCCCTGT TGC	
	III III	
	GGC GTCGGGACA ACG	
	_ CGG_ GG T	
GAM161 ATSV	GACACCC--C-CCCACTCTCC 2306 TG TCT	
	ACACCCT CCCACTCTCC	
	TGTGGGG GGGTGAGAGG	
	— —	
GAM161 CELSR3	CCCTGCACAGCCACTCTCC 2303 TGACACCCTTCTC	
	CCACTCTCCT	
	GGTGAGAGGG	
	GTGTC_____	
GAM161 ECM2	ACACCCTTCTGCCAGCTTTCCT 2300 TGAC C _ C A	
	ACCCTTCT CCA CT TCCT	
	TGGGAAGA GGT GA AGGA	
	_____ C C A A	
GAM161 GADD45B	ACTCCCTTCTCCTCTCTCTC 2299 TGACA CA _	
	CCCTTCTCC CTCTC CT	
	GGAAGAGG GAGAG GA	
	A_____ A_ A	
GAM161 HNRPD	CCCTTCGCCTCCCACTCTC 2302 TGACACCCT CT	
	TCTCCCACTCTC	
	GGAGGGTGAGAG	
	GC_____ CG	
GAM161 HOXC4	TGCCTCTCTCTCTCCCACTCTC 2308 TGACA _ _ CTA	
	CC CT TCTCCCACTCTC	
	GG GA AGAGGGTGAGAG	
	AC_ A GAG III	
GAM161 IGFBP5	ACACCTCTTTTCTCCCACT 2297 TGAC _ _ CTCCT	
	ACC CT TCTCCCACT	
	TGG GA AGAGGGTGA	
	_____ A AA A	
GAM161 IL4R	CCCTTCTGTTCCCACTCTCCT 2304 TGACACCCTTCTC	
	CCACTCTCCT	
	GGTGAGAGGA	
	GACAA_____	
GAM161 PAX4	ACACCACCTCTCCCACTGCCCT 2298 TGAC _ C A	
	ACC CTTCTCCCACT TCCT	

		TGG GGAGAGGGTGA GGGA		
		____ T C C		
GAM161 PIP5K1A		CCCTTCTCCGTCTTCCTA	2305 TGACAC	C__ TCTCCT
		CCTTCT CCAC		
		GGAAGG GGTG		
		GAGGCA ATT IIIATC		
GAM161 RNF4		TGACTCCCTTTCTCCCACTCT	2309 A _	CCTA
		TGAC CCCTT CTCCCACTCT		
		ACTG GGGAA GAGGGTGAGA		
		A A IIIA		
GAM161 SLC6A8		TGCCTCCCTTCTCCTCTCTCCT	2310 ACA	CA_ AI
		TG CCCTTCTCC CTCTCCT		
		AC GGGAAGAGG GAGAGGA		
		GGA AGA		
GAM161 STK38		CACCCATTGTGC-ACTCTCCTA	2301 TGACAC	TTCTCC
		CC CACTCTCCTA		
		GG GTGAGAGGAT		
		____ TAACAC		
GAM161 TFF3		TGACACCC-TCCCGCCCTCTCC	2311	C A TA
		TGACACCCCTTCT CC CTCTCC		
		ACTGTGGGAGGG GG GAGAGG		
		C _		
GAM161 UBTF		GACCCCCCACCCTCTCTCC	2307 TG A T	TA
		AC CCCT CTCCCACTCTCC		
		TG GGGG GGGGGTGAGAGG		
		_ G T CI		
GAM162 ABR		GAGTGTGTCTGCTTGT-CCAACAT	2322 C	A G I
		GA TGTGTCTGCT GT CCGGCAT		
		CT ACACAGACGA CA GGTTGTA		
		C A _ I		
GAM162 ABR		GAGTGTGTCTGCTTGT-CCAACAT	2322 AC_	A G I
		TGTGTCTGCT GT CCGGCA		
		ACACAGACGA CA GGTTGT		
		CTC A _ I		
GAM162 ADRA2A		CTGTGTCTGCCTG-GAAGGCAT	2320 _	AGTGCC I
		TGTGTCTGCT GGCA		
		ACACAGACGG CCGT		
		G ACCTT_ I		
GAM162 ADRA2A		CTGTGTCTGCCTG-GAAGGCAT	2320 GACT	AGTGCC
		GTGTCTGCT GGCAT		

	CACAGACGG CCGTA
	_____ ACCTT_
GAM162 CYP17	GTGGCTGG--GTGCCGGCA 2324 T CTA I
	GTG CTG GTGCCGGC
	CAC GAC CACGGCCG
	C C_ T
GAM162 DGAT1	GACTGTGTCTGGCCTGCTGTGCCAT 2321 _ A GC_ G II
	GACTGTGTCTG CT GT CG CAT
	CTGACACAGAC GG CG GC GTA
	C A ACA G II
GAM162 DGAT1	GACTGTGTCTGGCCTGCTGTGCCAT 2321 GA_ T AG GI
	CTG GTCTGCT TGCCG
	GAC CGGACGA GCGGT
	ACA _ CA AI
GAM162 F2R	CTGTGTCTGACATGGCCCTGGCAT 2316 GACT C GT _ I
	GTGTCTG TA GCC GGCAT
	CACAGAC GT CGG CCGTA
	_____ T AC GA C
GAM162 F2R	CTGTGTCTGACATGGCCCTGGCAT 2316 TG C GT _ I
	TGTCTG TA GCC GGCA
	ACAGAC GT CGG CCGT
	_ T AC GA I
GAM162 FCER2	CTGTGTCTGTCCTCCTAGTG 2314 _____ IIIC
	CTGTGTCTG CTAGT
	GACACAGAC GATCA
	AGGAG CIII
GAM162 FCER2	CTGTGTCTGTCCTCCTAGTG 2314 GA_ G G CCGGCA
	CTGT TCT CTAGTG
	GACA GGA GATCAC
	CACA _ G ACIIIT
GAM162 HDAC4	TGTGTCTGCGCGTCGCCGGC 2327 TA _ II
	TGTGTCTGC GT GCCGG
	ACACAGACG CA CGGCC
	CG G GI
GAM162 HDAC4	TGTGTCTGCGCGTCGCCGGC 2327 GACTGT TA _ A
	GTCTGC GT GCCGGC
	CAGACG CA CGGCCG
	_____ CG G C
GAM162 HDAC7A	TGTGTCTGCACAGGGCCTGGGGCA 2326 GTGT _ T _ I
	CTGC TAG GCC GGC

	GACG GTC CGG CCG	
	____ T C ACC I	
GAM162 IL10RA	CTGTGTCTGATACTGTCTTGGCAT 2317 GACT	C G CC__ I
	GTGTCTG TA TG GGCAT	
	CACAGAC AT AC CCGTA	
	____ T G AGAA C	
GAM162 IL10RA	CTGTGTCTGATACTGTCTTGGCAT 2317 TG	C G CC__ I
	TGTCTG TA TG GGCA	
	ACAGAC AT AC CCGT	
	____ T G AGAA I	
GAM162 MAPK8IP1	CTGTGTCTGGCAGGGCGCGGCA 2315 GACT	C T _
	GTGTCTG TAG GC CGGCAT	
	CACAGAC GTC CG GCCGTG	
	____ C C C	
GAM162 MAPK8IP1	CTGTGTCTGGCAGGGCGCGGCA 2315 T	C T _ I
	GTGTCTG TAG GC CGGC	
	CACAGAC GTC CG GCCG	
	____ C C C I	
GAM162 OGT	TGTGTCTGCCCTAGATCCAGGC 2325	AGTG__
	TGTGTCTGCT CCGG	
	ACACAGACGG GGTC	
	GATCTA CGI	
GAM162 OGT	TGTGTCTGCCCTAGATCCAGGC 2325 GACTGT	AGTG__ _ AT
	GTCTGCT CC GGC	
	CAGACGG GG CCG	
	____ GATCTA T GA	
GAM162 SHANK2	CTGAGTTTGCTGGTGCAGG 2318 T C A CGI	
	CTG GT TGCT GTGC	
	GAC CA ACGA CACG	
	T A C TCCI	
GAM162 SHANK2	CTGAGTTTGCTGGTGCAGG 2318 GACTGT C A C CA	
	GT TGCT GTGC GG	
	CA ACGA CACG CC	
	CT__ A C T CC	
GAM162 UCP2	CTGTGTCTG-TCG-GCTGGC 2319	CTA __ CGI
	CTGTGTCTG GT GC	
	GACACAGAC CG CG	
	AGC AC	
GAM162 UCP2	CTGTGTCTG-TCG-GCTGGC 2319 GACT	CTAGT C
	GTGTCTG GC GGC	

	CACAGAC CG CCG		
	_____ AGC__ A		
GAM162 ZAP70	GTGTCTGCTGAGCTCCGGCA 2323	_ G	II
	GTGTCTGCT AGT CCGGC		
	III		
	CACAGACGA TCG GGCCG		
	C A TI		
GAM162 ZAP70	GTGTCTGCTGAGCTCCGGCA 2323	GA CTGTGT	_ G
	CTGCT AGT CCGGCA		
	III		
	GACGA TCG GGCCGT		
	_____ C A		
GAM163 ADAR	GCAGCCATCACACGGCAC 2340	T	_ II
	GCAGCCATC CCGCG CA		
	II		
	CGTCGGTAG GGTGC GT		
	T C GI		
GAM163 ADAR	GCAGCCATCACACGGCAC 2340	TCGC	T _ AGT
	AGCCATC CCGCG CAC		
	III		
	TCGGTAG GGTGC GTG		
	_____ T C GTI		
GAM163 ARHGDIA	CGGAGCCATCTCCACAGCCCTGT 2335	C	_ ACAGI
	AGCCATCTCCGC GC		
	TCGGTAGAGGTG CG		
	C T GGAI		
GAM163 ARHGDIA	CGGAGCCATCTCCACAGCCCTGT 2335	TCGC	_ ACA GI
	AGCCATCTCCGC GC GT		
	II		
	TCGGTAGAGGTG CG CA		
	CC__ T GGA GI		
GAM163 BAZ1B	CGCAGAGTTC-CCGCGCACA 2336	_ CCA T	I
	GCAG TC CCGCGCAC		
	II		
	CGTC AG GGCGCGTG		
	G TCA _ I		
GAM163 BAZ1B	CGCAGAGTTC-CCGCGCACA 2336	TC CCA T	GT
	GCAG TC CCGCGCACA		
	II		
	CGTC AG GGCGCGTGT		
	_ TCA _ GI		
GAM163 BCL7A	CGCCGCTCACTCACTCGCGCACAG 2333	_ A_ T C	TGI
	TCGC GC CA CTC GCGCACAG		
	II		
	GGCG TG GT GAG CGCGTGTC		
	C AG A _ _ TII		
GAM163 BCL7A	CGCCGCTCACTCACTCGCGCACAG 2333	GCA _ T	_ I
	GC CA CTC CGCGCACA		

	CG GT GAG GCGCGTGT		
	___ A _ TGA I		
GAM163 CDX1	GCAGCCA--TCAGAGCCCAGTG 2341	TCC G CAGI	
	GCAGCCATC GC CA		
	CGTCGGTAG CG GT		
	TCT G CACI		
GAM163 CDX1	GCAGCCA--TCAGAGCCCAGTG 2341 TCGC	TCCGC A	
	AGCCATC GC CAGT		
	TCGGTAG CG GTCA		
	___ TCT__ G		
GAM163 DIO3	CCCTCTCCGCGCGCGACAG 2332 _ A	ACAIII	
	CC TCTCCGCGC		
	GG AGAGGCGCG		
	G _ CGCTGT		
GAM163 FKBP1B	GCAGCCATCTCCAGC-CAC 2339	C All	
	GCAGCCATCTCCG GC		
	CGTCGGTAGAGGT CG		
	_ GTG		
GAM163 FKBP1B	GCAGCCATCTCCAGC-CAC 2339 TCGC	_ G AG	
	AGCCATCTCC GC CAC		
	TCGGTAGAGG CG GTG		
	___ T _ GA		
GAM163 KCNK3	TCGCCGC--TCTCCGCGCA 2343 A CA	CAG	
	TCGC GC TCTCCGCGCA		
	AGCG CG AGAGGCGCGT		
	G _		
GAM163 KCNK3	TCGCCGC--TCTCCGCGCA 2343 A CA	I	
	TCGC GC TCTCCGCGC		
	AGCG CG AGAGGCGCG		
	G _ T		
GAM163 MN1	TCGCCGGAGTCTCCGCGCACCGT 2344 AGCCA	A GI	
	TCGC TCTCCGCGCAC GT		
	AGCG AGAGGCGCGTG CA		
	GCCTC G		
GAM163 MN1	TCGCCGGAGTCTCCGCGCACCGT 2344 CA A__	AGI	
	GCC TCTCCGCGCAC		
	CGG AGAGGCGCGTG		
	G_ CCTC		
GAM163 POLR2E	TCGCACCCCTTCTCCGCGC 2342 G A_	ACAGT	
	TCGCA CC TCTCCGCGC		

	AGCGT GG AGAGGCGCG			
	G GA III GT			
GAM163 POLR2E	TCGCACCCCTTCTCCGCGC	2342	G A_ II	
	TCGCA CC TCTCCGCG			
	II			
	AGCGT GG AGAGGCGCG			
	G GA GI			
GAM163 PRKAR2A	GCGGCCACTGTCTCCGCGCTCA	2338	A ____ ACIII	
	GC GCCA TCTCCGCGC			
	CG CGGT AGAGGCGCG			
	C GAC AGTII			
GAM163 PRKAR2A	GCGGCCACTGTCTCCGCGCTCA	2338	TCGCA ____ A GTG	
	GCCA TCTCCGCGC CA			
	CGGT AGAGGCGCG GT			
	C ____ GAC A GAI			
GAM163 PTPN11	AGCCAGCCGGCCGCGCACAG	2330	T ____ III	
	AGCCA CT CCGCGCACA			
	II			
	TCGGT GG GGCGCGTGT			
	C CC CII			
GAM163 PTPN11	AGCCAGCCGGCCGCGCACAG	2330	TCGC ATCT T	
	AGCC CCGCGCACAG			
	TCGG GGCGCGTGTC			
	____ CC__ T			
GAM163 PTPN7	AGCCATCTCTGAGCTAACCAGTG	2331	GCC C__ GCA_ I	
	ATCTC GC CAGT			
	II			
	TAGAG CG GTCA			
	____ ACT ATTG I			
GAM163 RGL	CGCAGCC-TCTAGCAGCGCACAGT	2334	G A CC__ I	
	CAGCC TCT GCGCACAG			
	GTCGG AGA CGCGTGTC			
	_ _ TCGT I			
GAM163 RGL	CGCAGCC-TCTAGCAGCGCACAGT	2334	TC A CC__ GI	
	GCAGCC TCT GCGCACAGT			
	CGTCGG AGA CGCGTGTC			
	____ _ TCGT GI			
GAM163 TCEA1	GCAGGTCTTCTCCGCGCCCA	2337	CCA_ ACII	
	GCAG TCTCCGCGC			
	CGTC AGAGGCGCG			
	CAGA GGTI			
GAM163 TCEA1	GCAGGTCTTCTCCGCGCCCA	2337	TCGCAGCCA A GT	
	TCTCCGCGC CA			

	AGAGGCGCG GT		
	TCCAGA___ G GG		
GAM164 ADRBK1	TGGCACAAGTG---CAGCCCACA 2361	CT	TTC
	TGGCAC GTG CAGCCCACA		
	ACCGTG CAC GTCGGGTGT		
	TT ___		
GAM164 ADRBK1	TGGCACAAGTG---CAGCCCACA 2361_	CT	TTC
	GGCAC GTG CAGCCCAC		
	CCGTG CAC GTCGGGTG		
	A TT ___		
GAM164 BRCA1	CACTCTGTGCTTCCAGCCC 2347 _ _		
	CAC CTGTGTT CCAGCC		
	GTG GACACGA GGTCGG		
	A A GII		
GAM164 BRCA1	CACTCTGTGCTTCCAGCCC 2347 TGGCAC	_	ACA
	CTGTGTT CCAGCCC		
	GACACGA GGTCGGG		
	A___ A ATT		
GAM164 CA6	GCAGC-GTGTTCCAGACACACAT 2354 CACCT	_ C	I
	GTGTTCCAG C CACA		
	CACAAGGTC G GTGT		
	GTCG_ T T I		
GAM164 CA6	GCAGC-GTGTTCCAGACACACAT 2354 TGGCACCT	_ C	
	GTGTTCCAG C CACAT		
	CACAAGGTC G GTGTA		
	TCG___ T T		
GAM164 CDH10	TGGAAGTTG-GTTCCAGCCAAAAT 2362	CACC T	CACATI
	TGG TG GTTCCAGCC		
	ACC AC CAAGGTCGG		
	TTCA _ TTTTAI		
GAM164 CDH10	TGGAAGTTG-GTTCCAGCCAAAAT 2362_	CACC T	CACAI
	GG TG GTTCCAGCC		
	CC AC CAAGGTCGG		
	A TTCA _ TTTTI		
GAM164 EPAC	CACCTG-G--CCAGCCCAC 2350	T TT	
	CACCTG G CCAGCCCA		
	GTGGAC C GGTCGGGT		

GAM164 ERH	CACCTGTGTTCCAAGCCCAC 2349	_	
	CACCTGTGTTCCA GCCCA		

	GTGGACACAAGGT CGGGT			
	T G			
GAM164 ERH	CACCTGTGTTCCAAGCCCAC 2349 TGGCAC	_	A	
	CTGTGTTCCA GCCCAC			
	GACACAAGGT CGGGTG			
	_____ T G			
GAM164 GNG5	CCTCTGTTCAGCTCCACA 2352 G	_	II	
	CCT TGTTCCAGC CCAC			
	GGA ACAAGGTCG GGTG			
	G A TI			
GAM164 GYPC	TGGCACCTGCTGTTCC-CCCCAAAT 2359	_	AG CATI	
	TGGCACCTG TGTTCC CCA			
	ACCGTGGAC ACAAGG GGGT			
	G G_ TTAI			
GAM164 GYPC	TGGCACCTGCTGTTCC-CCCCAAAT 2359	_	AG CAI	
	GGCACCTG TGTTCC CCA			
	CCGTGGAC ACAAGG GGGT			
	G G_ TTI			
GAM164 LDLR	GGCACCTGTGT--CTGGCCAAAT 2357		CCA CACI	
	GGCACCTGTGTT GCC			
	CCGTGGACACAG CGG			
	AC_ TTAA			
GAM164 LDLR	GGCACCTGTGT--CTGGCCAAAT 2357 TG		CCA CACAT	
	GCACCTGTGTT GCC			
	CGTGGACACAG CGG			
	_____ AC_ TTAA			
GAM164 MYO1C	GGCACCAGAGC-CCAGCCCACA 2356_ TGT T		I	
	GCACC GT CCAGCCCAC			
	CGTGG CG GGTCGGGTG			
	C TCT _ I			
GAM164 MYO1C	GGCACCAGAGC-CCAGCCCACA 2356 TG TGT T			
	GCACC GT CCAGCCCACAT			
	CGTGG CG GGTCGGGTGTG			
	_____ TCT _			
GAM164 NEO1	GGCGCCGCTGCTCCAGCCCA 2355 A TG		I	
	GC CC TGTTCCAGCCC			
	CG GG ACGAGGTCGGG			
	C CG I			
GAM164 NEO1	GGCGCCGCTGCTCCAGCCCA 2355 TG A TG		CA	
	GC CC TGTTCCAGCCCA			

	CG GG ACGAGGTCGGGT		
	__ C CG CI		
GAM164 PTPN12	TGGCACCTGAATTTTCCAG 2358	TG__	CCCACA
	TGGCACCTG TTCCAG		
	ACCGTGGAC AAGGTC		
	TTAA IIITAC		
GAM164 PTPN12	TGGCACCTGAATTTTCCAG 2358	TG__	III
	TGGCACCTG TTCCA		
	ACCGTGGAC AAGGT		
	TTAA CII		
GAM164 SMTN	TGGCACCTGT-CACCAGCTCA 2360	GTT	C CA
	TGGCACCTGT CCAGC CA		
	II		
	ACCGTGGACA GGTCG GT		
	GT_ A II		
GAM164 SMTN	TGGCACCTGT-CACCAGCTCA 2360_	GTT	CCI
	GGCACCTGT CCAGC		
	CCGTGGACA GGTCG		
	A GT_ AGI		
GAM164 STUB1	CACCTGCTTTTCCAGCCCACA 2348 A	G_	I
	CCTGT TTCCAGCCCAC		
	GGACG AAGGTCGGGTG		
	_ AA I		
GAM164 STUB1	CACCTGCTTTTCCAGCCCACA 2348	TGGCAC	G_ T
	CTGT TTCCAGCCCACA		
	GACG AAGGTCGGGTGT		
	_____ AA T		
GAM164 TSSC4	CCAGTGCTTCCAGCCCACA 2351	T _	II
	CC GTGTT CCAGCCCAC		
	II		
	GG CACGA GGTCGGGTG		
	T A TI		
GAM164 UBE3A	CTGCTGTTCCAGCCCACAT 2353	_	II
	CTG TGTTCAGCCCACA		
	GAC ACAAGGTCGGGTGT		
	G AI		
GAM165 ANGPT2	GCAAACCTGAGGGCAAACA 2370	AGGC	II
	GCAGAC GGGCAAAC		
	CGTTTG CCCGTTTG		
	AACT TI		
GAM165 CALD1	GCAAGCAGGCGGGCAGGCAG 2371	GA	AACAI
	CA CAGGCGGGCA		
	II		

	GT GTCCGCCCGT		
	TC CCGTI		
GAM165 CALD1	GCAAGCAGGCGGGCAGGCAG	2371 TGGC A	AA T
	AG CAGGCGGGCA CAG		
	TC GTCCGCCCGT GTC		
	T__ _ CC C		
GAM165 CARD12	CACACAGG---GCAAACAG	2367 CAGA G _	
	CA GC GGGCAAACA		
	GT TG CCCGTTTGT		
	__ G T		
GAM165 CDK5R2	GGCAGACAGGAGGGAAGATGGTG	2379 C CAAACAGTI	
	GCAGACAGG GGG		
	CGTCTGTCC CCC		
	T TTCTACCAI		
GAM165 CDK5R2	GGCAGACAGGAGGGAAGATGGTG	2379 TG C CAAACA I	
	GCAGACAGG GGG GTG		
	CGTCTGTCC CCC CAC		
	_ T TTCTAC T		
GAM165 DDX6	AGACAGTGTGGCAGCAAACAGT	2365 _ G	
	AGACA GGCGG CAAACAG		
	TCTGT CCGTC GTTTGTC		
	CACA _ AII		
GAM165 DDX6	AGACAGTGTGGCAGCAAACAGT	2365 _ A _ AACAGTG	
	TGGCAG CAGGCGG GCA		
	ACCGTC GTTTGTC TGT		
	TCAC _ A AIIIGTG		
GAM165 DFFB	TGGGAGACCGAGGCGGGCA	2380 C _ AACAGT	
	TGG AGAC AGGCGGGCA		
	ACC TCTG TCCGCCCGT		
	C GC IIIGTG		
GAM165 DFFB	TGGGAGACCGAGGCGGGCA	2380 C _	
	TGG AGAC AGGCGGGC		
	ACC TCTG TCCGCCCG		
	C GC TII		
GAM165 EIF2C1	GGCAGACAGGCAGGCAGGCAG	2374 AACAI	
	GCAGACAGGCGGGCA		
	CGTCTGTCCGTCCGT		
	CCGTI		
GAM165 EIF2C1	GGCAGACAGGCAGGCAGGCAG	2374 TG AA TG	
	GCAGACAGGCGGGCA CAG		

	CGTCTGTCCGTCCGT GTC		
	CC CI		
GAM165 FEZ1	TGGGAGGCCAAGGCGGGCAAA 2381 T___ AGAC CAGTG		
	GGC AGGCGGGCAAA		
	CCG TCCGCCCGTTT		
	ACCCT GT___ GT		
GAM165 FEZ1	TGGGAGGCCAAGGCGGGCAAA 2381 T___ AGAC		
	GGC AGGCGGGCAA		
	CCG TCCGCCCGTT		
	ACCCT GT___ T		
GAM165 GLRX2	TGGCAGACATGCTGGGGAAAC 2383 G _ C AGTG		
	TGGCAGACA GC GGG AAAC		
	ACCGTCTGT CG CCC TTTG		
	A A C G		
GAM165 GLRX2	TGGCAGACATGCTGGGGAAAC 2383 G G _ CAAAI		
	GCAGACA GC GGG		
	CGTCTGT CG CCC		
	_ A A CTTTI		
GAM165 GRLF1	GGCAGA--GGCGGGCACAGAGTG 2378 CA AA I		
	GGCAGA GGCGGGC ACAG		
	CCGTCT CCGCCCG TGTC		
	_ _ T		
GAM165 GRLF1	GGCAGA--GGCGGGCACAGAGTG 2378 TG CA AAC		
	GCAGA GGCGGGCA AGTG		
	CGTCT CCGCCCGT TCAC		
	_ _ GTC		
GAM165 GRM4	GGCGGGCAGGCGGGCAAGACAG 2372 _ GACA ACI		
	GGCA GGCGGGCAA		
	CCGT CCGCCCGTT		
	C _ CTG		
GAM165 GRM4	GGCGGGCAGGCGGGCAAGACAG 2372 T_ CAGA _ TG		
	GG CAGGCGGGCAA ACAG		
	CC GTCCGCCCGTT TGTC		
	CG C_ C TI		
GAM165 HAS3	GCAGACAGGCAGTCTGAAAACA 2369 GCAAAC		
	GCAGACAGGCGG		
	CGTCTGTCCGTC		
	AGACTTTTG		
GAM165 HAS3	GCAGACAGGCAGTCTGAAAACA 2369 TGGC GC_ GTG		
	AGACAGGCGG AAACA		

	TCTGTCCGTC TTTGT		
	_____ AGACT GTI		
GAM165 IGF1	TGGGAGGCTGAGGCGGGCAAA 2382 T_____ AGAC		CAGTG
	GGC AGGCGGGCAAA		
	CCG TCCGCCCGTTT		
	ACCCT AC_____ IIIGT		
GAM165 IGF1	TGGGAGGCTGAGGCGGGCAAA 2382 T_____ AGAC		
	GGC AGGCGGGCAA		
	CCG TCCGCCCGTT		
	ACCCT AC_____ TII		
GAM165 JAM3	TGGCAGACA-GCGAGGC-AACAGTG 2384	G _ A I	
	TGGCAGACAG CG GGCAA CAGTG		
	ACCGTCTGTC GC CCGTT GTCAC		
	_ T _ I		
GAM165 JAM3	TGGCAGACA-GCGAGGC-AACAGTG 2384 _	G _ A I	
	GGCAGACAG CG GGCAA CAGT		
	CCGTCTGTC GC CCGTT GTCA		
	A _ T _ I		
GAM165 KRT8	TGG-AGGCAGGCGGGCCGAACCAG 2385	C A	AAA_____ TGI
	TGG AG CAGGCGGGC CAG		
	ACC TC GTCCGCCCG GTC		
	_ C GCTTG		
GAM165 KRT8	TGG-AGGCAGGCGGGCCGAACCAG 2385	C A	A_ AI
	AG CAGGCGGGC AAC		
	TC GTCCGCCCG TTG		
	C C GC		
GAM165 LILRA1	TGGCAGACAGTCCAGATAACA 2387	G_ CA	GTG
	TGGCAGACAG CGGG AACA		
	ACCGTCTGTC GTCT TTGT		
	AG A_		
GAM165 LILRA1	TGGCAGACAGTCCAGATAACA 2387	G_ GC	ACI
	GGCAGACAG CGG AA		
	CCGTCTGTC GTC TT		
	AG TA GII		
GAM165 MAML1	GGCAGACAGAAAGGCCAACGGT 2377	C A	AGI
	GCAGACAGG GGGC AAC		
	CGTCTGTCT TCCG TTG		
	T G CCI		
GAM165 MAML1	GGCAGACAGAAAGGCCAACGGT 2377	TG C A A	
	GCAGACAGG GGGC AAC GTG		

	CGTCTGTCT TCCG TTG CAT	
	___ T G C	
GAM165 NFE2L1	GGCAG-CAGT--GGCAAACAGT 2376 A GCG I	
	GGCAG CAG GGCAAACA	
	CCGTC GTC CCGTTTGT	
	_ A_ C	
GAM165 NFE2L1	GGCAG-CAGT--GGCAAACAGT 2376 TG A GCG	
	GCAG CAG GGCAAACAGT	
	CGTC GTC CCGTTTGTCA	
	___ _ A_	
GAM165 Nrap	GACATGAACGGGCAAACAG 2368 ___	
	GACA GGCGGGCAAACA	
	CTGT TTGCCCGTTTGT	
	AC CII	
GAM165 Nrap	GACATGAACGGGCAAACAG 2368 TGGCAGACA	
	GGCGGGCAAACAGT	
	TTGCCCGTTTGTCTG	
	C_	
GAM165 SF3A2	TGGCGAAC-GGCGGGCAAA 2386 AG A CAG	
	TGGC AC GGCGGGCAAA	
	ACCG TG CCGCCCGTTT	
	CT _	
GAM165 SF3A2	TGGCGAAC-GGCGGGCAAA 2386 AG A I	
	TGGC AC GGCGGGCAA	
	ACCG TG CCGCCCGTT	
	CT _ T	
GAM165 SLC17A5	AGACAGACTGAACAAACAGTG 2366 G _ I	
	ACAGGC GGGCAAACAGT	
	TGTCTG CTTGTTTGTCA	
	_ A I	
GAM165 SLC17A5	AGACAGACTGAACAAACAGTG 2366 TGGCAGAC _	
	AGGC GGGCAAACAGTG	
	TCTG CTTGTTTGTAC	
	___ A	
GAM165 SLC29A1	GGCAGACAGTCTGACAGACA 2373 ___ AAACI	
	GCAGACAG GCGGGC	
	CGTCTGTC TGTCTG	
	AGAC IIICA	
GAM165 SLC29A1	GGCAGACAGTCTGACAGACA 2373 TG GCG A GT	
	GCAGACAG GGCA ACA	

	CGTCTGTC CTGT TGT		
	___ AGA C GI		
GAM165 SLC29A1	GGCAGACAGGGAGGGAGGCAG 2375	C___	AACAI
	GCAGACAGG GGGCA		
	CGTCTGTCC TCCGT		
	CTCCC IIIAC		
GAM165 SLC29A1	GGCAGACAGGGAGGGAGGCAG 2375 TG	C CAAA	TG
	GCAGACAGG GGG CAG		
	CGTCTGTCC TCC GTC		
	___ C CTCC CI		
GAM165 TEM6	TGGCTTAGATGATGGCAAACAGTG 2388	___ CAGGCG	I
	TGGC AGA GGCAAACAGTG		
	ACCG TCT CCGTTTGTAC		
	AA ACTA___ I		
GAM165 TEM6	TGGCTTAGATGATGGCAAACAGTG 2388	___ CAGGCG	I
	GGC AGA GGCAAACAGT		
	CCG TCT CCGTTTGTCA		
	AA ACTA___ I		
GAM166 ADORA2B	TATTTGTCAATCC-TTGGAGC 2397	A CACC	TA
	TATT GTC CCTTGGAGC		
	ATAA CAG GGAACCTCG		
	A TTA_ II		
GAM166 ADORA2B	TATTTGTCAATCC-TTGGAGC 2397	ATTA_ CACC	I
	GTC CCTTGGAG		
	CAG GGAACCTC		
	ATAAA TTA_ I		
GAM166 IGF1	TTATACCACCCCTTTGAGGTAG 2399	TAGT G CI	
	CCACCCCTT GAG		
	GGTGGGGAA CTC		
	AT___ A CA		
GAM166 IGF1	TTATACCACCCCTTTGAGGTAG 2399	TATTAGT G C	
	CCACCCCTT GAG TAG		
	GGTGGGGAA CTC ATC		
	TAT___ A C		
GAM166 NOS1	TCCAGGCCCTTGATGCTA 2398	___ _	
	TCCA CCCCTTGGA GCT		
	AGGT GGGGAACCT CGA		
	CC A TII		
GAM166 PIGA	TATTAGTCCAGGCACCCCGTGG 2394	___ T AGCTAG	
	TATTAGTCC ACCCC TGG		

	ATAATCAGG TGGGG ACC		
	TCCG C IIGAT		
GAM166 PIGA	TATTAGTCCAGGCACCCCGTGG 2394	TTGIIIC	
	TATTAGTCC ACCCC		
	ATAATCAGG TGGGG		
	TCCG CACCI		
GAM166 PITX3	TAGTCCACCCCTCAGGGCT 2393	TG A II	
	TAGTCCACCCCT G GC		
	ATCAGGTGGGGA C CG		
	GT C AI		
GAM166 PITX3	TAGTCCACCCCTCAGGGCT 2393	TATTAG TG A A	
	TCCACCCCT G GCT		
	AGGTGGGGA C CGA		
	GT C C		
GAM166 POLG	TATT--TCCACTGCCTTGGAGC 2395	ATTAG C_ I	
	TCCAC CCTTGGAG		
	AGGTG GGAACCTC		
	ATAA_ AC I		
GAM166 POLG	TATT--TCCACTGCCTTGGAGC 2395	TATTAG C_ TA	
	TCCAC CCTTGGAGC		
	AGGTG GGAACCTCG		
	ATAA__ AC II		
GAM166 SLC18A1	ATGAGTC-ACCCCTTGCAG 2391	ATT C GAI	
	AGTC ACCCCTTG		
	TCAG TGGGGAAC		
	TAC _ GTC		
GAM166 SLC18A1	ATGAGTC-ACCCCTTGCAG 2391	TATT C G CT	
	AGTC ACCCCTTG AG		
	TCAG TGGGGAAC TC		
	AC_ _ G TI		
GAM166 TGFBR3	ATTGGTCCTGCCCTTGGAG-TAG 2392	TA AC CI	
	GTCC CCCTTGGAG		
	CAGG GGGAACCTC		
	AC AC AI		
GAM166 TGFBR3	ATTGGTCCTGCCCTTGGAG-TAG 2392	TATTA AC C	
	GTCC CCCTTGGAG TAG		
	CAGG GGGAACCTC ATC		
	AAC_ AC _		
GAM166 ZNF146	TATTTTCC--CCCTTGGAG 2396	ATTAGTCCA I	
	CCCCTTGA		

	GGGGAACCT		
	ATAAAAAG_ I		
GAM166 ZNF146	TATTTTCC--CCCTTGGAG	2396	TATTAGTCCA CT
	CCCCTTGGAG		
	GGGGAACCTC		
	ATAAAAAG_ II		
GAM167 ADAMTS13	GCAGTGGCAGTG	2407	II
	GCGGTGGCAGT		
	CGTCACCGTCA		
	CI		
GAM167 APPBP2	GCGGTGGCAGCCACGCGGGC-GCAC	2405	C_ TG AG T A I
	GG GC TGC GGC GCA		
	II II III III III		
	CC CG GCG CCG CGT		
	CA GT GT C _ I		
GAM167 APPBP2	GCGGTGGCAGCCACGCGGGC-GCAC	2405	GTGC ____ T A I
	GGTGGCAGT GC GGC GCAC		
	II III III		
	CCACCGTCG CG CCG CGTG		
	____ GTG C _ C		
GAM167 ASS	GCGGTGGCAG-GC-GGCAG	2408	T T I
	GCGGTGGCAG GC GGCA		
	II III		
	CGCCACCGTC CG CCGT		
	_ _ C		
GAM167 ASS	GCGGTGGCAG-GC-GGCAG	2408	GTGC T T C
	GGTGGCAG GC GGCAG		
	II III		
	CCACCGTC CG CCGTC		
	____ _ _ T		
GAM167 AVPR2	GTGCGGTGGCAGT-ATGGC	2415	C AGC
	GTGCGGTGGCAGTG TGGC		
	III		
	CACGCCACCGTCAT ACCG		
	_ III		
GAM167 AVPR2	GTGCGGTGGCAGT-ATGGC	2415	C I
	GTGCGGTGGCAGTG TGG		
	III		
	CACGCCACCGTCAT ACC		
	_ G		
GAM167 BSN	GCGGTGACTCACCTGGCAGCA	2410	AGTG I
	CGGTGGC CTGGCAGC		
	GCCACTG GACCGTCG		
	AGTG I		
GAM167 CALCA	GCGGTGGCAGCGGCGGCGGC	2409	C AGI
	CGGTGGCAGTG TGGC		
	III		

	GCCACCGTCGC GCCG		
	C CCI		
GAM167 CALCA	GCGGTGGCAGCGGCGGCGGC 2409 GTGC	C A A	
	GGTGGCAGTG TGGC GC		
	CCACCGTCGC GCCG CG		
	_____ C C C		
GAM167 CDKN2C	GTGCCCTGGAGCAGAGCCTGGCAGCAC2413	___ T T _	
	GTGC GG GGCAG GC TGGCAGCAC		
	CACG CC TCGTC CG ACCGTCGTG		
	GGA _ T G		
GAM167 CDKN2C	GTGCCCTGGAGCAGAGCCTGGCAGCAC2413 TGC T T _ I		
	GG GGCAG GC TGGCAGCA		
	CC TCGTC CG ACCGTCGT		
	GGA _ T G I		
GAM167 COL6A1	CGGGGTCAGTGCTGGTCAGCA 2402 GGT _ _ I		
	GG CAGTGCTGG CAGC		
	CC GTCACGACC GTCG		
	C _ A A I		
GAM167 COL6A1	CGGGGTCAGTGCTGGTCAGCA 2402 GTGCGGT _ _ C		
	GG CAGTGCTGG CAGCA		
	CC GTCACGACC GTCGT		
	_____ A A C		
GAM167 CSNK2A2	GTGGCAGCTGCTTGAAGG 2418 I		
	GTGCGGTGGCAGT		
	CACGTCACCGTCA		
	I		
GAM167 CXCR4	TGCGGTGGC--TACTGG-AGCAC 2421 _ AG C		
	GCGGTGGC TGCTGG AGCA		
	CGCCACCG ATGACC TCGT		
	A _ _		
GAM167 CXCR4	TGCGGTGGC--TACTGG-AGCAC 2421 GT AG C		
	GCGGTGGC TGCTGG AGCA		
	CGCCACCG ATGACC TCGT		

GAM167 DFFB	GCGGTGGCACCTGCTGCCAGC 2404 CG G_ G_ I		
	GTGGCA TGCTG CAG		
	CACCGT ACGAC GTC		
	_ GG GG I		
GAM167 DFFB	GCGGTGGCACCTGCTGCCAGC 2404 GTGC G_ G_ AC		
	GGTGGCA TGCTG CAGC		

	CCACCGT ACGAC GTCG		
	_____ GG GG AC		
GAM167 EMP1	GTGGCAGGTGCTGGCAGCA 2419 _	II	
	GTGGCAG TGCTGGCAGC		
	CACCGTC ACGACCGTCG		
	C TI		
GAM167 FGD1	GCGGTGGCAGTAGCAGCAGCA 2406 _	_ T GI	
	GCGGTGGCAGT GC GGCA		
	CGTCATCGTCG CG TCGT		
	C T _ II		
GAM167 FGD1	GCGGTGGCAGTAGCAGCAGCA 2406 _ _	_ T ACI	
	GTG CCGTGGCAGT GC GGCAGC		
	CAC GTCATCGTCG CG TCGTCG		
	C C T _ III		
GAM167 GAL	GTGCGGTGGCGGGTCTGGGCGGCA 2414	A_ G _ A CI	
	GTGCGGTGGC GT CTGG C GCA		
	CACGCCACCG CA GACC G CGT		
	CC _ C C II		
GAM167 GAL	GTGCGGTGGCGGGTCTGGGCGGCA 2414 T	A_ G _ A I	
	GCGGTGGC GT CTGG C GC		
	CGCCACCG CA GACC G CG		
	_ CC _ C C I		
GAM167 GPR4	GTG-GGTGGGAGTGCTGGCA 2416 C C	GCA	
	GTG GGTGG AGTGCTGGCA		
	CAC CCACC TCACGACCGT		
	_ C III		
GAM167 GPR4	GTG-GGTGGGAGTGCTGGCA 2416 _ C C	I	
	TG GGTGG AGTGCTGGC		
	AC CCACC TCACGACCG		
	C _ C I		
GAM167 LANGERIN	GCAGTGCTG 2403	II	
	GCAGTGCT		
	CGTCACGA		
	CI		
GAM167 MAF	TGCGGTGGCGGCGGTGGTGGCTGC 2420 GC	A C AI	
	GGTGGC GTG TGGC		
	CCGCCG CAC ACCG		
	A_ C C AC		
GAM167 MAF	TGCGGTGGCGGCGGTGGTGGCTGC 2420 GT	A_ C A ACI	
	GCGGTGGC GTG TGGC GC		

		CGCCACCG CAC ACCG CG		
		— CCGC C A CII		
GAM167 PAX8	GCAGTGCTG	2403 II		
	GCAGTGCT			
	CGTCACGA			
	CI			
GAM167 PPP1R12B	GTGCGGT--CAGTGCTGGCA	2417 GG GC		
	GTGCGGT CAGTGCTGGCA			
	CACGCCA GTCACGACCGT			
	II			
GAM167 PPP1R12B	GTGCGGT--CAGTGCTGGCA	2417_ GG I		
	TGCGGT CAGTGCTGGC			
	ACGCCA GTCACGACCG			
	C _ I			
GAM167 TNNI1	GGTGGCAGTG-AGACAGCAC	2411_ CT I		
	GTGGCAGTG GGCAGCA			
	CACCGTCAC CTGTCGT			
	C T_ I			
GAM167 TNNI1	GGTGGCAGTG-AGACAGCAC	2411 GTGCGGTG CT		
	GCAGTG GGCAGCA			
	CGTCAC CTGTCGT			
	T_			
GAM167 WEE1	GTGGGCGTGGCAGTG--GGCAGC	2412__ T G CT AC		
	G GCG TGGCAGTG GGCAGC			
	I			
	C CGC ACCGTCAC CCGTCG			
	CA C _ _ II			
GAM167 WEE1	GTGGGCGTGGCAGTG--GGCAGC	2412 T__ G CT I		
	GCG TGGCAGTG GGCAG			
	CGC ACCGTCAC CCGTC			
	CACC _ _ I			
GAM168 ABCC3	ATGAGGTTGGCTGGAGAAT	2425 TATGA_ AT CTGC		
	TG CTGGAGAATT			
	AC GACCTCTTAG			
	ACTCCA C_ IIIT			
GAM168 CLN5	ATGTTAATATGCAGCAATTCTGCT	2426 TA A C G _ I		
	TG TGAT TG AG AATTCTGCT			
	AC ATTA AC TC TTAAGACGA			
	_ A T G G C			
GAM168 EVA1	TGATGATCTGG-GAGTCCT	2431 TATG A A G		
	ATGATCTGG GA TTCT			

	TACTAGACC CT AGGA	
	_____ _ C G	
GAM168 LDB3	TGA-GTTCTTG-GAATTCTGCT 2432 TATGATGA GGA	
	TCT GAATTCTGC	
	AGA CTTAAGACG	
	TCA_____ AC_	
GAM168 MPP3	ATGATGGAATTTGTGGAGAATTCT 2424 TA ATC_____ GCTI	
	TGATG TGGAGAATTCT	
	ACTAC ACCTCTTAAGA	
	_____ CTAAAC G	
GAM168 PXF	GATGATCTGCAGACTTGTGCT 2429 TATGAT G A C	
	GATCTG AGA TT TGCT	
	CTAGAC TCT AA ACGA	
	_____ G G C	
GAM168 ST7	GATGATCTGAATGATTTCT 2428 TATGAT _ A GC	
	GATCTGGA GA TTCT	
	CTAGACTT CT AAGA	
	_____ A A AT	
GAM168 TCF12	GATGTAAGTGGAGAATATATGC 2427 TATGA T TC_ T	
	TGA CTGGAGAAT TGC	
	ATT GACCTCTTA ACG	
	C_____ TAT T	
GAM168 VSX1	TATGATGATAT-CAG-ATTCTTCT 2430 CT_ GAA GCT	
	TATGATGAT GGA TTCT	
	ATACTACTA TCT AAGA	
	TAG AAG	
GAM168 ZNF193	TGGTGATCTGGAAAAGT-TGCT 2433 TATGA C	
	TGATCTGGAGAATT TGCT	
	ACTAGACCTTTTGA ACGA	
	C_____ _	
GAM169 ARNTL	CAGATCCAGCTTGGGAGGA 2441 TAGCAG _____ T AGCG	
	ATCCAGC GGA GA	
	TAGGTCG CCT CT	
	_____ AAC C CAAI	
GAM169 CTNND2	AGAGTCACAACGGATGAAG 2436 TAGCAGA _ C	
	TC CAGCGGATGAAG G	
	AG GTTGCCTACTTC C	
	_____ T T	
GAM169 CYP3A4	GCAG-TCCATTGGATGAAGC 2445 TAGC A GC G	
	AG TCCA GGATGAAGC	

	TC AGGT CCTACTTCG		
	____ _ AA G		
GAM169 GNLY	GCAGATCCA-CCGATGAGGC 2446 TAGC	G G	A G
	AGATCCA C GATGA GC		
	TCTAGGT G CTACT CG		
	____ _ G C G		
GAM169 GRAF	CAGATCCAGCTGCCTGTAGC 2442 TAGCAG	GGA_	A
	ATCCAGC TG AGCG		
	TAGGTCG AC TCGT		
	____ _ ACGG A		
GAM169 GRIK3	AGAAGATCTGAGGAGGATGAAGC 2439 TAGC	C_ C_	GGI
	AGATC AG GGATGAAGC		
	TCTAG TC CCTACTTCG		
	CT__ AC CT GII		
GAM169 GUCA2B	TACCAGATCCAGCTGCTCAGGC 2447 G	GGATGAA	GG
	TA CAGATCCAGC GC		
	AT GTCTAGGTCG CG		
	G ACGAGTC		
GAM169 IMPA1	CAGAATCCAGCGGCAATGAAG 2440 TAGCA	__	CGG
	GATCCAGCGG ATGAAG		
	TTAGGTCGCC TACTTC		
	____ _ GT AAT		
GAM169 JAM3	AGCAGTGTCTCCGGCGGATGAA 2437 TA	A__ A	CGG
	GCAG TCC GCGGATGAAG		
	CGTC AGG CGCCTACTTT		
	__ ACAG C		
GAM169 PYGB	CAGATCCAGC--ATGCAAG 2443 TAGCAG	GG _	C
	ATCCAGC ATG AAG		
	TAGGTCG TAC TTC		
	____ _ G C		
GAM169 TBX6	CAGATCCA--GGATCACAGC 2444 TAGCAG	GC	GA_
	ATCCA GGAT AGC		
	TAGGT CCTA TCG		
	____ _ GTG		
GAM169 TNR	AGCAGATGTTAGCCAGCGGAT 2438 TA	____	GAAGCGG
	GCAGAT CCAGCGGAT		
	CGTCTA GGTGCGCTA		
	__ CAATC A GGC		
GAM170 CKTSF1B1	AACAGGTCTCT--TGCCCTCAG 2453	GTGA	I
	AACAGGTCT TGCCCTT		

	TTGTCCAGA ACGGGAG		
	GA__ T		
GAM170 CKTSF1B1	AACAGGTCTCT--TGCCCTCAG 2453 TA	GTGA	
	ACAGGTCT TGCCCTTAG		
	TGTCCAGA ACGGGAGTC		
	__ GA__		
GAM170 DYRK2	AACAGGTCTGAGCTACTCCTT 2451 A	TGA _ I	
	CAGGTCTG TGC CCT		
	GTCCAGAC ATG GGA		
	_ TCG A I		
GAM170 DYRK2	AACAGGTCTGAGCTACTCCTT 2451 TA	TGA _ AGT	
	ACAGGTCTG TGC CCTT		
	TGTCCAGAC ATG GGAA		
	_ TCG A AII		
GAM170 EMP1	AGGTCTGTG--GACCTCAGT 2455_	ATGC I	
	GGTCTGTG CCTTAG		
	CCAGACAC GGAGTC		
	T CT__ I		
GAM170 ENTPD5	ACAGGGCTCTCTGTGATGCTCT 2454	_____ CCIIIA	
	ACAGG TCTGTGATGC		
	TGTCC AGACACTACG		
	CGAG AGAIII		
GAM170 ENTPD5	ACAGGGCTCTCTGTGATGCTCT 2454 TAAC	_____ C TAGT	
	AGG TCTGTGATGC CT		
	TCC AGACACTACG GA		
	_____ CGAG A CCII		
GAM170 GFER	AACAGGCTCTGGCTGTGATGCACTT 2450 ACA_ T	C I	
	GG CTGTGATGC CT		
	CC GACACTACG GA		
	GAGA _ T I		
GAM170 GFER	AACAGGCTCTGGCTGTGATGCACTT 2450 TA	_____ C AGTII	
	ACAGGT CTGTGATGC CTT		
	TGTCCG GACACTACG GAA		
	_ AGACC T AIIIT		
GAM170 NUFIP1	CAGGTCTGTGACGTCACTAG 2456	CCCTTAI	
	AGGTCTGTGATG		
	TCCAGACACTGC		
	AGTGATI		
GAM170 NUFIP1	CAGGTCTGTGACGTCACTAG 2456 TAACAG	CCC	
	GTCTGTGATG TTAG		

		CAGACACTGC GATC			
		AGT			
GAM170 OAS3	GTCTAAGAAGGTGCCCTTAG	2457	T ____	III	
	GTCTG GA TGCCCTTA				
	CAGAT CT ACGGGAAT				
	T TCC CII				
GAM170 PCDHGA1	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I	
	AGGTC GTGATGCCCT				
	TCCAG TACTACGGGA				
	TTC _ I				
GAM170 PCDHGA1	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG	
	AGGTC GTGATGCCCTT				
	TCCAG TACTACGGGAA				
	TC_ _ GI				
GAM170 PCDHGA10	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I	
	AGGTC GTGATGCCCT				
	TCCAG TACTACGGGA				
	TTC _ I				
GAM170 PCDHGA10	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG	
	AGGTC GTGATGCCCTT				
	TCCAG TACTACGGGAA				
	TC_ _ GI				
GAM170 PCDHGA11	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I	
	AGGTC GTGATGCCCT				
	TCCAG TACTACGGGA				
	TTC _ I				
GAM170 PCDHGA11	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG	
	AGGTC GTGATGCCCTT				
	TCCAG TACTACGGGAA				
	TC_ _ GI				
GAM170 PCDHGA12	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I	
	AGGTC GTGATGCCCT				
	TCCAG TACTACGGGA				
	TTC _ I				
GAM170 PCDHGA12	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG	
	AGGTC GTGATGCCCTT				
	TCCAG TACTACGGGAA				
	TC_ _ GI				
GAM170 PCDHGA2	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I	
	AGGTC GTGATGCCCT				

		TCCAG TACTACGGGA			
		TTC _ I			
GAM170 PCDHGA2		AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
		AGGTC GTGATGCCCTT			
		TCCAG TACTACGGGAA			
		TC__ _ GI			
GAM170 PCDHGA3		AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
		AGGTC GTGATGCCCT			
		TCCAG TACTACGGGA			
		TTC _ I			
GAM170 PCDHGA3		AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
		AGGTC GTGATGCCCTT			
		TCCAG TACTACGGGAA			
		TC__ _ GI			
GAM170 PCDHGA4		AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
		AGGTC GTGATGCCCT			
		TCCAG TACTACGGGA			
		TTC _ I			
GAM170 PCDHGA4		AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
		AGGTC GTGATGCCCTT			
		TCCAG TACTACGGGAA			
		TC__ _ GI			
GAM170 PCDHGA5		AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
		AGGTC GTGATGCCCT			
		TCCAG TACTACGGGA			
		TTC _ I			
GAM170 PCDHGA5		AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
		AGGTC GTGATGCCCTT			
		TCCAG TACTACGGGAA			
		TC__ _ GI			
GAM170 PCDHGA6		AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
		AGGTC GTGATGCCCT			
		TCCAG TACTACGGGA			
		TTC _ I			
GAM170 PCDHGA6		AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
		AGGTC GTGATGCCCTT			
		TCCAG TACTACGGGAA			
		TC__ _ GI			
GAM170 PCDHGA7		AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
		AGGTC GTGATGCCCT			

	TCCAG TACTACGGGA			
	TTC _ I			
GAM170 PCDHGA7	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
	AGGTC GTGATGCCCTT			
	TCCAG TACTACGGGAA			
	TC__ _ GI			
GAM170 PCDHGA8	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
	AGGTC GTGATGCCCT			
	TCCAG TACTACGGGA			
	TTC _ I			
GAM170 PCDHGA8	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
	AGGTC GTGATGCCCTT			
	TCCAG TACTACGGGAA			
	TC__ _ GI			
GAM170 PCDHGA9	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
	AGGTC GTGATGCCCT			
	TCCAG TACTACGGGA			
	TTC _ I			
GAM170 PCDHGA9	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
	AGGTC GTGATGCCCTT			
	TCCAG TACTACGGGAA			
	TC__ _ GI			
GAM170 PCDHGB1	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
	AGGTC GTGATGCCCT			
	TCCAG TACTACGGGA			
	TTC _ I			
GAM170 PCDHGB1	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
	AGGTC GTGATGCCCTT			
	TCCAG TACTACGGGAA			
	TC__ _ GI			
GAM170 PCDHGB2	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
	AGGTC GTGATGCCCT			
	TCCAG TACTACGGGA			
	TTC _ I			
GAM170 PCDHGB2	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
	AGGTC GTGATGCCCTT			
	TCCAG TACTACGGGAA			
	TC__ _ GI			
GAM170 PCDHGB3	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
	AGGTC GTGATGCCCT			

	TCCAG TACTACGGGA			
	TTC _ I			
GAM170 PCDHGB3	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
	AGGTC GTGATGCCCTT			
	TCCAG TACTACGGGAA			
	TC__ _ GI			
GAM170 PCDHGB4	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
	AGGTC GTGATGCCCT			
	TCCAG TACTACGGGA			
	TTC _ I			
GAM170 PCDHGB4	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
	AGGTC GTGATGCCCTT			
	TCCAG TACTACGGGAA			
	TC__ _ GI			
GAM170 PCDHGB5	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
	AGGTC GTGATGCCCT			
	TCCAG TACTACGGGA			
	TTC _ I			
GAM170 PCDHGB5	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
	AGGTC GTGATGCCCTT			
	TCCAG TACTACGGGAA			
	TC__ _ GI			
GAM170 PCDHGB6	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
	AGGTC GTGATGCCCT			
	TCCAG TACTACGGGA			
	TTC _ I			
GAM170 PCDHGB6	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
	AGGTC GTGATGCCCTT			
	TCCAG TACTACGGGAA			
	TC__ _ GI			
GAM170 PCDHGB7	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
	AGGTC GTGATGCCCT			
	TCCAG TACTACGGGA			
	TTC _ I			
GAM170 PCDHGB7	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
	AGGTC GTGATGCCCTT			
	TCCAG TACTACGGGAA			
	TC__ _ GI			
GAM170 PCDHGC3	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
	AGGTC GTGATGCCCT			

	TCCAG TACTACGGGA			
	TTC _ I			
GAM170 PCDHGC3	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
	AGGTC GTGATGCCCTT			
	TCCAG TACTACGGGAA			
	TC__ _ GI			
GAM170 PCDHGC4	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
	AGGTC GTGATGCCCT			
	TCCAG TACTACGGGA			
	TTC _ I			
GAM170 PCDHGC4	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
	AGGTC GTGATGCCCTT			
	TCCAG TACTACGGGAA			
	TC__ _ GI			
GAM170 PCDHGC5	AAGAGGTCA-TGATGCCCTT	2452	AC_ T	I
	AGGTC GTGATGCCCT			
	TCCAG TACTACGGGA			
	TTC _ I			
GAM170 PCDHGC5	AAGAGGTCA-TGATGCCCTT	2452	TAAC T	AG
	AGGTC GTGATGCCCTT			
	TCCAG TACTACGGGAA			
	TC__ _ GI			
GAM171 ANK1	GGGGGCTCTGACGTGGAGGGGGCT	2476	ACCC CT	I
	GGGGGC ATG GAGGGGGCT			
	CCCCCG TGC CTCCCCGA			
	AGAC AC I			
GAM171 ANKRD3	GGTGCACTCCAGCGACCTGAGGGGGGCT	2463	GGGG _ _ _	
	GCAC CCA TG CTGAGGGGGCT			
	CGTG GGT GC GACTCCCCCGA			
	CA__ A C TG GII			
GAM171 BCL11B	GGGTCACCCATGCTAGAGG	2468	G GG GA	
	GG CACCCATGCT GGGGGC			
	CC GTGGGTACGA TCTCCG			
	_ A_ _			
GAM171 BMP1	GGGGGCGTCC---CCGAGGGGGGCT	2475	AC ATG	
	GGGGGC CC CTGAGGGGGGCT			
	CCCCCG GG GGCTCCCCCGA			
	CA _			
GAM171 ESPN	GGGGGCTGC-ATCCTGGAGGGGGGCT	2471	ACC G _	I
	GGGGGC CAT CTG AGGGGGGCT			

	CCCCCG GTA GAC TCCCCGA		
	AC_ G C I		
GAM171 GNA11	GGGGC-CCCATGCTGGCTGGCGGGGGCT2467	GG A A_____ III	
	GGGC CCCATGCTG GGGGGCT		
	CCCG GGGTACGAC CCCCCGA		
	__ _ CGACCG GII		
GAM171 GTF2I	GGAGCAGCCTCGGCTGAGGGGAGCT 2466	GG C AT_ _ II	
	GGGCA CC GCTGAGGGG GCT		
	CTCGT GG CGACTCCCC CGA		
	_ C AGC T CI		
GAM171 HTR6	GGGGCACCCGATGAGCCGAGG 2464	GG AT___ GGGCT	
	GGGCACCC GCTGAGG		
	CCCGTGCG CGGCTCC		
	_ CTACT GIIT		
GAM171 NELL1	GGGGGCACCGAAGCT-AGGTGG 2473	CAT G _ GCT	
	GGGGGCACC GCT AGG GG		
	CCCCCGTGG CGA TCC CC		
	CTT _ A III		
GAM171 NR1I2	GGGGGCACCCATGTCCTTCCTGAGG 2469	_____ GGGCTII	
	GGGGGCACCCATG CTGAGG		
	CCCCCGTGGGTAC GACTCC		
	AGGAAG IIITCGG		
GAM171 PACE	GGGGGCACCCCTGGGCAGATGGCT 2474	A CTG GG I	
	GGGGGCACCC TG AG GGCT		
	CCCCCGTGGG AC TC CCGA		
	G CCG TA I		
GAM171 RFP	GGGAGCCATGCTGACAGGGC 2460	GGGGGCAC G	
	CCATGCTGA GGGGC		
	GGTACGACT TCCCG		
	TC_____ G		
GAM171 SCRT1	GGGGGCACCC-TG--GAGGGG 2472	A CT G	
	GGGGGCACCC TG GAGGGG		
	CCCCCGTGGG AC CTCCCC		
	_ _ I		
GAM171 SLC2A6	GGGGCACCCGCTGCTGAGG 2465	GG A_ GGGC	
	GGGCACCC TGCTGAGG		
	CCCGTGCG ACGACTCC		
	_ CG GIII		
GAM171 TARBP2	GGGGTTGCACTCAGACTGCTGAGGGG 2462	_ C _ GCTII	
	GGGG GCAC CA TGCTGAGGGG		

	CCCC CGTG GT ACGACTCCCC	
	AA A CTG IIITC	
GAM171 XRCC3	GGGCACGGTCCCAAGGCTGAGGGGG 2461 GGG_ CA T_ CTII	
	GG CCCA GCTGAGGGGG	
	II III IIIIIIIII	
	CC GGGT CGACTCCCCC	
	CGTG A_ TC AGII	
GAM171 ZNF205	GGGGGCACC--TGCGGCAGTGGG 2470 CA TGA _ CT	
	GGGGGCACC TGC GG GGG	
	IIIIIIII III II III	
	CCCCCGTGG ACG TC CCC	
	_ CCG A II	
GAM172 ABL2	CGGCTCCGCACCCGGCCTC 2497 _ III	
	CGGCTCCGCGCC GCCT	
	IIIIIIIIII IIII	
	GCCGAGGCGTGCG CGGA	
	GC GII	
GAM172 ABL2	CGGCTCCGCACCCGGCCTC 2497 TCA _ G CGCCT	
	CACTCGGC TCC CGC	
	IIIIIIII III III	
	GTGGGCCG AGG GTG	
	C_ G A CCIII	
GAM172 ADAM12	TCGCGCACGGC-CCGCGCCGCC 2515 CAACT_ T I	
	CGGC CCGCGCCGC	
	IIII IIIIIIIII	
	GCCG GCGCGGGCG	
	AGCGCGT _ I	
GAM172 ADAM12	TCGCGCACGGC-CCGCGCCGCC 2515 TCACACT T TC	
	CGGC CCGCGCCGCC	
	IIII IIIIIIIII	
	GCCG GCGCGGGCGG	
	AGCGCGT _ II	
GAM172 ADPRT	CACGCTTGCCGCCTCGCCGCCTC 2490 A CG _ G I	
	AC CT GCT CC CGCCGCCT	
	II II III II IIIIIII	
	TG GA CGG GG GCGGCGGA	
	C A_ C A I	
GAM172 ADPRT	CACGCTTGCCGCCTCGCCGCCTC 2490 TC A CG _ G I	
	AC CT GCT CC CGCCGCCTC	
	II II III II IIIIIII	
	TG GA CGG GG GCGGCGGAG	
	_ C A_ C A C	
GAM172 ARHGAP6	CACTGCCCTCCGCGCCCGCCTC 2492 ACTCGG _ I	
	CTCCGCGCC GCCT	
	IIIIIIII IIII	
	GAGGCGCGG CGGA	
	GACGG_ G I	
GAM172 ARHGAP6	CACTGCCCTCCGCGCCCGCCTC 2492 TCACACTCGG _	
	CTCCGCGCC GCCTC	
	IIIIIIII IIII	

		GAGGCGCGG CGGAG		
		ACGG_____ G		
GAM172 ARIH1	TCAGACGCGGCTCCGCTCCGGCCTC	2513	C T	G _ II
	TCA AC CGGCTCCGC CCG CCTC			
	AGT TG GCCGAGGCG GGC GGAG			
	C C A C II			
GAM172 ARIH1	TCAGACGCGGCTCCGCTCCGGCCTC	2513	CAC T	G _ I
	AC CGGCTCCGC CCG CCT			
	TG GCCGAGGCG GGC GGA			
	TC_ C A C I			
GAM172 ARSB	CTCGGCCCC-CGCCGCCTC	2507	G	I
	CTCGGCTCC CGCCGCCT			
	GAGCCGGGG GCGGCGGA			
	_____ G			
GAM172 ASCL2	ACCCTC--CTCCGCGCCGCC	2480	C GG	I
	ACTC CTCCGCGCCGC			
	TGGG GAGGCGCGGCG			
	_ AG I			
GAM172 ASCL2	ACCCTC--CTCCGCGCCGCC	2480	TCACA GG	
	CTC CTCCGCGCCGCC			
	GAG GAGGCGCGGCGG			
	G_____			
GAM172 BRCA2	CACAG-CGGCTCCGCCTCTGCCGCCT	2489	ACACT	_____ I
	CGGCTCCGC GCCGCC			
	GCCGAGGCG CGGCGG			
	C_____ GAGA I			
GAM172 BRCA2	CACAG-CGGCTCCGCCTCTGCCGCCT	2489	TC CT	_____ CII
	ACA CGGCTCCGC GCCGCCT			
	TGT GCCGAGGCG CGGCGGA			
	_ C_ GAGA TII			
GAM172 CACNA1S	CACTCGGCTCCCCGCTGCC	2493	G C II	
	CACTCGGCTCC CGC GC			
	GTGAGCCGAGG GCG CG			
	G A GI			
GAM172 CACNA1S	CACTCGGCTCCCCGCTGCC	2493	TCACAC	G C T
	TCGGCTCC CGC GCC			
	AGCCGAGG GCG CGG			
	_____ G A C			
GAM172 CD81	CAGACTCGGCTCTCGAACCG	2488	C _ C II	
	CA ACTCGGCTC CG GCC			

	GT TGAGCCGAG GC TGG	
	C A T C I	
GAM172 CD81	CAGACTCGGCTCTCGAACCG 2488 TCAC _ C CCT	
	ACTCGGCTC CG GCCG	
	TGAGCCGAG GC TGGC	
	TC_ A T C II	
GAM172 CDR2	CAGACTCCGCT--GCGCCGCCTC 2491 AC_ G CC I	
	ACTC GCT GCGCCGCCT	
	TGAG CGA CGCGGCGGA	
	GTC G _ I	
GAM172 CDR2	CAGACTCCGCT--GCGCCGCCTC 2491 TCAC G CC	
	ACTC GCT GCGCCGCCTC	
	TGAG CGA CGCGGCGGAG	
	TC_ G _	
GAM172 CRAT	CACACCGGGCAAAGTCCGCGCCGCC 2487 AACTC _ _ I	
	GGC TCCGCGCCGC	
	CCG AGGCGCGGCG	
	GC_ TTTC I	
GAM172 CRAT	CACACCGGGCAAAGTCCGCGCCGCC 2487 TC C _ TCII	
	AACT GGC TCCGCGCCGC	
	TGTGG CCG AGGCGCGGCGG	
	_ C TTTC CIII	
GAM172 DYRK1A	TCAGCCTCGGGCTCCCGCGCCGCTC2510 CA _ _ _ III	
	TCA CTCGG CTCC GCGCCGC CTC	
	AGT GAGCC GAGG CGCGGCG GAG	
	CG C G C III	
GAM172 DYRK1A	TCAGCCTCGGGCTCCCGCGCCGCTC2510 CACA _ _ _ I	
	CTCGG CTCC GCGCCGC CT	
	GAGCC GAGG CGCGGCG GA	
	G_ C G C I	
GAM172 FGF18	CACATGTCCGCTCCGCGCGGCC 2484 ACAC G C I	
	TC GCTCCGCGC GC	
	AG CGAGGCGCG CG	
	GTAC G C I	
GAM172 FGF18	CACATGTCCGCTCCGCGCGGCC 2484 TC C_ G C TC	
	ACA TC GCTCCGCGC GCC	
	TGT AG CGAGGCGCG CGG	
	_ AC G C C I	
GAM172 FGFR4	TCAC-CT-GGCTCCTCCGCGCCTC 2512 CA TC G_ I	
	CAC GGCTCC CGCCGCCT	

	GTG CCGAGG GCGGCGGA	
	A_ GA AG I	
GAM172 FGFR4	TCAC-CT-GGCTCCTCCGCCGCTC 2512 TCA TC G_ I	
	CAC GGCTCC CGCCGCCTC	
	GTG CCGAGG GCGGCGGAG	
	A__ GA AG I	
GAM172 FOXD2	CACTCTCCGGCTCCGCTCCG 2485 A _ G II	
	CAC CTC GGCTCCGC CC	
	GTG GAG CCGAGGCG GG	
	A G A CI	
GAM172 FOXD2	CACTCTCCGGCTCCGCTCCG 2485 TC A _ G CCT	
	AC CTC GGCTCCGC CCG	
	TG GAG CCGAGGCG GGC	
	_ A G A CII	
GAM172 GCN5L1	TCAC-CTCGGCTCCCCGGGGCC 2514 A G CC TC	
	TCAC CTCGGCTCC CG GCC	
	AGTG GAGCCGAGG GC CGG	
	_ G CC II	
GAM172 GCN5L1	TCAC-CTCGGCTCCCCGGGGCC 2514 _ A G CC I	
	CAC CTCGGCTCC CG GC	
	GTG GAGCCGAGG GC CG	
	A _ G CC I	
GAM172 GUCY1A2	CTGGGGGGCCGCCGCCGCCTC 2503 CTC CT _ II	
	GG CCGC GCCGCCT	
	CC GGCG CGGCGGA	
	GAC CC G GI	
GAM172 GUCY1A2	CTCG-CGCGGCGCCGCCTC 2506 _ TCC I	
	CTCG GC GCGCCGCCT	
	GAGC CG CGCGGCGGA	
	G C_ G	
GAM172 HDAC4	ACTCGGCTCTGGGTC-CCTC 2482 _ CGCG_ GCCTI	
	CTCGGCTC CC	
	GAGCCGAG GG	
	T ACCCA GAIII	
GAM172 HIC1	CTCGCGCTCAGCCAGCGGCC 2498 _____ CC _ GCIII	
	CTCGGCT GCG CC	
	GAGTCGG CGC GG	
	GAGCGC T_ C IIICG	
GAM172 HIC1	CTCGCGCTCAGCCAGCGGCC 2498 TCACA CC _ _	
	CTCGGCT GCG CCGC CT	

	GAGTCGG CGC GGCG GA	
	C_____ T_ C A	
GAM172 IL6R	CTCGGCCCGCGCCGCGCTC 2505 _ II	
	CTCGGCTCCGCGCCGC CT	
	GAGCCGGGGCGCGGCG GA	
	C GI	
GAM172 IL6ST	CACTCAGG-CCGCGCCGCCTC 2494 _ CT I	
	ACTCGG CCGCGCCGCCT	
	TGAGTC GGCGCGGCGGA	
	G C_ I	
GAM172 IL6ST	CACTCAGG-CCGCGCCGCCTC 2494 TCACAC CT	
	TCGG CCGCGCCGCCT	
	AGTC GGCGCGGCGGA	
	_____ C_	
GAM172 LDB1	CTCGGCTCTCCCGGCCGCGCCTC 2501 _ G TIII	
	CTCGGC TCC CGCCGCC	
	GAGCCG AGG GCGGCGG	
	AG G CGGAG	
GAM172 LDB1	CTCGGCTCTCCCGGCCGCGCCTC 2501 TCACA GG _ I	
	CTC CTCCGC GCCGCCTC	
	GAG GGGGCG CGGCGGAG	
	_____ A_ G A	
GAM172 MAN2A2	TCAGCGCCCGGCCTCCGCGCCGC 2509 CA_ _ CTCI	
	TCA CTCGGC TCCGCGCCGC	
	AGT GGGCCG AGGCGCGGCG	
	CGC G IIIC	
GAM172 MAN2A2	TCAGCGCCCGGCCTCCGCGCCGC 2509 CACA _ I	
	CTCGGC TCCGCGCCG	
	GGGCCG AGGCGCGGC	
	CGC_ G I	
GAM172 MAP3K5	CACAGCTCGGGGCTGCTCCGCGCCCGCC2483 AACTCG _ I	
	GCTCCGCGCC GC	
	CGAGGCGCGG CG	
	CCCCGA_ G I	
GAM172 MAP3K5	CACAGCTCGGGGCTGCTCCGCGCCCGCC2483 TC _ _ TCIII	
	ACA CTCG GCTCCGCGCC GCC	
	TGT GAGC CGAGGCGCGG CGG	
	_ C CCCGA G CIIC	
GAM172 MAP3K7IP2	CTCGGCCGCGCCGCGCCTC 2500 _ _ III	
	CTCGGCT CCGC GCCGCCT	

	GAGCCGG GGCG CGGCGGA		
	C G GII		
GAM172 MET	CACACGCGCGCTCCGCGCCTCC 2486 A T _ GCI		
	CAC CG GCTCCGCGCC		
	GTG GC CGAGGCGCGG		
	_ C G AGI		
GAM172 MET	CACACGCGCGCTCCGCGCCTCC 2486 TC T _ G C		
	ACAC CG GCTCCGCGCC CCT		
	TGTG GC CGAGGCGCGG GGG		
	_ C G A I		
GAM172 MLF2	CTCGGCCTTCCACGCCGCCTC 2499 _ III		
	CTCGGC TCCGCGCCGCCT		
	GAGCCG AGGTGCGGCGGA		
	GA GII		
GAM172 MLF2	CTCGGCCTTCCACGCCGCCTC 2499 TCACACTCGGC		
	TCCGCGCCGCCTC		
	AGGTGCGGCGGAG		
	GGA_____		
GAM172 NEO1	CTCGGCTCCCGGGCGCCGC 2502 _ III		
	CTCGGCTCC GCGCCG		
	GAGCCGAGG CGCGGC		
	GCC GII		
GAM172 NEO1	CTCGGCTCCCGGGCGCCGC 2502 TCACA CTCC _		
	CTCGG GCGCCGC CT		
	GGGCC CGCGGCG GA		
	GA_____ AC		
GAM172 PTPRF	TCCCACTCCTCTGCCGCCGCCGCCTC 2511 A GG _ _ II		
	TC CACTC CT CCGC GCCGCCTC		
	AG GTGAG GA GGCG CGGCGGAG		
	G GA C G II		
GAM172 PTPRF	TCCCACTCCTCTGCCGCCGCCGCCTC 2511 CA GG _ _ I		
	CACTC CT CCGC GCCGCCT		
	GTGAG GA GGCG CGGCGGA		
	_ GA C G I		
GAM172 SMURF1	CGGCCCGCGCCGCCGCCTC 2495 _ TIIIG		
	CGGCTCCGC GCCGCC		
	GCCGGGGCG CGGCGG		
	G CGGAG		
GAM172 SRRM2	CGCCTCCGCCGCCGCCTC 2496 G _ III		
	CG CTCCGC GCCGCCT		

	GC GAGGCG CGGCGGA	
	G GG GII	
GAM172 TEF	ACTCGGCTCGCGCACCTCGCCTC 2481 CTC _ _ I	
	GGCTC CGCGCC GCCT	
	CCGAG GCGTGG CGGA	
	_ C AG I	
GAM172 TNFRSF1B	CTCGGCTCCCTGCAACCTC 2508 GC C II	
	CTCGGCTCC GC GCCT	
	GAGCCGAGG CG TGGA	
	GA T GI	
GAM172 TNFRSF1B	CTCGGCTCCCTGCAACCTC 2508 TCACA G T_ GCG	
	CTC GC CC CCGCCT	
	GGG CG GG GGTGGA	
	GA_ A TT A_	
GAM172 YY1	CTCGGCTCCCCGCCTCGCCTC 2504 G _ III	
	CTCGGCTCC CGCC GCCT	
	GAGCCGAGG GCGG CGGA	
	G AG GII	
GAM172 YY1	CTCGGCTCCCCGCCTCGCCTC 2504 TCACA G TC GC	
	CTC GC CGC CGCCTC	
	GGG CG GCG GCGGAG	
	GA_ G GA GA	
GAM172 ZNF18	ACACTCGGC-CCGCGGCGCC 2479 _ T C I	
	CACTCGGC CCGCG CGC	
	GTGAGCCG GGCGC GCG	
	T _ C I	
GAM172 ZNF18	ACACTCGGC-CCGCGGCGCC 2479 TCAC T C T	
	ACTCGGC CCGCG CGCC	
	TGAGCCG GGCGC GCGG	
	_ _ C C	
GAM173 ABCB9	TCGCTCCGCTCTTCCCGCT 2522 G_ G TTCGA	
	TCGCTCCGC TTC CGCT	
	AGCGAGGCG AAG GCGA	
	AG G IIICA	
GAM173 ABCB9	TCGCTCCGCTCTTCCCGCT 2522 G_ G II	
	TCGCTCCGC TTC CGC	
	AGCGAGGCG AAG GCG	
	AG G AI	
GAM173 EN2	CGCTC-GCC--CGCGCTTTC 2519 _ CGC	
	GCTC GTTCGCGCTTT	

	CGAG CGGGCGCGAAA			
	G _ _ _			
GAM173 EN2	CGCTC-GCC--CGCGCTTTC	2519 TC	CGC	G
	GCTC GTTCGCGCTTTC			
	CGAG CGGGCGCGAAAG			
	_ _ _ G			
GAM173 NPTX2	CGCTCCGCGGGAGGCGCCTTCG	2518 G	TTC_	I
	CTCCGCG GCGCTTTC			
	GAGGCGC CGCGGAAG			
	_ CCTC I			
GAM173 NPTX2	CGCTCCGCGGGAGGCGCCTTCG	2518 TC	TTC_	AC
	GCTCCGCG GCGCTTTCG			
	CGAGGCGC CGCGGAAGC			
	_ CCTC GI			
GAM173 PDE5A	GCTCCAGTCGGGCCGCTTTCGAC	2521 CTC_	C T C	I
	CG GT CG GCTTTCGA			
	GC CG GC CGAAAGCT			
	GGTCA C _ _ I			
GAM173 PRKAB1	GCTCTCGCAATCGCGCTTT	2520 _ T	II	
	GCTC CGCG TCGCGCTT			
	CGAG GCGT AGCGCGAA			
	A T AI			
GAM173 PRKAB1	GCTCTCGCAATCGCGCTTT	2520 TCG C T	CGA	
	CTC GCG TCGCGCTTT			
	GAG CGT AGCGCGAAA			
	A _ _ T TGI			
GAM173 UBTF	TCGCTCCGC-TTCGCCATCTCG	2523	G GC AC	
	TCGCTCCGC TTCGC TTTCG			
	AGCGAGGCG AAGCG AGAGC			
	_ GT II			
GAM173 UBTF	TCGCTCCGC-TTCGCCATCTCG	2523 _	G GC I	
	CGCTCCGC TTCGC TTTC			
	GCGAGGCG AAGCG AGAG			
	A _ GT I			
GAM174 COG3	ATGCCCTCATTTCTTTGGAAAG	2526	G_ III	
	ATGCCCTCAT TTGGGAA			
	TACGGGAGTA AACCTTT			
	AAGA CII			
GAM174 DYT1	GGGATGCCCTCCTGTTTCAGGAA	2529	A _ GCA	
	GGGATGCCCTC TGTT GGGAA			

	CCCTACGGGAG ACAA TCCTT	
	G G III	
GAM174 DYT1	GGGATGCCCTCCTGTTCAGGAA 2529 G A _ I	
	GATGCCCTC TGTT GGG A	
	CTACGGGAG ACAA TCCT	
	_ G G I	
GAM174 IL1RAP	GATGCCTT--TCTTGGGAAGC 2528 CTCATG I	
	GATGCC TTGGGAA	
	CTACGG AACCTT	
	AAAG_ C	
GAM174 IL1RAP	GATGCCTT--TCTTGGGAAGC 2528 GGGA CTCATG	
	TGCC TTGGGAAGC	
	ACGG AACCTTCG	
	____ AAAG_	
GAM174 RGS14	CCCTCCATGTTGGGCAAGC 2527 _ _ III	
	CCCTC ATGTTGGG AAG	
	GGGAG TACAACCC TTC	
	G G GII	
GAM174 SLC21A3	GGCATTGCCTCAC-TTGGGAAGC 2530 G GC G A	
	GG AT CCTCAT TTGGGAAGC	
	CC TA GGAGTG AACCTTCG	
	G AC _ I	
GAM174 SLC21A3	GGCATTGCCTCAC-TTGGGAAGC 2530 GGA_ C G I	
	TGCC TCAT TTGGGAAG	
	ACGG AGTG AACCTTC	
	CCGTA _ _ I	
GAM174 SOST	GGGAAGCC---AGGCTGGGAAGCA 2531 T CTCAT	
	GGGA GCC GTTGGGAAGCA	
	CCCT CGG CGACCCTTCGT	
	T TC_	
GAM174 SOST	GGGAAGCC---AGGCTGGGAAGCA 2531 _ T CTCAT	
	GGA GCC GTTGGGAAGC	
	CCT CGG CGACCCTTCG	
	C T TC_	
GAM175 CDS2	CCTGCTCAGTTCTGTTCT 2536 A _ II	
	CCT CT AGTTCTGTTCC	
	GGA GA TCAAGACAAGG	
	C G AI	
GAM175 CDS2	CCTGCTCAGTTCTGTTCT 2536 TATCCTAC CT	
	TAGTTCTGTTCT	

	GTCAAGACAAGGA		
	CGA_____CA		
GAM175 CRY2	TCCTACCACTACGTTCTGTTC	2538	_____IIIG
	TCCTACTA GTTCTGTT		
	AGGATGGT CAAGACAA		
	GATG GIII		
GAM175 CRY2	TCCTACCACTACGTTCTGTTC	2538 TATC	_ CTCTG
	CTACTA GTTCTGTTC		
	GGTGAT CAAGACAAG		
	GAT_ G TCIII		
GAM175 GPR61	ATCCTGTTGGCTCTGTTCCT	2535 ACTA	I
	TCCT GTTCTGTTCC		
	AGGA CGAGACAAGG		
	CAAC I		
GAM175 GPR61	ATCCTGTTGGCTCTGTTCCT	2535 TA ACTA	CT
	TCCT GTTCTGTTCCCT		
	AGGA CGAGACAAGGA		
	_ CAAC CI		
GAM175 OTX1	TATCTTAA-AGTTCTGTTTCCT	2537 C CT	_ CTG
	TATC TA AGTTCTGTT CCT		
	ATAG AT TCAAGACAA GGA		
	A T_ A III		
GAM175 OTX1	TATCTTAA-AGTTCTGTTTCCT	2537 C CT	_ I
	ATC TA AGTTCTGTT CC		
	TAG AT TCAAGACAA GG		
	A T_ A I		
GAM175 POP4	TCCTGCCAGT-CTGTTTCCTC	2539_ A T	I
	CCT CTAGT CTGTTTCCT		
	GGA GGTCA GACAAGGA		
	A C _ I		
GAM175 POP4	TCCTGCCAGT-CTGTTTCCTC	2539 TATC A T	
	CT CTAGT CTGTTTCCTCT		
	GA GGTCA GACAAGGAGG		
	_____C _		
GAM175 TFE3	ATCCT-C-ACTTCTGTTTCCT	2534 _ AC G	I
	TCCT TA TTCTGTTCC		
	AGGA GT AAGACAAGG		
	T _ G I		
GAM175 TFE3	ATCCT-C-ACTTCTGTTTCCT	2534 TA AC G	C
	TCCT TA TTCTGTTTCCT		

	AGGA GT AAGACAAGGA		
	— — G A		
GAM176 ADCY6	TACCCTCACCCCTACCCCATGGCACC 2562	— A —	CII
	TACCCTCACCCC ATC CA GCACC		
	ATGGGAGTGGGG TGG GT CGTGG		
	A G AC III		
GAM176 ASPH	ACCCTCA-CCAATCAGAGCA 2546 TA	CC C CC	
	CCCTCACC ATCA AGCA		
	GGGAGTGG TAGT TCGT		
	— T_ C TI		
GAM176 ATF5	CCCTCACCCAGACACAGCCCC 2557 TACC	CAT A	
	CTCACCC CACAGC CCC		
	GAGTGGG GTGTCTG GGG		
	— TCT —		
GAM176 CDKN1A	ACCCTCACCCC--CACAGC 2545 TA	AT AC	
	CCCTCACCCC CACAGC		
	GGGAGTGGGG GTGTCTG		
	— — AI		
GAM176 CELSR2	CCCCCACCCACATCACAGCA 2553 TACC	— CC	
	CTCACCC CATCACAGCA		
	GGGTGGG GTAGTGTCTG		
	— T TT		
GAM176 ENO2	ACCCTGACGCTCCCATCACAG 2542 TA	C — CACCC	
	CCCT AC CCCATCACAG		
	GGGA TG GGGTAGTGTC		
	— C CGA TIIC		
GAM176 FADD	CCTCTCCCCACCACAGCACCC 2561 TACCCTCA		
	CCCCATCACAGCACCC		
	GGGGTGGTGTCTGTTGG		
	GA—		
GAM176 FLNA	CCCTCACCCC-TCCAGAACCC 2558 TACC	A A C	
	CTCACCCC TC CAG ACC		
	GAGTGGGG AG GTC TGG		
	— — G T		
GAM176 FUT1	CCCTCACCCCACGTTTACA 2555 TACC	— GCACC	
	CTCACCCCA TCACA		
	GAGTGGGGT AGTGT		
	— GCA AAI		
GAM176 GAS1	ACCCTCACCCC--CAGTTCAC 2547 TA	AT AG C	
	CCCTCACCCC CAC CAC		

	GGGAGTGGGG GTG GTG		
	— — CA A		
GAM176 GJB1	CCCTCACCCCA-GACACCTCC 2559 TACC	TCACA	
	CTCACCCCA GCACC		
	GAGTGGGGT TGTGG		
	— — C —		
GAM176 GJB1	CACCCACATGTCCACAGCACCC 2550 TACCCTCACCCCA		
	TCACAGCACCC		
	GGTGTCTGTGGG		
	GTACA —		
GAM176 GYPC	CCCTCACCTCAACA-AGGAC 2554 TACC	_ T C C C	
	CTCACCC CA CA AG AC		
	GAGTGGG GT GT TC TG		
	— — A T _ C A		
GAM176 HAP1	CCCTCACCCACCCACA-CAC 2556 TACC	CA G C	
	CTCACCC TCACA CAC		
	GAGTGGG GGTGT GTG		
	— — TG _ T		
GAM176 HMGE	ACACCCACCCCATCAACAGCA 2543 TACC	_ CCC	
	CTCACCCCATCA CAGCA		
	GGGTGGGGTAGT GTCGT		
	GT_ T CII		
GAM176 LRP5	CCCTGCCCACCCCATCACAG 2551 TACC	CACC	
	CTCACCCCATCACAG		
	GGGTGGGGTAGTGTC		
	GAC_ AAI		
GAM176 LTB	CCCTCACCCACCATCACGGCCCC 2552 TACC	_ _ A I	
	CTCACCCCATCA CA GC CCC		
	GAGTGGGGTGGT GT CG GGG		
	— — A GC _ T		
GAM176 MTNR1A	TACTCTACCCAGCCCTGAACC 2563 C	_ ACAGC CI	
	TAC CTCACCCCA TC ACC		
	ATG GAGTGGGGT GG TGG		
	A C GACT_ II		
GAM176 PDYN	ACCCTT-CCCCATCACAG-ACCC 2549 TA CA	C	
	CCCT CCCCATCACAG ACCC		
	GGA GGGGTAGTGTC TGGG		
	— A_ —		
GAM176 SGCA	ACTCTACCCACCCACCCCC 2548 TACC	ACA A	
	CTCACCCCATC GC CCC		

	GAGTGGGGTGG TG GGG	
	GA__ GG_ G	
GAM176 SLC6A8	ACCCTCACCCAGCCCCAGC 2544 TA CA A ACC	
	CCCTCACCC TC CAGC	
	GGGAGTGGG GG GTCG	
	__ TC G GII	
GAM176 ZNF205	CCTCACCCCATGCCCTCACC 2560 CAC A A ACC	
	TACCCT CCC TCAC GC	
	GTGGGG GGG AGTG CG	
	TAC _ G GII	
GAM177 ACADS	GGGACAGGTGTGTTTATTA 2575 A ATTII	
	GGGA AGGTGTGTT	
	CCCT TCCACACAA	
	G ATAAT	
GAM177 ATBF1	ATTTTGTAAATTGGTTTGTTATTAA 2572 GG AA G I	
	TTTG A GGT TGTTATTA	
	AAAC T CCA ACAATAAT	
	TT AA A I	
GAM177 ATBF1	ATTTTGTAAATTGGTTTGTTATTAA 2572 AA GG AA G II	
	TTTG A GGT TGTTATTAA	
	AAAC T CCA ACAATAATT	
	AA TT AA A AI	
GAM177 CANX	ATTGGGGAAA-GTCTGCTAT 2573 _ G G I	
	TTTGGGAAAG T TGTTA	
	AAACCCTTTC A ACGAT	
	T _G I	
GAM177 CANX	ATTGGGGAAA-GTCTGCTAT 2573 AA G G TA	
	TTTGGGAAAG T TGTTAT	
	AAACCCTTTC A ACGATA	
	_ _G CI	
GAM177 DAPP1	AATTCTGGGAAAGGGATTGTTAT 2566 A TG_ I	
	TTTGGGAAAGG TGTTA	
	AGACCCTTTCC ACAAT	
	_ CTA I	
GAM177 DAPP1	AATTCTGGGAAAGGGATTGTTAT 2566 AA_ TG_ TAAI	
	TTTGGGAAAGG TGTTAT	
	AGACCCTTTCC ACAATA	
	TTA CTA IIIA	
GAM177 DIBD1	TTTGGGGCCACAGGTGTGTT 2580 AA__ III	
	TTTGGG AGGTGTGT	

	AAACCC TCCACACA		
	CGGTG AII		
GAM177 DIBD1	TTTGGGGCCACAGGTGTGTT 2580 AATTT AA__ ATTA		
	GGG AGGTGTGTT		
	III		
	CCC TCCACACAA		
	AC__ GGTG CIII		
GAM177 FBXL7	AATCTGGGAAAGGGCCATGTGTTTATTA2568 ____ _ AIII		
	AATTTGGGAAAGG TGTGTT ATTA		
	TTAGACCCTTTCC ACACAA TAAT		
	CGGT A IIIA		
GAM177 FBXL7	AATCTGGGAAAGGGCCATGTGTTTATTA2568 TG ____ ATTI		
	GGAAAGG TGTGTT		
	CCTTTCC ACACAA		
	__ CGGT AIII		
GAM177 FNTB	TGCACCAAGCGTGG-CCTTG 2576 _ A CGTI		
	GCG CAAGCGTGGTC		
	III		
	CGT GTTCGCACCGG		
	A G AAI		
GAM177 FNTB	TGCACCAAGCGTGG-CCTTG 2576 TGTTGCGA CGTG		
	CAAGCGTGGTC		
	GTTCGCACCGG		
	TG____ AACC		
GAM177 GPR85	AATATGG-AATTCTGTGTTATTA 2570 AATTTG AGG A		
	GGAA TGTGTTATTA		
	III		
	CCTT ACACAATAAT		
	TTATA_ AAG I		
GAM177 GPR85	AATATGG-AATTCTGTGTTATTA 2570 ATTTG AGG I		
	GGAA TGTGTTATT		
	III		
	CCTT ACACAATAA		
	TTATA AAG I		
GAM177 KCNK4	TGGGACA-GCGTGGT-CGTG 2578 C A CGI		
	TG GACA GCGTGGTC		
	II		
	AC CTGT CGCACCAG		
	C _ CAC		
GAM177 KCNK4	TGGGACA-GCGTGGT-CGTG 2578 TGTTGC A C		
	GACA GCGTGGTC GT		
	III II		
	CTGT CGCACCAG CA		
	____ _		
GAM177 KPNA1	ATTTGGGAAAATTGGAGGGTTTTT 2571 AA ____ TGT ATTAAI		
	TTTGGGAAA GG GTT		
	II III		

	AAACCCTTT CC CAA		
	___ TAA TCC AAAAII		
GAM177 LDB3	TTTGGGAAAGCTGCTTGTT	2582	G GTIII
	TTTGGGAAAG TGT		
	AAACCCTTTC ACG		
	G AACAA		
GAM177 LDB3	TTTGGGAAAGCTGCTTGTT	2582 AATT	G ___ ATTA
	TGGGAAAG TGT GTT		
	ACCCTTTC ACG CAA		
	___ G AA CGII		
GAM177 MAP3K4	GACAGAGGCGATGGTCCGTG	2574	A___ _ III
	GACA GCG TGGTCCGT		
	CTGT CGC ACCAGGCA		
	CTC T CII		
GAM177 MLN	AATTTGCTTTGGAAAGGTGTTTT	2567	___ GTIIIA
	AATTTG GGAAAGGTGT		
	TTAAAC CCTTCCACA		
	GAAA AAIII		
GAM177 MLN	AATTTGCTTTGGAAAGGTGTTTT	2567	___ GTTATTAI
	AATTTG GGAAAGGTGT		
	TTAAAC CCTTCCACA		
	GAAA AAIIIAAT		
GAM177 SHOX	TTTGGGAAACGGTGTGTGATT	2581 AATT	_ T AA
	TGGGAAA GGTGTGT ATT		
	ACCCTTT CCACACA TAA		
	___ G C AC		
GAM177 SHOX	TTTGGGAAACGGTGTGTGATT	2581 T	_ TATI
	TGGGAAA GGTGTGT		
	ACCCTTT CCACACA		
	_ G CTAI		
GAM177 SORBS1	TGAGATAAGATAGTGTATTAA	2579 AATTTGGA	_
	AAGGT GTGTATTAA		
	TTCTA CACAATAATT		
	TA_____ T		
GAM177 SORBS1	TGAGATAAGATAGTGTATTAA	2579 GGGA	_ I
	AAGGT GTGTATTAA		
	TTCTA CACAATAAT		
	CTA_ T I		
GAM177 TPMT	AATTTGGG-AATGTTTGTT	2569	AG G ATT
	AATTTGGGAA GT TGTT		

	TTAAACCCTT CA ACAA			
	A_ A III			
GAM177 TPMT	AATTTGGG-AATGTTTGT	2569	AGG_ GTI	
	AATTTGGGAA TGT			
	III			
	TTAAACCCTT ACA			
	ACAA AII			
GAM177 YWHAG	TGCTA-AAGA-TGGTCCGTG	2577_	GAC C I	
	GC AAG GTGGTCCGT			
	II III			
	CG TTC TACCAGGCA			
	A AT_ _ I			
GAM178 CPD	TATAAGCAGC-AGCACCTGT	2591	ATCATCATC I	
	TAGCACCTG			
	GTCGTGGAC			
	ATATTCGTC I			
GAM178 CPD	TATAAGCAGC-AGCACCTGT	2591	TATCATCATC CCG	
	TAGCACCTGT			
	GTCGTGGACA			
	ATATTCGTC_ III			
GAM178 CTSL	TCTTCCAGTCCCTGTCCGG	2594	A CA II	
	TC TCTAG CCTGTCCG			
	II			
	AG AGGTC GGACAGGC			
	A AG CI			
GAM178 MTMR3	TATCATAACCTCTTGGCACCTGTC	2590	C A___ CGGI	
	TATCAT ATCT GCACCTGTC			
	ATAGTA TGGA CGTGGACAG			
	T GAAC IIIG			
GAM178 MTMR3	TATCATAACCTCTTGGCACCTGTC	2590	ATC A A_ I	
	ATC TCT GCACCTGT			
	TGG AGA CGTGGACA			
	TAT _ AC I			
GAM178 NFKB2	TCCTCCAGCCGCTGTCCGG	2593	A A_ II	
	TC TCTAGC CCTGTCCG			
	II			
	AG AGGTCTG GGACAGGC			
	G GC CI			
GAM178 RFC4	ATCATCATCCAG--CTTGTCC	2586_	ACC I	
	TCATCATCTAGC TGTC			
	AGTAGTAGGTCTG ACAG			
	T A_ I			
GAM178 RFC4	ATCATCATCCAG--CTTGTCC	2586	TA ACC G	
	TCATCATCTAGC TGTC			

	AGTAGTAGGTCG ACAGG		
	___ A___ A		
GAM178 SCD	ATCATCATCTTTAGCATCCTG 2585	___ _ III	
	ATCATCATCT AGCA CCT		
	TAGTAGTAGA TCGT GGA		
	AA A CII		
GAM178 SCD	ATCATCATCTTTAGCATCCTG 2585 TA	___ _ TCCGG	
	TCATCATCT AGCA CCTG		
	AGTAGTAGA TCGT GGAC		
	___ AA A CIIIG		
GAM178 SLC7A7	TATTGTCATCCAGCACCTGT 2592 CA	CCG	
	TAT TCATCTAGCACCTGT		
	ATA AGTAGGTCGTGGACA		
	AC		
GAM178 SLC7A7	TATTGTCATCCAGCACCTGT 2592 ATCA	I	
	TCATCTAGCACCTG		
	AGTAGGTCGTGGAC		
	TAAC I		
GAM178 TDG	ATCCT-TACCGCCTGTCCGG 2587 TCA A A_	I	
	TCT GC CCTGTCCG		
	GGA TG GGACAGGC		
	TA_ A GC I		
GAM178 TSNAX	CAACATCTGGGCACCTGTC 2588 T A_	II	
	CA CATCT GCACCTGT		
	GT GTAGA CGTGGACA		
	T CC GI		
GAM178 TSNAX	CAACATCTGGGCACCTGTC 2588 TATCAT A_	CG	
	CATCT GCACCTGTC		
	GTAGA CGTGGACAG		
	___ CC TT		
GAM178 WRN	CATCTTCC--CACCTGTCC 2589 A AG	I	
	CATC TCT CACCTGTC		
	GTAG AGG GTGGACAG		
	A ___ G		
GAM178 WRN	CATCTTCC--CACCTGTCC 2589 TATCATCA AG		
	TCT CACCTGTCC		
	AGG GTGGACAGG		
	GA_____		
GAM179 MKKS	TTTTTATTTTGTAACACAT 2598 TATTTT GC_	GA	
	TTATTT AACTACAT		

	AATAAA TTGGTGTA		
	_____ ACAT AA		
GAM179 NDP	TTTTATATTTGCAAC-ACA 2599 TATTTT	T	
	TATTTGCAAC ACAT		
	ATAAACGTTG TGTG		
	AAT_____		
GAM179 PCDHGA8	ATTGTTTTATTTGGTTTAAACTAC 2597 TATT	C_____ ATGAI	
	TTTTATTTG AACTAC		
	AAAATAAAC TTGATG		
	AAC_ CAAAT AIIIA		
GAM180 ADORA2B	ATTTGTCAATCCTTGGAGCCTA 2606 ATTTCTG	GC	
	GATCCTTGGAGCTTA		
	TTAGGAACCTCGGAT		
	TAAACAG II		
GAM180 BRCA1	TTTCTGGATGCCTCTCAGCT 2615 AT	_ GG TAG	
	TTCTGGAT CCTT AGCT		
	AAGACCTA GGAG TCGA		
	_ C AG CII		
GAM180 CRY2	CTGAGTCCTTGGAGCTCAGC 2608 ATTTCTGGA		
	TCCTTGGAGCTTAG		
	AGGAACCTCGAGTC		
	C_____		
GAM180 DRD3	ATTTCTGGAGACCGAGGAGTTTA 2602	T_ TT C GCI	
	ATTTCTGGA CC GGAG TTA		
	II		
	TAAAGACCT GG CCTC AAT		
	CT CT A III		
GAM180 GIP	ATTTCTGGA-CCTTCTGAGC 2603	T G_ TTAG	
	ATTTCTGGA CCTT GAGC		
	TAAAGACCT GGAA CTCG		
	_ GA IIIC		
GAM180 GRF2	TTCAGGGACCCTGGAGCTTAG 2611 ATTTCT	T C	
	GGATCCT GGAGCTTAG		
	CCTGGGA CCTCGAATC		
	GTC_____ C		
GAM180 HUNK	TTTTGGGATCCTTGGA-CTGAG 2618 ATTTCT	G T C	
	GGATCCTTGGA CT AG		
	II II		
	CCTAGGAACCT GA TC		
	AAAC_____ C T		
GAM180 ITGA5	TTCTGATTCCCCTTGGAGCT 2610 ATTT	A_ TAG	
	CTGG TCCTTGGAGCT		

	<p> GACT GGGAACCTCGA ____ AAG CCI TTCCTTGGAT--TTGGAGCTT 2614 A TC CC AG TT TGGAT TTGGAGCTT AG ACCTA AACCTCGAA A GA _ CI </p>
GAM180 NOV	
	<p> ATCTCTGGATCCCTGTGAG 2604 _ CTTAG ATTCTGGATCCTTG GAG TAGAGACCTAGGGAC CTC A CG </p>
GAM180 PCDHA9	
	<p> TTGCTGGATCC-TGGAGCT 2616 ATTT T TA CTGGATCCT GGAGCT GACCTAGGA CCTCGA AC_ _ CI </p>
GAM180 PCDHB16	
	<p> TTTCTG-ATCCTTGA-ATTAG 2617 AT G C TTCTG ATCCTTGGAG TTAG AAGAC TAGGAACCTT AATC </p>
GAM180 PIK3C2B	
	<p> _ _ _ TTCGGGCTCCT--GAGCTTAGC 2613 ATTTCT A_ TG GG TCCT GAGCTTAG CC AGGA CTCGAATC G_ CG _ </p>
GAM180 PIK3C2B	
	<p> TCTGGATTATTGCAGGTCTTA 2609 ATTTCT CC G _ GGAT TTG AG CTTAGC CCTA AAC TC GAATTG _ AT G CA </p>
GAM180 PTTG1	
	<p> ATCTCAGGA-CCT-GGAGCTTAGC 2607 T T T ATTTC GGA CCT GGAGCTTAGC TAGAG CCT GGA CCTCGAATCG T _ _ </p>
GAM180 SLC21A9	
	<p> ATTTGGGG--CTTGGAGCTTA 2605 ATTTC ATC G TGG CTTGGAGCTTA ACC GAACCTCGAAT TAA_ CC_ I </p>
GAM180 TGFBR2	
	<p> TTCTG---CTTGGAGCTGAG 2612 ATTT GATC T CTG CTTGGAGCT A GAC GAACCTCGA T _ _ C </p>
GAM180 ZNF26	
	<p> GGGTGGCAGAGGTTGCAGTGA 2634 TG G T CAG AGTG GG GG GG GCAGTGA </p>
GAM181 ADCY6	

	CC TC CC CGTCACT	
	___ G T AA_ CGTT	
GAM181 CAMLG	GGGGTGGCAGTGGCGGTGATGT 2632 TGGGGG	___ A A G
	GTGGCA GGC GTGA GT	
	CACCGT CCG CACT CA	
	_____ CA C A A	
GAM181 CASP8	TGGCGGGGTACAGGCAGGCAG-GAAG 2635	_ _ T TGII
	TGG GGGGT GGCAGGCAG GAAG	
	ACC CCCCA CCGTCCGTC CTTC	
	G TGT _ IIIG	
GAM181 CSF1R	TGGGGAAGTGGCAGGCAGGTGCAG 2637	_ _ A TGI
	TGGGGG GTGGCAGGCAG TG AG	
	ACCCCT CACCGTCCGTC AC TC	
	T C G III	
GAM181 EFNB1	TGGGGGGTGG--GG--GTGAA 2642	CA CA G
	TGGGGGGTGG GG GTGAA	
	ACCCCCCACC CC CACTT	
	_ _ I	
GAM181 FOXD2	GGGGGACTGAGGCAGGCAGGGA 2621 T	G _ T AGTG
	GGGGG T GGCAGGCAG GA	
	CCCCT A CCGTCCGTC CT	
	_ G CT C CII	
GAM181 GAS11	TGGGCGGTGGCAGGTAGGTGA 2640	G CA_ AGTG
	TGGG GGTGGCAGG GTGA	
	ACCC CCACCGTCC CACT	
	G ATC IIIG	
GAM181 GPT	GGAGGTGGCAGGACCAGAAGTG 2628 TGGG	_ AGT
	GGGTGGCAGG C GAAGTG	
	TCCACCGTCC G CTTAC	
	_____ T GT_	
GAM181 HHLA1	TGGGGGGTGGTATGGAGAGA 2641	CA_ C T AGT
	TGGGGGGTGG GG AG GA	
	ACCCCCCACC CC TC CT	
	ATA _ T III	
GAM181 KRTHB1	TGTGGGGTGGCAGAGCCCAGAAGTG 2639 TGG	_ AGT II
	GGGGTGGCAG GC GAAGTG	
	CCCCACCGTC CG CTTAC	
	ACA T GGT II	
GAM181 MASP1	TGGGGTGTGCCCAGGCAGTG 2638	G G_ AAGT
	TGGGG GTG CAGGCAGTG	

	ACCCC CAC GTCCGTCAC			
	A GG III G			
GAM181 MGAT4B	GGGGGGTGGCTGCTGCAGT	2622 TG	AG__	GAAGT
	GGGGGTGGC GCAGT			
	CCCCACCG CGTCA			
	__ ACGA AIIIG			
GAM181 MPP2	GGGGTGGCAGGGGGCAGTG	2631 TGGGGG	__	AAGT
	GTGGCA GGCAGTG			
	CACCGT CCGTCAC			
	_____ CCC ACGI			
GAM181 NDRG3	GGGGGTGGGCAGGCAGAGA	2626 TGGG	_	T AGT
	GGGTGG CAGGCAG GA			
	CCCACC GTCCGTC CT			
	_____ C T CTI			
GAM181 NFE2L1	GGAGTGGCAAGGCAGTGAA	2633 TGGGGG	_	GT
	GTGGCA GGCAGTGAA			
	CACCGT CCGTCACTT			
	_____ T AC			
GAM181 NIPSNAP1	GGAGGGAGGCAGGCAGGGAA	2624 TG	T	T T
	GGGGG GGCAGGCAG GAAG			
	CTCCC CCGTCCGTC CTTT			
	_____ T C I			
GAM181 PLXNB3	GGGAGGTGGCAGGCAGGGA	2623 TG		T AGT
	GGGGGTGGCAGGCAG GA			
	CCTCCACCGTCCGTC CT			
	_____ C CII			
GAM181 RGS14	GGTGGCGGGCAGGCAGTGGAG	2625 TGGGGG	_	A TG
	GGTGG CAGGCAGTG AG			
	CCGCC GTCCGTCAC TC			
	CA__ C C TI			
GAM181 RNF26	TGGAGGGGTGGGCAGGCAGGGAAG	2636	_	_ T TGI
	TGG GGGGTGG CAGGCAG GAAG			
	ACC CCCACC GTCCGTC CTTC			
	T C C III			
GAM181 SRC	GGGGGTGGCA--CA--GAAGTG	2629 TGGG	AG	GT
	GGGTGGC GCA GAAG			
	CCCACCG TGT CTTC			

GAM181 TNNI3	GGGGGTGGCGGGTACTG-AGTG	2630 TGGG	A CAG	A
	GGGTGGC GG TGA GTG			

	CCCACCG CC ACT CAC			
	_____ C ATG _			
GAM181 TUBA2	GGGGGTGGCAGTGGAGTGGAG	2627	TGGG	GC_ A TG
	GGGTGGCAG AGTG AG			
	CCCACCGTC TCAC TC			
	_____ ACC C TT			
GAM182 BMP4	TGCCCACTCACCT-AGCTTCC	2663	GT CT CG	
	TGCCCACT CCT GCTTCC			
	ACGGTGTGA GGA CGAAGG			
	GT T_ II			
GAM182 BMP4	TGCCCACTCACCT-AGCTTCC	2663_	GT CT I	
	GCCCACT CCT GCTTC			
	CGGTGTGA GGA CGAAG			
	A GT T_ I			
GAM182 CAPN10	TGCCAACTGGGTCCTCTGCT	2658	C _ TCCCG	
	TGCCA ACT GTCCTCTGCT			
	ACGGT TGA CAGGAGACGA			
	T CC IGC			
GAM182 CAPN10	TGCCAACTGGGTCCTCTGCT	2658	C _	
	TGCCA ACT GTCCTCTGC			
	ACGGT TGA CAGGAGACG			
	T CC AII			
GAM182 CLASP1	TGGCACCCAG-CCTCTGCTT	2662	C A T CCC	
	TG CAC CTG CCTCTGCTT			
	AC GTG GGT GGAGACGAA			
	C _ C			
GAM182 CLASP1	TGGCACCCAG-CCTCTGCTT	2662_	C A T I	
	G CAC CTG CCTCTGCT			
	C GTG GGT GGAGACGA			
	A C _ C I			
GAM182 FCMD	TGGCTCACTGCAGACTCTGCTTCCCG	2659	GCCA C_ I	
	CACTGT CTCTGCTTCCC			
	GTGACG GAGACGAAGGG			
	GA_ TCT I			
GAM182 FCMD	TGGCTCACTGCAGACTCTGCTTCCCG	2659	T_ CA C_ II	
	GC CACTGT CTCTGCTTCCCG			
	CG GTGACG GAGACGAAGGGC			
	AC A_ TCT II			
GAM182 GAA	CACACAGGC-TCTGCTTCCC	2646_	TGTC I	
	ACAC CTCTGCTTCC			

	TGTG GAGACGAAGG	
	G TCC_ I	
GAM182 GAA	CACACAGGC-TCTGCTTCCC 2646 TGCCACACTGTC	
	CTCTGCTTCCC	
	GAGACGAAGGG	
	TGTCC_____	
GAM182 GAA	CACTGTCCTACCTGCTGCC 2649 _ TCIII	
	CACTGTCCT CTGCT	
	GTGACAGGA GACGA	
	TG CGGII	
GAM182 GAA	CACTGTCCTACCTGCTGCC 2649 TGCCACA T _ CC	
	CTG CCT CTGCTTC	
	GAT GGA GACGGAG	
	AG_____ _ C TA	
GAM182 GJB3	TGCCCACTG-CC-CTGCATTTCCT 2660 T T _ GI	
	TGCCCACTG CC CTGC TTCCC	
	ACGGTGTGAC GG GACG AAGGG	
	_ _ TA II	
GAM182 GJB3	TGCCCACTG-CC-CTGCATTTCCT 2660 T T _ I	
	GCCCACTG CC CTGC TTCC	
	CGGTGTGAC GG GACG AAGG	
	_ _ TA I	
GAM182 GNA11	TGCAACACCTACCTCTGCTT 2661 C GT CCC	
	TGC AACT CCTCTGCTT	
	ACG TGTGG GGAGACGAA	
	T AT III	
GAM182 GNA11	TGCAACACCTACCTCTGCTT 2661 C GT I	
	GC AACT CCTCTGCT	
	CG TGTGG GGAGACGA	
	T AT I	
GAM182 GNGT2	GCCCACTGTCCTCAGAGTGTTCCC 2656 CCA _ C I	
	CACTGTCCTC TG TTCC	
	GTGACAGGAG AC AAGG	
	_ TCTC _ I	
GAM182 GNGT2	GCCCACTGTCCTCAGAGTGTTCCC 2656 TG _ C II	
	CCCACTGTCCTC TG TTCCCG	
	GGTGTGACAGGAG AC AAGGGT	
	_ TCTC _ II	
GAM182 KITLG	CACTGTCC-CTGCTTCCCG 2650 T I	
	CACTGTCC CTGCTTCCC	

	GTGACAGG GACGAAGGG	
	— C	
GAM182 MYO1D	TGCCCCGCT-TCCT--GCTTCCCG 2665	ACA CC
	TGCC CTGT TCTGCTTCCCG	
	ACGG GGCG GGACGAAGGGC	
	— AA	
GAM182 MYO1D	TGCCCCGCT-TCCT--GCTTCCCG 2665	_ ACA CC
	GCC CTGT TCTGCTTCCC	
	CGG GGCG GGACGAAGGG	
	A — AA	
GAM182 MYO1F	CCACGCCG--CTCTGCTTCACG 2654	A TC CI
	CCAC CTG CTCTGCTTC	
	GGTG GGC GAGACGAAG	
	C — TG	
GAM182 MYO1F	CCACGCCG--CTCTGCTTCACG 2654	TGCCACACT _ C
	GTC CTCTGCTTC C	
	CGG GAGACGAAG G	
	TG_____ C T	
GAM182 PLCB4	CCTCAGTGTCTCTG-TTCCC 2652	CA_ C C I
	CA TGTCTCTG TTCC	
	GT ACAGGAGAC AAGG	
	GGA C _ I	
GAM182 PLCB4	CCTCAGTGTCTCTG-TTCCC 2652	TGCCA C C
	CA TGTCTCTG TTCCC	
	GT ACAGGAGAC AAGGG	
	A_____ C _	
GAM182 RARB	CCACAGCTTTCACTCTGCTTC 2651	_ G _
	CCACA CT TC CTCTGCTT	
	GGTGT GA AG GAGACGAA	
	C A T GII	
GAM182 RARB	CCACAGCTTTCACTCTGCTTC 2651	TGCC _ G _ CCG
	ACA CT TC CTCTGCTTC	
	TGT GA AG GAGACGAAG	
	_____ C A T TAI	
GAM182 SCN2B	CACTGCAACCTCTGCTTCCCG 2648	_
	CACTGT CCTCTGCTTCCC	
	GTGACG GGAGACGAAGGG	
	TT CII	
GAM182 SCN2B	CACTGCAACCTCTGCTTCCCG 2648	TGCCACACTGT
	CCTCTGCTTCCCG	

		GGAGACGAAGGGC		
		GTT_____		
GAM182 SMG1	CACACGG-CCACTGCTTCCC	2647_ T T T I		
	ACAC G CC CTGCTTCC			
	TGTG C GG GACGAAGG			
	G C_ T I			
GAM182 SYNGR1	TGCCCACTCTCCCCTACAGCCC	2664 G TT GI		
	TGCCCACT TCCTCTGC CCC			
	ACGGTGTGA AGGGGATG GGG			
	G TC II			
GAM182 SYNGR1	TGCCCACTCTCCCCTACAGCCC	2664 G TT I		
	GCCCACT TCCTCTGC CC			
	CGGTGTGA AGGGGATG GG			
	G TC I			
GAM182 TLX1	CCTCTCTGGCTTCTGCTTCCC	2653 CACA TCC I		
	CTG TCTGCTTCC			
	GAC AGACGAAGG			
	GAGA CGA I			
GAM182 TLX1	CCTCTCTGGCTTCTGCTTCCC	2653 TGCCACA TCC G		
	CTG TCTGCTTCCC			
	GAC AGACGAAGGG			
	AGA___ CGA G			
GAM182 TOP3A	GCCCAACTGTCCTCTAAGTTTCC	2655 C CTTCI		
	AACTGTCCTCTG			
	TGTGACAGGAGAT			
	_____ TCAAA			
GAM182 TOP3A	GCCCAACTGTCCTCTAAGTTTCC	2655 TG _ C_ CGI		
	CCA CACTGTCCTCTG TTCC			
	GGT GTGACAGGAGAT AAGG			
	___ T TCA TII			
GAM182 TRAP100	TGCCTCATCTTTCCTCACTGCTTCCC	2657 A _ G _ GII		
	TGCC CA CT TCCTC TGCTTCCC			
	ACGG GT GA AGGAG ACGAAGGG			
	A A A TG III			
GAM182 TRAP100	TGCCTCATCTTTCCTCACTGCTTCCC	2657 GCCA _ G _ I		
	CA CT TCCTC TGCTTCC			
	GT GA AGGAG ACGAAGG			
	A___ A A TG I			
GAM182 ZNF289	CACA---TCCTCTGCTTCCC	2645 A T		
	CAC GTCCTCTGCTTCC			

GTG TAGGAGACGAAGG

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GAM182 ZNF289      CACA---TCCTCTGCTTCCC    2645 TGCCACACT
                   GTCCTCTGCTTCC
                   |||||
                   TAGGAGACGAAGG

GAM183 ADAM19      ACAGCAGTGGCTGGCTTGA    2671  A    A GII
                   ACA CAGTGGGCTGG CT
                   ||| ||||| ||
                   TGT GTCACCGACC GA
                   C    _ ACT

GAM183 ADCY6       ACAGTGGCTTACACCTGTAATCC  2673 CA    GGA__ A  I
                   GTGGCT  CTG AATC
                   ||||| ||| |||
                   CACCGA  GAC TTAG
                   _  ATGTG A  I

GAM183 CBFA2T2     ACAGTGGCTCATGCCTGTAATCC  2676 CA    GGA__ A  I
                   GTGGCT  CTG AATC
                   ||||| ||| |||
                   CACCGA  GAC TTAG
                   _  GTACG A  I

GAM183 CHST6       ACAGTGGCTCATGCCTGTAATCC  2676 CA    GGA__ A  I
                   GTGGCT  CTG AATC
                   ||||| ||| |||
                   CACCGA  GAC TTAG
                   _  GTACG A  I

GAM183 CIAS1       ACAGTGGCTCACGCCTGTAATCC  2675 CA    GGA__ A  I
                   GTGGCT  CTG AATC
                   ||||| ||| |||
                   CACCGA  GAC TTAG
                   _  GTGCG A  I

GAM183 CYP8B1      ACAGTGGCTCATGCCTGTAATCC  2676 CA    GGA__ A  I
                   GTGGCT  CTG AATC
                   ||||| ||| |||
                   CACCGA  GAC TTAG
                   _  GTACG A  I

GAM183 DSCR3       ACAGTGGCTCACACCTGTAATC  2677 CA    _G GAAATI
                   GTGGCT G ACT
                   ||||| |||
                   CACCGA T TGG
                   _  G G ACATTA

GAM183 DSCR3       AACAGTGGCAGGATTTGAA    2668    T CTGAI
                   AACAGTGGC GGA
                   ||||| |||
                   TTGTCACCG CCT
                   T AAAC TT

GAM183 GALR1       AACAG---CTCGGCTGAAATCC  2670 AC TG  _ A
                   AG GCT GG CTGAAATC
                   || ||| || |||||
```

	TT CGA CC GACTTTAG		
	__ GT G _		
GAM183 GPRK5	AACAGTGGCTGCACAGAAA	2669	G T II
	AACAGTGGCTG AC GAA		
	TTGTCACCGAC TG CTT		
	G T TI		
GAM183 HTR1D	ACAGTGGCTCATGCCTGTAATCC	2676 CA	GGA__ A I
	GTGGCT CTG AATC		
	CACCGA GAC TTAG		
	__ GTACG A I		
GAM183 MEFV	ACAGTGGCTCATGCCTGTAATCC	2676 CA	GGA__ A I
	GTGGCT CTG AATC		
	CACCGA GAC TTAG		
	__ GTACG A I		
GAM183 PRIM2A	ACAGTGGCTCACAACCTGTAATCC	2674 CA	G__ A I
	GTGGCT GACTG AATC		
	CACCGA TTGAC TTAG		
	__ GTG A I		
GAM183 RAD54B	CAGTGGCTGGATTCCAATC	2680	__ TG AATII
	CAGTGGCTGGA C A		
	GTCACCGACCT G T		
	AA GT AGIII		
GAM183 RTN4	ACAACAGTGCATGG-CTAAAA	2672 _	G _ A I
	CAACAGTG C TGG CTGAA		
	GTTGTCAC G ACC GATTT		
	T _ T _ I		
GAM183 SCA1	CATCCGTG-CAGG-CTGAAATCC	2679 AACA_	G T A I
	GTG C GG CTGAAATC		
	CAC G CC GACTTTAG		
	GTAGG _ T _ I		
GAM183 SH3BP2	ACAGTGGCTCATGCCTGTAATCC	2676 CA	GGA__ A I
	GTGGCT CTG AATC		
	CACCGA GAC TTAG		
	__ GTACG A I		
GAM183 SH3GL3	ACAGTGGCTCACACCTGTAATCC	2678 CA	GGA__ A I
	GTGGCT CTG AATC		
	CACCGA GAC TTAG		
	__ GTGTG A I		
GAM183 SNAP23	ACAGTGGCTCACGCCTGTAATCC	2675 CA	GGA__ A I
	GTGGCT CTG AATC		

	CACCGA GAC TTAG			
	___ GTGCG A I			
GAM183 UBE2I	GGCTGGACTCCGAAACTCC	2681	___	CIII
	GGCTGGACT GAAAT			
	CCGACCTGA CTTTG			
	GG AGGI			
GAM184 DLC1	TGAGCCGGC-GCTCCTGATGC	2691	AG A	AG
	TGAG GGC GCTCCTGATGC			
	ACTC CCG CGAGGACTACG			
	GG _ II			
GAM184 DLC1	TGAGCCGGC-GCTCCTGATGC	2691	_ AG A	I
	GAG GGC GCTCCTGATG			
	CTC CCG CGAGGACTAC			
	A GG _ I			
GAM184 IGJ	GAGACGCCAGCTCCTGCTCCA	2686	GGG	ATGCI
	AGA CAGCTCCTG			
	TCT GTCGAGGAC			
	GCG GAGGI			
GAM184 IGJ	GAGACGCCAGCTCCTGCTCCA	2686	TG GGG	ATG GC
	AGA CAGCTCCTG CA			
	TCT GTCGAGGAC GT			
	_ GCG GAG GI			
GAM184 INS	GATGGCCTCTTCTGATGCAGC	2689	AG AG C	I
	GGC CT CTGATGCAG			
	CCG GA GACTACGTC			
	TA GA A I			
GAM184 POU3F2	AGCGGGCAGCTCC-GACGC	2684	A T I	
	AG GGGCAGCTCC GATG			
	TC CCCGTCGAGG CTGC			
	G _ G			
GAM184 POU3F2	AGCGGGCAGCTCC-GACGC	2684	TGAGA T A	
	GGGCAGCTCC GATGC			
	CCCGTCGAGG CTGCG			
	G _ _ G			
GAM184 RRP22	GAGAGGGCAG-GCCCGAGGCAG	2687	_ CT T I	
	AGAGGGCAG CCTGA GCA			
	TCTCCCGTC GGGCT CGT			
	C C_ C I			
GAM184 RRP22	GAGAGGGCAG-GCCCGAGGCAG	2687	TG CT T C	
	AGAGGGCAG CCTGA GCAG			

	TCTCCCGTC GGGCT CGTC		
	___ C_ C C		
GAM184 SNCAIP	AGGGCCAAGCTCCTGAGGC 2685	___	TGIII
	AGGGC AGCTCCTGA		
	TCCCG TCGAGGACT		
	GT CCGII		
GAM184 SNCAIP	AGGGCCAAGCTCCTGAGGC 2685	TGAGAGGGC	T AG
	AGCTCCTGA GC		
	TCGAGGACT CG		
	GGT_____ C AC		
GAM184 TP73	GAGGGCAGCTCGCT-CTGCAGC 2688	_ GA	I
	AGGGCAGCTC CT TGCAG		
	TCCCGTCGAG GA ACGTC		
	C G_ I		
GAM184 TP73	GAGGGCAGCTCGCT-CTGCAGC 2688	TGAGAG	_ GA
	GGCAGCTC CT TGCAGC		
	CCGTCGAG GA ACGTCG		
	_____ C G_		
GAM184 VCAM1	TGGGAGGGTATTTCAGCTCCTGAAGC 2690	A	___ T AGCII
	TG GAGGG CAGCTCCTGA GC		
	AC CTCCC GTCGAGGACT CG		
	C ATAA T IIICG		
GAM184 VCAM1	TGGGAGGGTATTTCAGCTCCTGAAGC 2690	AGA	___ TGI
	GGG CAGCTCCTGA		
	CCC GTCGAGGACT		
	___ ATAA TII		
GAM185 AQP6	GACACATGAGGCCAAGAGG 2702	AAAAGII	
	GACACATGAGGC		
	CTGTGTACTCCG		
	GTTCTCC		
GAM185 AQP6	GACACATGAGGCCAAGAGG 2702	TG	AAA_ CTCC
	ACACATGAGGC AGG		
	TGTGTACTCCG TCC		
	___ GTTC TIII		
GAM185 B4GALT1	ACACAT-AGGCCAAAAGG-TCC 2695	G	_ I
	ACACAT AGGCCAAAAGG CT		
	TGTGTA TCCGTTTTCC GG		
	_ A I		
GAM185 B4GALT1	ACACAT-AGGCCAAAAGG-TCC 2695	TGAC	G C
	ACAT AGGCCAAAAGG TCC		

TGTA TCCGTTTTCC AGG

GAM185 B4GALT3	TGTCACA-GAGGGCAGAGAAAGGCTCC2705 GAC T _ _ _ I ACA GAGG CA AAAGGCTC TGT CTCC GT TTTCCGAG _ _ C CTC I
GAM185 B4GALT3	TGTCACA-GAGGGCAGAGAAAGGCTCC2705 TGA T _ _ _ GII CACA GAGG CA AAAGGCTCC GTGT CTCC GT TTTCCGAGG ACA _ C CTC III
GAM185 EPS15	CACAGGCAGGCAAAA-GCTC 2701 TG_ G II CACA AGGCAAAAG CT GTGT TCCGTTTTC GA CCG _ GI
GAM185 EPS15	CACAGGCAGGCAAAA-GCTC 2701 TGACACATG G _ AGGCAAAAG CTC C I TCCGTTTTC GAG G TCCG_ _ T
GAM185 KIAA0442	ACATTACACAAGAAGGCTCCG 2697 _ TG CAAA I CA AGG AGGCTCC GT TCT TCCGAGG TAAT GT _ I
GAM185 KIAA0442	ACATTACACAAGAAGGCTCCG 2697 TGAC TG CAAA ACA AGG AGGCTCCG TGT TCT TCCGAGGC A_ GT _
GAM185 LIMD1	CACAATGAGGCAAAGGCCT 2699 _ A II CACA TGAGGCAAA GGC GTGT ACTCCGTTT CCG T _ GA
GAM185 LIMD1	CACAATGAGGCAAAGGCCT 2699 TGACAC A CC ATGAGGCAAA GGCT TACTCCGTTT CCGG T_ _ AT
GAM185 P53AIP1	ACAGGAGGAACAAAAGGCTCC 2696 T _ III ACA GAGG CAAAAGGCTC TGT CTCC GTTTTCCGAG C TT GII
GAM185 PFKFB4	CACAGGCCAGG-AAAGGCTCCG 2700 ACATG A_ I AGGC AAAGGCTCC

	TCCG TTTCCGAGG	
	TG__ GTCC I	
GAM185 SLC8A2	TGGCAC-TGAGGGCAAAGG 2704 A A _ CTCC	
	TG CAC TGAGG CAAAAGG	
	II III IIII IIIII	
	AC GTG ACTCC GTTTTCC	
	C _ C IIIG	
GAM185 SLC8A2	TGGCAC-TGAGGGCAAAGG 2704 A A _ II	
	TG CAC TGAGG CAAAAG	
	II III IIII IIIII	
	AC GTG ACTCC GTTTTC	
	C _ C CI	
GAM185 TDG	ACAGATGAGTGGCAAAGG 2694 C _ III	
	ACA ATGA GGCAAAG	
	III IIII IIIII	
	TGT TACT CCGTTTTTC	
	C CA CII	
GAM185 TDG	ACAGATGAGTGGCAAAGG 2694 TGACAC _ C C	
	ATGA GGCAAAGG TC	
	III IIIIIII II	
	TACT CCGTTTTTCC AG	
	TC__ CA _ I	
GAM185 USH2A	TGAAACAATCAGGCAAAG 2703 C _ G GCTCC	
	TGA ACA T AGGCAAAG	
	III III I IIIIIII	
	ACT TGT A TCCGTTTTTC	
	T T G IIIGC	
GAM185 USH2A	TGAAACAATCAGGCAAAG 2703 C _ G II	
	TGA ACA T AGGCAAAA	
	III III I IIIIIII	
	ACT TGT A TCCGTTTTT	
	T T G CI	
GAM185 WHSC1	CACACTAAGGCAAAGGGCTC 2698 _ _ III	
	CACA TGAGGCAAAGG CT	
	III IIIIIIIII II	
	GTGT ATTCCGTTTTTCC GA	
	G C GII	
GAM185 WHSC1	CACACTAAGGCAAAGGGCTC 2698 TGACACA _ CG	
	TGAGGCAAAGG CTC	
	IIIIIIII III	
	ATTCCGTTTTTCC GAG	
	TG__ C AG	
GAM186 ACCN1	TGACTT--TGGACCTGGAATCTGGT 2713 GT G_ I	
	TGACTT TGGAC GGAATCTGGT	
	IIII IIII IIIIIII	
	ACTGAA ACCTG CCTTAGACCA	
	_ GA I	
GAM186 ADAMTS13	CTTGGTG-ACTGGGAATCTGGT 2708 TGACTTGTTG _	
	GAC GGGAATCTGGT	
	III IIIIIIIII	

	CTG CCCTTAGACCA	
	CCA_____ A	
GAM186 GAD1	GAGTTGTTGGAC---AAGCTGGT 2710 TGAC	AAT
	TTGTTGGACGGG CTGG	
	AACAACCTGTTC GACC	
	TC_____	
GAM186 GLUD1	TGACTTGTTGAGAATGGTATC 2712	_ CG A TGGT
	TGACTTGTTG GA GG ATC	
	ACTGAACAAC CT CC TAG	
	T TA A T	
GAM186 LNK	TTGGACGGGAAGCAGTCTGG 2714 TGACTTG_____	_ AATCTGG
	TTGGACG GG	
	GACCTGC CC	
	CCTTCGTCA A C TGG	
GAM186 NEBL	TGACTTTTATGCTCAGTGAATCTGGT 2711	GT_ GA _
	TGACTT TG CGG GAATCTGGT	
	ACTGAA AC GTC CTTAGACCA	
	AAT GA A	
GAM186 TEC	CTTGT-GCTTGGAATCTGG 2709 TGACTTGTTGGAC	
	GGGAATCTGG	
	CCCTTAGACC	
	CACGAA_____	
GAM187 ABCB4	AATTCCCTCTTGCAATTCCT 2717 TGAGAATT	G T
	TCTCTTGCAAT CCT	
	GGAGAACGTA GGA	
	G_____ A C	
GAM187 AFG3L2	GAGAATTTCTGCTGGC---CCTT 2725 TG	C CAT
	AGAATTTCT TTG GCCTT	
	TCTTAAAGA GAC CGGGA	
	_____ C _____	
GAM187 AKAP2	TGAGAATTTTAGTC-TCCATGCC 2730	C_ G TTA
	TGAGAATTT TCTT CATGCC	
	ACTCTTAAA AGAG GTACGG	
	ATC _	
GAM187 ATF4	TGAGAATTTTCATCCTTCCA---CTTA 2732	_ G GCCTTAI
	TGAGAATTTT TCTT CAT	
	ACTCTTAAAG GGAA GTG	
	TA G AAT A	
GAM187 BCAS1	AGCATTTCTCTTCTATAACTTA 2724 TGAGA	GC C
	ATTTCTCTT ATG CTTA	

	TAAAGAGAA TAT GAAT	
	G_____ GA T	
GAM187 DIRC1	AGAATTTCTACTCCA-GCC 2723 TGAG C G T T	
	AATTTCT TT CA GCC	
	TTAAAGA GA GT CGG	
	_____ T G _ T	
GAM187 EPHA3	TGAGAAATTTCTCT--CCTG-CTTA 2729 _____ ATGCCTTA	
	TGAGAA TTTCTCTTGC	
	ACTCTT AGAGAGGACG	
	TAA AATIIAT	
GAM187 FGA	AGAATGTTTCTCTTGCCTTCCT 2720 TGAGAA ATG TA	
	TTTCTCTTGC CCT	
	AAAGAGAACG GGA	
	TTAC_____ GAA CC	
GAM187 FGFR1	AGAAAGCTCTCACTTGCATGCCT 2719 T AA T TAI	
	GAG TTTC CTTGCATGCCT	
	TTC AGAG GAACGTACGGA	
	T G_ T CAI	
GAM187 FUT6	AGAATTTCTACCTTCC--GCCTT 2721 TGAG _ GCA A	
	AATTTCT CTT TGCCTT	
	TTAAAGA GGA GCGGAA	
	_____ T AG_ A	
GAM187 NOTCH2	TGACGAATTGCTTCTCTTGCAT 2727 _ _ GCCTTA	
	TGA GAATT TCTCTTGCAT	
	ACT CTAA AGAGAACGTA	
	G CGA IIIATT	
GAM187 PPP1R2	TGAGCATG-CTGCTTGGCATGCCTTA 2733 AATT _ _ II	
	TGAG CT CTTG CATGCCTTA	
	ACTC GA GAAC GTACGGAAT	
	GTAC_ C C II	
GAM187 PRDM2	TGAGAATTTCAAGTCTGGAAATGCCT 2731 _____ TGC_ TAI	
	TGAGAATTTCT TCT ATGCCT	
	ACTCTTAAAG AGA TACGGA	
	TTC CCTT IIIA	
GAM187 PTPN1	AGAATTTCTCTGTAC-TGGCTT 2722 TGAG _ A C A	
	AATTTCTCT TGC TG CTT	
	TTAAAGAGA ATG AC GAA	
	_____ C _ C G	
GAM187 SH3GL2	GAGAATTTCT-TTTCAGTCCCT 2726 TG C G TG A	
	AGAATTTCT TT CA CCTT	

	TCTTAAAGA AA GT GGA	
	— A _ CA G	
GAM187 SPK	AATGTCTCGCTTGCATGCCT 2718 TGAGAA T	
	TTTC CTTGCATGCCTT	
	AGAG GAACGTACGGAG	
	— C	
GAM187 TNFSF15	TGAAATATTTCTCTTTCAATCCT 2728 _ G TG TAI	
	TGAGA ATTTCTCTT CA CCT	
	ACTTT TAAAGAGAA GT GGA	
	A A TA	
GAM188 NCOR2	CATCG---AATTCATTCTGC 2736 GCG GI	
	CATC GAATTCATTC	
	GTAG CTTAAGTAAG	
	— AC	
GAM188 NCOR2	CATCG---AATTCATTCTGC 2736 TATCATCGCG G	
	GAATTCATTC G	
	CTTAAGTAAG C	
	G — A	
GAM189 CYBB	AAAGGCTATA--TTCGCACAG 2739 TCAA AGACT G	
	AGGT TTCGCACAG	
	TCCG AAGCGTGTC	
	— ATAT_ G	
GAM189 MECP2	TCAAAGGTAGGATTTCTCCAGG 2743 AC GCA TI	
	TCAAAGGTAG TTTC CAGG	
	AGTTTCCATC AAAG GTCC	
	CT GAG	
GAM189 TCEA1	AAATGTAGACTTT-GCAACAG 2740 TCAAAG C _ G	
	GTAGACTTT GCA CAG	
	CATCTGAAA CGT GTC	
	TA — _ T A	
GAM189 TEM8	TCAAAGGTATACATTTGGAAC 2742 G TTTCGCACAGGT	
	TCAAAGGTA AC	
	AGTTTCCAT TG	
	A TAAACCTTG	
GAM189 TRIM14	CAAAGGTAGACTCAAGTCTCGCAGAG 2741 TC — C GTII	
	AAAGGTAGACTT TCGCA AG	
	TTTCCATCTGAG AGCGT TC	
	— TTCAG C A	
GAM190 HNRPD	CAAAATCAACTGTGCCTTAATT 2747 TGCCAAT _	
	GTCGATTG GCCTTAATT	

TAGTTGAC CGGAATTAA
 T_____ A
 GAM190 MKI67 TGCAGATGTCCAATAGCCTTAATT 2751 CA GAT I
 TGC ATGTC TGGCCTTAATT
 ||| |||| |||||
 ACG TACAG ATCGGAATTAA
 TC GTT I
 GAM190 MS4A4A TGCCAATGT-AAT--GCCTTTAT 2750 CGATTG AAT
 TGCCAATGT GCCTT
 ||||| ||||
 ACGGTTACA CGGAA
 TTA___ ATA
 GAM190 PITX1 TGTGCTCCGTGGCCTTAAT 2752 TGCCAATG AT
 TCG TGGCCTTAAT
 ||| |||||
 GGC ACCGGAATTA
 A_____ _
 GAM190 SHANK2 TGCCACTCCC--TTGGCCTTA 2749 ATG GA AT
 TGCCA TC TTGGCCTTA
 |||| || |||||
 ACGGT GG AACCGGAAT
 GA_ G_ II
 GAM190 SLC9A5 GCCAGAGTAGA--GGCCTTAAT 2748 TG AT C TT
 CCA GT GA GGCCTTAAT
 ||| || |||||
 GGT CA CT CCGGAATTA
 _ CT T _
 GAM190 ZNF265 CAATGTCTCCATTGGCCTT 2746 TGCCAATG G AAT
 TC ATTGGCCTT
 || |||||
 AG TAACCGGAA
 ACAG___ G AGT
 GAM191 ADRA2A GCAATTATGCTGTTAGGCA 2758 CAG TCII
 GC TATGCTGTTAG
 || |||||
 CG ATACGACAATC
 TTA CGTI
 GAM191 ADRA2A GCAATTATGCTGTTAGGCA 2758 TGC _ T AGA
 CAGT ATGCTGTTAG CA
 ||| ||||| ||
 GTTA TACGACAATC GT
 _ A C GII
 GAM191 BMP6 GTATGCTGTATAGTAAAAAG 2759 _ C II
 GTATGCTGT TAGT AAGA
 ||||| ||| |||
 CATACGACA ATCA TTTT
 T T CI
 GAM191 CACNB2 ATGCTGTAGTTATACAAGA 2755 _ IIIT
 ATGCTGTAGT CAAG
 ||||| |||

	TACGACAATCA GTTC		
	ATAT TIII		
GAM191 COL9A3	GTATGCTGTCAGGCGACAG 2760	TCAAGAI	
	GTATGCTGTTAG		
	CATACGACAGTC		
	CGCTGTCTI		
GAM191 GSTM3	TGCCAGTATCGCAGCGATTCAA 2761	_ T TAG GAG	
	TGCCAGTAT GC GT TCAA		
	ACGGTCATA CG CG AGTT		
	G T CTA III		
GAM191 GSTM3	TGCCAGTATCGCAGCGATTCAA 2761 G	_ T TAG I	
	CCAGTAT GC GT TCA		
	GGTCATA CG CG AGT		
	_ G T CTA I		
GAM191 PLCB4	CCAG-A-GCTGTTAGTCTAG 2757	TAT AI	
	CCAG GCTGTTAGTC		
	GGTC CGACAATCAG		
	T_ AT		
GAM191 PLCB4	CCAG-A-GCTGTTAGTCTAG 2757	TGCCAGTAT A	
	GCTGTTAGTC AG		
	CGACAATCAG TC		
	TCT_____ A		
GAM191 PRDM2	TGTCAATATGCTGTTGATTCCCAGAG 2762 C	AG_ A_ II	
	TG CAGTATGCTGTT TC AGAG		
	AC GTTATACGACAA AG TCTC		
	A CTA GG II		
GAM191 PRDM2	TGTCAATATGCTGTTGATTCCCAGAG 2762 GC	AG_ A_ I	
	CAGTATGCTGTT TC AGA		
	GTTATACGACAA AG TCT		
	_ CTA GG I		
GAM191 STC1	CAGTATAGGTCTAAGTCAAGAG 2756 A	CT _ I	
	GTATG GTT AGTCAAGA		
	CATAT CAG TCAGTTCT		
	_ C_ AT I		
GAM192 ABCG1	GATCCA---ACCCAGCTGG 2771	TGCGAG TTC	
	CCA ACCCAGCTG		
	GGT TGGGTCGAC		

GAM192 ARHGEF1	TGCGGGGCCAGTAACCCAGCTGG 2779	A_ TTCA_ TCI	
	TGCG GCCA CCCAGCTGG		

	ACGC CGGT GGGTCGACC	
	CC CATTG III	
GAM192 ATP7B	GAGGCCCTCACTCCAGCTGGTC 2770 TGCGA A _	
	GCC TTCAC CCAGCTGGTC	
	III IIII IIIIIIIII	
	CGG GAGTG GGTGCGACCAG	
	_____ A	
GAM192 COG3	GCTAGAGATCCACACAGCTGGTC 2777 TGC CC C I	
	GAG ATTCAC CAGCTGGTC	
	III IIII IIIIIIIII	
	CTC TAGGTG GTCGACCAG	
	GAT _ T G	
GAM192 CYP4F3	AGCTCTTTACCCAGGCTGG 2765 TGCGAGCCA _ T	
	TTCACCCAG CTGG	
	IIIIIIII III	
	AAGTGGGTC GACC	
	GA_____ C T	
GAM192 EIF2B1	TGCGAGCCAGTCTGACAGC 2781 T ACC TGGT	
	TGCGAGCCA TC CAGC	
	IIIIIIII II III	
	ACGCTCGGT AG GTCG	
	C ACT IIIC	
GAM192 EPRS	GAGCCATATAACCCAGCTG 2768 TGCGAG TC_ GT	
	CCAT ACCCAGCTG	
	III IIIIIII	
	GGTA TGGGTCGAC	
	_____ TAT AT	
GAM192 FMR2	GAGGC-TTCCCACAGCTGGTC 2773 TGCGAGCCA A _	
	TTC CC CAGCTGGT	
	III II IIIIIII	
	AAG GG GTCGACCA	
	CG_____ T	
GAM192 HOXC4	GCGAGGCAGGGTCCCAGCTGG 2776 TG C TTCA TC	
	CGAG CA CCCAGCTGG	
	III II IIIIIII	
	GCTC GT GGGTCGACC	
	_ C CCCA TI	
GAM192 HTR1D	TGCTGAGACAACTACC-AGCTGGT 2778 _ C TTCAC CI	
	TGC GAG CA CCAGCTGGT	
	III III II IIIIIII	
	ACG CTC GT GGTGACCA	
	A T TGAT_ II	
GAM192 KIFC3	GCGAGCCA-TC-CCCGGCT 2775 TG T A A GG	
	CGAGCCAT C CCC GCT	
	IIIIII I III III	
	GCTCGGTA G GGG CGA	
	_ _ C GI	
GAM192 KLF8	GAGTCGATTCAGACCCAGCTGG 2767 TG GC TTC TC	
	CGA CA ACCCAGCTGG	
	III II IIIIIII	

	GCT GT TGGGTCGACC	
	A_ AA C__ CG	
GAM192 MSH3	TGCCAG--ATTCACCCAGTTG 2782 TGCGA _ C GT	
	GCCA TTCACCCAG TG	
	CGGT AAGTGGGTC AC	
	A__ CT A II	
GAM192 NFKBIL2	GAGC---TCCCCCAGCTGGT 2772 TGCGAGCCA A	
	TTC CCCAGCTGG	
	AGG GGGTCGACC	
	G_____ _	
GAM192 RARA	GAGCCAGCTCCCCCAGCTGG 2769 TGCGAG _ A T	
	CCA TTC CCCAGCTGG	
	GGT GAG GGGTCGACC	
	_____ C G C	
GAM192 SCN1B	TGCGAGCCAAGCCCCCTGC 2780 TTCA A TGGT	
	TGCGAGCCA CCC GC	
	ACGCTCGGT GGG CG	
	TCGG A IIIC	
GAM192 TSLP	AGCCCTTATTCACCCATGCTG 2766 TGCGAGCC _ GTC	
	ATTCACCCA GCTG	
	TAAGTGGGT CGAC	
	GAA_____ A AAC	
GAM192 ZNF10	GCGACTCCATTCA-CCAGC 2774 TG G_ C TGG	
	CGA CCATTCACC AGC	
	GCT GGTAAGTGG TCG	
	_ GA _ CII	
GAM193 CHST6	TCCCGGGCCT--AGCGCCTGC 2793 AC G GG	
	TCCCGGGCCT AGCG CTGC	
	AGGGCCCGGA TCGC GACG	
	_ G II	
GAM193 CSF3	CCAGGGGCTCACAGCGGCT 2785 TCCC C GCGG	
	GGGC TACAGCGGCT	
	CCCG GTGTGCGCCGA	
	GTC_ A GIII	
GAM193 HK3	CCCGG--CTCCAGCAAGGCTGCGGC 2786 TC G CTA _ I	
	CCGG C CAGC GGCTGCGGC	
	GGCC G GTCG CCGACGCCG	
	_ _AG_ TT C	
GAM193 KCNA7	TCCCGCCCCCTACAGCGAGCTGGGG 2791 GG_ _ C CII	
	TCCCG CCTACAGCG GCTG GG	

	AGGGC GGATGTCGC CGAC CC	
	GGG T _ CII	
GAM193 LFG	TCCCGGGCCCCATCTGCAGC 2792	TA GCGG
	TCCCGGGCC CA CTGCGGC	
	AGGGCCCGG GT GACGTCG	
	GG A__	
GAM193 MLC1	TCCCGGGCCAGGACAGAGGC 2790	T__ C TGCGG
	TCCCGGGCC ACAG GGC	
	AGGGCCCGG TGTC CCG	
	TCC T IIICG	
GAM193 PRX	CCCGGGCCTCCA-CCTCTGC 2787 TC	ACA GG G
	CCGGGCCT GC CTGCG	
	GGCCCGGA TG GACGT	
	__ GG_ GA I	
GAM193 SHC1	CCCGGGCCTA---GGCTG-GGC 2789 TC	CAGC C
	CCGGGCCTA GGCTG G	
	GGCCCGGAT CCGAC C	
	__ _ _	
GAM193 SURF4	CCCCTGCCACAGCGGCTGCGGC 2788 T GG	I
	CCC GCCTACAGCGGCTGCGGC	
	GGG CGGGTGTGCGCCGACGCCG	
	_ A_ A	
GAM194 ATP11B	TATAATGGCCTCAGCAACAG 2801	ATT C GCA
	TATAATGGCCT CA CAG	
	ATATTACCGGA GT GTC	
	GTC T III	
GAM194 ATP11B	TATAATGGCCTCAGCAACAG 2801	ATT C I
	ATAATGGCCT CA CA	
	TATTACCGGA GT GT	
	GTC T I	
GAM194 FGFR2	TAAAATGGCCTACTTATCTGTGCAC 2802 AT	CACCAG_ I
	AATGGCCTATT GCA	
	TTACCGGATGA CGT	
	T_ ATAGACA I	
GAM194 FGFR2	TAAAATGGCCTACTTATCTGTGCAC 2802 TAT	CACCAG_ II
	AATGGCCTATT GCAC	
	TTACCGGATGA CGTG	
	ATT ATAGACA II	
GAM194 ICA1	TGGCC---CACCAGGCAC 2805	TATT
	TGGCC CACCAGGCA	

ACCGG GTGGTCCGT

GAM194 INMT TGGCCTATTCTTGACCAAAGCAC 2803 _____ IIIG
TGGCCTATTC ACCAG GCA
||||||| |||||
ACCGGATAAG TGGTT CGT
GAAC T GIII

GAM194 INMT TGGCCTATTCTTGACCAAAGCAC 2803 TATAATGG ATTC _ I
CCT ACCAG GCAC
||| |||||
GGA TGGTT CGTG

GAM194 ITPR3 ATCATGG---AGTCACCAGGC 2797 TA_ CCTAT
ATGG TCACCAGG
||||| |||||
TACC AGTGGTCC
TAG TC_

GAM194 ITPR3 ATCATGG---AGTCACCAGGC 2797 TATA CCTAT
ATGG TCACCAGGC
||||| |||||
TACC AGTGGTCCG
AG_ TC_

GAM194 LPIN2 AAAGGCCCA--CACCAGGCA 2796 AT_ TT I
GGCCTA CACCAGGC
||||| |||||
CCGGGT GTGGTCCG
TTT _ I

GAM194 LPIN2 AAAGGCCCA--CACCAGGCA 2796 TATAAT TT
GGCCTA CACCAGGC
||||| |||||
CCGGGT GTGGTCCG

GAM194 MEF2C TATAA---CTTATTCACCA 2800 TATA C
ATGGC TATTCACC
||||| |||||
TATTG ATAAGTGG
A_ A

GAM194 MEF2C TATAA---CTTATTCACCA 2800 TATA C GG
ATGGC TATTCACCA
||||| |||||
TATTG ATAAGTGGT
A_ A II

GAM194 NDRG1 TGGCCTTCTGACCAGGCAC 2806 A C II
TGGCCT TT ACCAGGCA
||||| || |||||
ACCGGA GA TGGTCCGT
A C GI

GAM194 PES1 GGCCTCTTCTCTGACCAGGCAC 2798 A _ IIIG
GGCCT TTC ACCAGGCA
||||| ||| |||||

	CCGGA AAG TGGTCCGT		
	G AGAC GIII		
GAM194 PES1	GGCCTCTTCTCTGACCAGGCAC	2798 TATAA TATT	G C
	TGGCC CACCAG CA		
	ACTGG GTGGTC GT		
	AAGAG TCC_ _ C		
GAM194 SLC1A4	TAATGGCCTGTT-A-CAGG	2799	ATTCACCAGI
	TAATGGCCT		
	ATTACCGGA		
	CAATGTCCII		
GAM194 SLC1A4	TAATGGCCTGTT-A-CAGG	2799 TATA	A CAC C
	ATGGCCT TT CAGG		
	TACCGGA AA GTCC		
	____ C T_ C		
GAM194 TARBP2	TGGACAGTTCCACCAGGCAC	2804 _CTA	II
	TGG C TTCACCAGGCA		
	ACC G AGGTGGTCCGT		
	T TCA GI		
GAM194 TARBP2	TGGACAGTTCCACCAGGCAC	2804 TATAATGGCCTA	
	TTCACCAGGCA		
	AGGTGGTCCGT		
	TCA_____		
GAM195 ADCY8	GGGATGGGGAGCAGGGGCGGA	2814	C ____ IIIT
	GGGATGGGGA C GCGG		
	CCCTACCCCT G CGCC		
	C TCCC TIII		
GAM195 ADCY8	GGGATGGGGAGCAGGGGCGGA	2814 TG	C ____ AGTTCC
	GGATGGGGA C GCGGA		
	CCTACCCCT G CGCCT		
	____ C TCCC CIIIC		
GAM195 ARHGEF1	GGCTGGTGTCCGCGCGGAAGT	2811 A GGAC__	III
	GG TGG CGCGGAAG		
	CC ACC GCGCCTTC		
	G ACAGGC AII		
GAM195 ARHGEF1	GGCTGGTGTCCGCGCGGAAGT	2811 TG A GGGAC	TCC
	GG TG CGCGGAAGT		
	CC AC GCGCCTTCA		
	GA _ AGGC_ CTI		
GAM195 CAPN7	GGA CTGGGAGCGCCGCGGAAG	2810 TGGGATG ____	TTCC
	GGA CCGCGGAAG		

	CCCT GGCGCCTTC			
	TGAG___ CGC CTII			
GAM195 CAPN7	GGA	CTCGGGAGCGCCGCGGAAG	2810	G_ ___ IIIC
	GGAT GGG	CCGCGGAA		
	CCTG CCCT	GGCGCCTT		
	AG CGC CII			
GAM195 CELSR1	TGGGCGGGGCTGGACCGCGG	2822	A ___	AAGTTC
	TGGG TGGG	ACCGCGG		
	ACCC GCCC	TGGCGCC		
	_ GACC	IIICCT		
GAM195 CELSR1	TGGGCGGGGCTGGACCGCGG	2822	A ___	III
	TGGG TGGG	ACCGCG		
	ACCC GCCC	TGGCGC		
	_ GACC	CII		
GAM195 CYP1B1	TGGGATGGGGA-CGGAGAAG	2824		C C TTC
	TGGGATGGGGAC G	GGAAG		
	ACCCTACCCCTG C	TCTTC		
	_ C	III		
GAM195 CYP1B1	TGGGATGGGGA-CGGAGAAG	2824	_	CGC AI
	GGGATGGGGAC	GGA		
	CCCTACCCCTG	CCT		
	A	___ CT		
GAM195 DAG1	GGGA---GGACCGCGGCAG	2817	TGG	AA
	GGGA	GGACCGCGG		
	CCCT	CCTGGCGCC		
	___	GT		
GAM195 DAG1	GGGA---GGACCGCGGCAG	2817	TGGGAT	A T
	GGGGACCGCGG	AG		
	CTCCTGGCGCC	TC		
	C	___ G C		
GAM195 FOXE3	GGGATGGGGGACGGAGAAG	2818		ACC AII
	GGGATGGGG	GCGGA		
	CCCTACCCC	TGCCT		
	C	___ CTT		
GAM195 FOXE3	GGGATGGGGGACGGAGAAG	2818	TG	AC C TTC
	GGATGGGG	CG GGAAG		
	CCTACCCC	GC TCTTC		
	___	CT C CII		
GAM195 FXYD6	GATGGGGACTCCTCGTGGAAG	2809	___	C IIIC
	GATGGGGAC	CG GGAA		

	CTACCCCTG GC CCTT		
	AGGA A CIII		
GAM195 HOXD1	GGGATGGGGGTGCGCTGGGACTTC 2815	AC ____	AGTTI
	ATGGGG CGC GGA		
	TACCCC GCG CCT		
	CA GAC GIIIT		
GAM195 HOXD1	GGGATGGGGGTGCGCTGGGACTTC 2815 TG	AC ____	AG CI
	GGATGGGG CGC GGA TTC		
	CCTACCCC GCG CCT AAG		
	____ CA GAC G_ AI		
GAM195 MYO1D	GGAAGGAGA--GAGGAAGTTCC 2812 T	CCGC	I
	GGA GGGGA GGAAGTT		
	CCTCCTCT CCTTCAA		
	T CT__ G		
GAM195 MYO1D	GGAAGGAGA--GAGGAAGTTCC 2812 TGGGAT	CCGC	
	GGGGA GGAAGTTC		
	CCTCT CCTTCAAG		
	TT____ CT__		
GAM195 PRKACA	TGGGATGGGGA----GAAGTT 2825	CCGCG	
	TGGGATGGGGA GAAGTT		
	ACCCTACCCCT CTTCAA		

GAM195 PRKACA	TGGGATGGGGA----GAAGTT 2825 _	CCGCG	
	GGGATGGGGA GAAG		
	CCCTACCCCT CTTCA		
	A _____		
GAM195 RELA	GGGATGGGGGACC-CCACAGTTCC 2813	_ G GA	I
	GGATGGGG ACC CG AGTTC		
	CCTACCCC TGG GT TCAAG		
	C G G_ I		
GAM195 RELA	GGGATGGGGGACC-CCACAGTTCC 2813 TG	_ G GA	I
	GGATGGGG ACC CG AGTTCC		
	CCTACCCC TGG GT TCAAGG		
	_ C G G_ G		
GAM195 RFNG	TGGGATGGGCAGGTCAGCGGAA 2821	GACC____	GTTCC
	TGGGATGGG GCGGAA		
	ACCCTACCC CGCCTT		
	GTCCAGT IIICC		
GAM195 RFNG	TGGGATGGGCAGGTCAGCGGAA 2821	GACC____	
	TGGGATGGG GCGGA		

	ACCCTACCC	CGCCT	
	GTCCAGT	TII	
GAM195 TBX6	GGGATGGGGCCGGTGGAGGT	2820	A C_ AGI
	GGATGGGG CCG GGA		
	CCTACCCC GGC CCT		
	_ CA CCI		
GAM195 TBX6	GGGATGGGGCCGGTGGAGGT	2820 TG	A C_ A TC
	GGATGGGG CCG GGA GT		
	CCTACCCC GGC CCT CA		
	_ _ CA C CI		
GAM195 TCIRG1	GGGCTTGGGACTGTGGGAAGTTCC	2816 GGATG	CGC_ I
	GGGAC GGAAGTTC		
	CCCTG CCTTCAAG		
	CGAA_ ACAC I		
GAM195 TCIRG1	GGGCTTGGGACTGTGGGAAGTTCC	2816 TG ATG	CGC_ I
	GG GGGAC GGAAGTTCC		
	CC CCCTG CCTTCAAGG		
	_ GAA ACAC C		
GAM195 THPO	GGGATGGGGGCGTTGGAAG	2819	ACC GAII
	GGGATGGGG GCG		
	CCCTACCCC CGC		
	_ AACCT		
GAM195 THPO	GGGATGGGGGCGTTGGAAG	2819 TG	AC C_ TTC
	GGATGGGG CG GGAAG		
	CCTACCCC GC CCTTC		
	_ C_ AA CII		
GAM195 VASP	TGGGATGGGGAGTG-GGAA	2823	CCGC GTT
	TGGGATGGGGA GGAA		
	ACCCTACCCCT CCTT		
	CAC_		
GAM195 VASP	TGGGATGGGGAGTG-GGAA	2823	CCGC I
	TGGGATGGGGA GGA		
	ACCCTACCCCT CCT		
	CAC_ T		
GAM196 CARD10	CTGGATGGT-GGGAGTCAC	2832 _ T	CTAC
	CTGG TGGT GGGAGTCAC		
	GACC ACCA CCCTCAGTG		
	T _ G		
GAM196 CHS1	TGGTACAGAGGCACCTACTG	2844 CTGGTGGTTG	T
	GGAG CACCTACT		

		TCTC GTGGATGA	
		TG_____ C	
GAM196 FVT1	ACATTCCTGAAGAGCACTGGT	2828 TGAC	CCC__ ATG
	ATTCCTGAA CTGGT		
	TAAGGACTT GACCA		
	_____ CTCGT GGI		
GAM196 GALNT2	ACATTCCTGAGCACCCAGGTA	2829 TGAC	__ CT TG
	ATTCCTGA ACCC GGTA		
	TAAGGACT TGGG CCAT		
	_____ CG T_ CT		
GAM196 GP9	CTGGTGGTTTGGGCTGACC	2834	_ AGTC TACT
	CTGGTGGTT GGG ACC		
	GACCACCAA CCC TGG		
	A GAC_ G		
GAM196 GRLF1	ACACGCCTGAACCCTGGGTTTG	2831 TGACATT	CT ATG
	CCTGAACCC GGT		
	GGACTTGGG CCA		
	TGC_____ AC AAC		
GAM196 HD	TGGGGGTGGGG-GACACCTACTG	2842 CT_ TT GT	
	GGTGG GGGG CACCTACTG		
	CCACC CCCT GTGGATGAC		
	CCC _ _		
GAM196 LARGE	GGTGGTTGGTAGAGGCAGCT	2836 C_____ TT G CACCTACT	
	TGGTGG GG AGT		
	ACCATC CC TCG		
	ACCA T_ G ACT GT		
GAM196 MMP14	TGACAG--CTGCACCCCTGGT	2841 TTC A AT	
	TGACA CTG ACCCCTGGT		
	ACTGT GAC TGGGGACCA		
	C_ G		
GAM196 MYO1D	GGTTGGGAGGCAGCAGCTG	2837 CT_____ TG AGTCACCTACT	
	GG GTTGGG		
	TC CGACCT		
	CCTCCG GT GAC GTCAT		
GAM196 PARK2	TCCTGGGGAACCCCTGGTATG	2839 TGACATTCCT	
	GAACCCCTGGTATG		
	CTTGGGGACCATAC		
	C_____		
GAM196 PPIL1	GTAGTAAGTAGTCACCTATTG	2838 CTGGTGGT _ CTG	
	TGGG AGTCACCTA		

	ATTC TCAGTGGAT		
	C_____ A AAC		
GAM196 PPP4R1	TGAC--TCTTGAAATCCCTGGTAT 2840	AT C C_ G	
	TGAC TC TGAA CCCTGGTAT		
	ACTG AG ACTT GGGACCATA		
	__ A TA I		
GAM196 RPH3AL	TGGGGGTTGGGAGTCACAT-CTG 2843	CT T CTA	
	GG GGTTGGGAGTCAC CTG		
	CC CCAACCCTCAGTG GAC		
	C_ _ TA_		
GAM196 RPH3AL	CTGGGGGTTGGGAGTCACAT-CTG 2835	T CTA I	
	CTGG GGTTGGGAGTCAC CTG		
	GACC CCAACCCTCAGTG GAC		
	C TA_ I		
GAM196 SLC13A3	TTCTAGAACTTCCCCTGGTATG 2845	TGACATTCCTGAA	
	CCCCTGGTATG		
	GGGGACCATAC		
	CTTGAA_____		
GAM196 ST3GALVI	CTGGTGGTTATGAATCACC 2833	G TACT	
	CTGGTGGTTG GAGTCACC		
	GACCACCAAT CTTAGTGG		
	A G		
GAM196 TNF	ACATTCCTGAATCCCAGGT 2830	TGAC C T AT	
	ATTCCTGAA CCC GGT		
	TAAGGACTT GGG CCA		
	_____ A T AA		
GAM197 COL19A1	AAGTCACTTTGAATTACAT 2849	TGGCAAGT CAG	
	CACTTTGA ACAT		
	GTGAAACT TGTA		
	_____ TAA		
GAM197 FGF12	TGGCAAAAGTCACTT---CAG-CATT 2856	___ TGA A	
	TGGCA AGTCACTT CAG CATT		
	ACCGT TCAGTGAA GTC GTAA		
	TT _____		
GAM197 FMO2	TGGCACCGTCTCTTTGACAGA 2857	A_ A CATT	
	TGGCA GTC CTTTGACAGA		
	ACCGT CAG GAAACTGTCT		
	GG A T		
GAM197 NAPB	AATTCACCTTTGACACTCAT 2850	TGGCAAGT GA	
	CACTTTGACA CAT		

	GTGAAACTGT GTA	
	_____ GA	
GAM197 NAT1	AAGTCACTTTTGTGGACATT 2851 TGGCAAGT GACA	
	CACTTT GACAT	
	GTGAAA CTGTA	
	_____ ACAC	
GAM197 NRXN1	TCACTTCTACATGACAGACAT 2855 TGGCAAGTC TT	
	AC TGACAGACATT	
	TG ACTGTCTGTAG	
	A_____ T_	
GAM197 PDE1A	GCTATTGACTTTGACAGGCAT 2852 TGGCAAGTC A T	
	ACTTTGACAG CAT	
	TGAAACTGTC GTA	
	ATAAC_____ C T	
GAM197 PRKR	AAGTCAACCGCTGGTTGACAGACA 2848 TGGCA GT A ____ TTI	
	A C CT TTGACAGACA	
	T G GA AACTGTCTGT	
	G_____ TG C CC CGC	
GAM197 SLC29A1	GGCA-GACAGTCTGACAGACA 2854 TG A T C	
	GCA G CA TTTGACAGACAT	
	CGT C GT AGACTGTCTGTG	
	__ _ T C	
GAM197 SLC7A6	GGCAAGTCAGCCTTTGCATAAGACA 2853 TG ____ AC__ TII	
	GCAAGTCA CTTTG AGACAT	
	CGTTCAGT GAAAC TCTGTG	
	_____ CG GTAT III	
GAM198 ATBF1	CAGTCGTGCCGGGCGCAGGCC 2866 TC T C CC	
	AGTTGT CC GGCGCAGGCC	
	TCAGCA GG CCGCGTCCGG	
	_____ C C CI	
GAM198 CCFN	CAGT-GTGCAGGGACGCAGGCCCC 2863 TC _ TCCC I	
	AGT TGT GGCGCAGGCC	
	TCA ACG CTGCGTCCGGGG	
	_____ C TCC_ G	
GAM198 CLDN5	TCAGCTG---CGGGCGCAGGC 2872 TCCC C	
	TCAGTTGT GGCGCAGGC	
	AGTCGACG CCGCGTCCG	
	C_____ I	
GAM198 COX41	CAGGTG---CAGGCGCAGGCC 2865 TCAGTTGTTCCC	
	GGCGCAGGCC	

CCGCGTCCGG
TCCACGT_____

GAM198 CST1 TCTGTCTGTCTCTTGGCGCAGGC 2869 TCA _ _ CC CCCI
GT TGT TC GGCGCAGGC
|| ||| || |||||
CA ACA AG CCGCGTCCG
AGA G G AA IIIC

GAM198 EZH2 GTTGTTCCTCCGCGCGTCGCCCCC 2868 TCAGTT G AG_
GTTCCCG CGC GCCCC
||||| ||| ||||
CAAGGGC GCG CGGGG

GAM198 FUT3 _____ _ CAG
GTTCCCGGCAGCCCAGGCACC 2867 TCAGTT T_ _ AG_ CC
GT CCC GGCGC GCC
|| ||| ||||| |||
CG GGG CCGTG CGG
C_____ TC T GTA CI

GAM198 KCNK10 TCAGTTGTTTATGGCACAG 2871 CCC GCCC
TCAGTTGTT GGCGCAG
||||||| |||||
AGTCAACAA CCGTGTC
ATA IIIC

GAM198 KDR AGTGATGCCCGGCGCAGGC 2862 TCAGTTGTT CC
CCCGGCGCAGGC
|||||||
GGGCCGCGTCCG
ACTAC_____ TC

GAM198 LAD1 TCAGTGGCTG--GGAGCAGGCCCC 2873 T CCC C
TCAGT GTT GG GCAGGCCCC
||||| ||| || |||||
AGTCA CGA CC CGTCCGGGG
C C_ T

GAM198 MKI67 AGTTGTTCTGCCACCGTGCCC 2861 TCAG CG _ AG_ C
TTGTTCC GC GC GCCC
||||| || || ||||
AACAAGG CG TG CGGG
_____ A_ G GCA A

GAM198 MYO1D CAGTT--TCACGGGCGCAGGCCCC 2864 TC GTTCCC
AGTT GGCGCAGGCCCC
||| |||||
TCAA CCGCGTCCGGGG
_ AGTGC_

GAM198 PTPRG AGTTGTGGCTCCGGCGCAGGC 2860 TCA T C CCC
GT GTTCC GGCGCAGGC
|| ||||| |||||
CA CGAGG CCGCGTCCG
AA_ C _ ACI

GAM198 TNP2 TCATTCTGCCCTGTGCAGGCCCC 2870 GT_ T GGC II
TCA TGT CCC GCAGGCCCC
||| ||| ||| |||||

	AGT ACG GGG CGTCCGGGG		
	AAAG _ ACA II		
GAM199 ADCY6	CACCCAGTGAGCACAGAGTCCA 2876	_____ T	GIII
	CACCCAGTGA AG GTCCA		
	II		
	GTGGGTCACT TC CAGGT		
	CGTG T III G		
GAM199 BAIAP3	CACCCAGTG--GTG-CCAG 2877	AA T	
	CACCCAGTG GTG CCAG		
	III		
	GTGGGTCACT CAC GGTC		
	— —		
GAM199 EGFL4	CCAAGTAGACAGTGTCCAG 2879	CACCC _ _	I
	AGT GA AGTGTCCAG		
	III II		
	TCA CT TCACAGGTC		
	T_____ T G C		
GAM199 WT1	CACCCAGTGATGCATCTAG 2878	A CAGI	
	CACCCAGTGA GTGTC		
	GTGGGTCACT CGTAG		
	A ATCI		
GAM200 ADRBK1	GGTTGG-GGCAAGAGGGGACAG 2884	TG T CC	
	GTTGG GGCA AGGGGACAG		
	CAACC CCGT TCCCCTGTC		
	— — TC		
GAM200 APOC1	TTGGTGGCACCTGGGGCCA 2895	TGGTTG A A	
	GTGGCACC GGGG CA		
	II		
	CACCGTGG CCCC GT		
	_____ A G		
GAM200 BACE2	GTTGGTGGCACATGTAGACA 2885	TGGT CAGG G	
	TGGTGGCAC GGACA		
	ACCACCGTG TCTGT		
	_____ TACA G		
GAM200 CASP2	TTGGTGGCAGCAGCCAACAG 2896	TGGT TG _ _ CAG	
	TGG GCA CCAG GGA		
	ACC CGT GGTT TCCT		
	C___ GT C G AII		
GAM200 DLEC1	TGGTTGGTGTACTCCAGGAG-CAG 2891	_ A A I	
	TGGTTGGTG GC CCAGGGG CAG		
	II		
	ACCAACCAC TG GGTCCTC GTC		
	A A _ I		
GAM200 EGLN2	TGGTAGGAGGGGAGCAGGGGACAG 2892	T T CAC_	II
	TGGT GG GG CAGGGGACAG		

	ACCA CC CC GTCCCCTGTC		
	T T CCTC II		
GAM200 EZH1	GGTGGCACACAGCCTGGGACAG	2882	TGGTTG TG ACCAG I
	G GC GGGACAG		
	I II IIIII		
	T CG CCCTGTC		
	GTGG_ GT GA_ C		
GAM200 G6PD	GTTGGTGGGAC-AGGGGACA	2886	TGGT CAC
	TGGTGG CAGGGGACA		
	IIII IIIIIII		
	ACCACC GTCCCCTGT		
	CT_		
GAM200 JDP1	TGTTGGCAGCATAGGGGACAG	2889	TGGTT TG CC
	GG GCA AGGGGACAG		
	II III IIIIIII		
	CC CGT TCCCCTGTC		
	GT A_		
GAM200 KLHL3	TTGGTGGCATCTGTGGGCAG	2897	TGGTTG CCAG_ A
	GTGGCA GGG CAG		
	IIII III III		
	CACCGT CCC GTC		
	AGACA _		
GAM200 NDST1	TGATGGGTGACGACAGGGGACAG	2893	T AC I
	TGGT GGTGGC CAGGGGACAG		
	III IIIII IIIIIII		
	ACTA CCACTG GTCCCCTGTC		
	C CT I		
GAM200 NTSR1	GGTTGGTGGCCCTTGGGCAC	2883	TG A A_ G AG
	GTTGGTGGC CC GGG AC		
	IIIIII II III II		
	CAACCACCG GG CCC TG		
	AA G AI		
GAM200 PCTK1	TGTTTGGGCAGGCAGCAGGGGACA	2890	TG _ _ C GII
	GTT GGT GGCA CAGGGGACA		
	III III III IIIIIII		
	CAA CCG CCGT GTCCCCTGT		
	A_ AC T C III		
GAM200 PKD2L1	TTGCTGCAAGCCCCAGGGGAC	2894	TGGT GT A AG
	TG GGC CCAGGGGAC		
	II III IIIIIII		
	AC TCG GGTCCCCTG		
	G_ GT G GT		
GAM200 TUFT1	TGGGTGCAGCCAGGGGACAG	2888	TGGTTGGTG _
	GCA CCAGGGGACAG		
	III IIIIIII		
	CGT GGTCCCCTGTC		
	A_ C		
GAM200 WHN	TGGCTTAGTGGCAT-AGGGGACAG	2887	_ CC I
	TGGTT GGTGGCA AGGGGACAG		
	IIII IIIII IIIIIII		

	ACCGA TCACCGT TCCCCTGTC		
	A A_ I		
GAM201 BRCA1	TGTCTGTTCAATTTGGCTTGTTA 2913	ATG	ATGA
	TGTCTGTTTCAT TTGGTT		
	ACAGACAAGTA AACCGA		
	____ ACAA		
GAM201 BRCA1	TGTCTGTTCAATTTGGCTTGTTA 2913	ATG	I
	TCTGTTTCAT TTGGTT		
	AGACAAGTA AACCGA		
	____ A		
GAM201 BTC	CATTTTCA--AATGAGCAA 2903	AAA	TC
	CATTT CGAATGAGCAA		
	GTAAA GTTTACTCGTT		
	A_ II		
GAM201 BTC	CATTTTCA--AATGAGCAA 2903	AAA	I
	CATTT CGAATGAGCA		
	GTAAA GTTTACTCGT		
	A_ T		
GAM201 C18orf1	TGTCTGTTACATCTCTGTGAT 2915	G G	TATGA
	TGTCTGTTTCATAT TT GT		
	ACAGACAAGTGTA AG CA		
	G A CTAII		
GAM201 C18orf1	TGTCTGTTACATCTCTGTGAT 2915	G G	TAI
	GTCTGTTTCATAT TT GT		
	CAGACAAGTGTA AG CA		
	G A CTI		
GAM201 C5R1	TGTCAATATCCTGGTTATGA 2917	C G	I
	GTT ATAT TTGGTTATG		
	CAG TATA GACCAATAC		
	T G I		
GAM201 C5R1	TGTCAATATCCTGGTTATGA 2917	TGTCTGTTC	G
	ATAT TTGGTTATG		
	TATA GACCAATAC		
	T_____ G		
GAM201 COG3	CATTTAAACGAGGCAGTTATCA 2905	ATGA	____ GI
	CATTTAAACGA GCA ATCA		
	GTAAATTTGCT CGT TAGT		
	C_____ CAA II		
GAM201 COG3	CATTTAAACGAGGCAGTTATCA 2905	ATGA	ATCI
	ATTTAAACGA GCA		

	TAAATTTGCT CGT			
	C__ CAAT			
GAM201 CXCL6	CATTTCTATGTAAATTAGCAATCAG	2901	AAAC__ G	II
	CATTT GAAT AGCAATCAG			
	GTAAA TTTA TCGTTAGTC			
	GATACA A II			
GAM201 CXCL6	CATTTCTATGTAAATTAGCAATCAG	2901	ATTTAAAC G	I
	GAAT AGCAATCA			
	TTTA TCGTTAGT			
	AAGATACA A I			
GAM201 EXT2	TCTGTTCTTAAATGGTTATGA	2911	A TGT I	
	CTG TTC TA TGGTTATG			
	GACAAG AT ACCAATAC			
	A TTT I			
GAM201 EXT2	TCTGTTCTTAAATGGTTATGA	2911	TGTC A TGT	
	TG TTC TA TGGTTATGA			
	ACAAG AT ACCAATACT			
	__ A TTT			
GAM201 FBLN1	CATTAAAA--AATGAGCAA	2902	CAT C TC	
	TTAAA GAATGAGCAA			
	AATTT TTTACTCGTT			
	GT_ _ II			
GAM201 FBLN1	CATTAAAA--AATGAGCAA	2902	CAT C I	
	TTAAA GAATGAGCA			
	AATTT TTTACTCGT			
	GT_ _ T			
GAM201 FBXL3A	TCTTCTCATATGTTGCTGTAGGA	2909	TG GTTATI	
	TTCATATGTTG			
	GAGTATACAAC			
	A_ GACATC			
GAM201 FBXL3A	TCTTCTCATATGTTGCTGTAGGA	2909	TGTCTG GTTATGAI	
	TTCATATGTTG			
	GAGTATACAAC			
	AA__ GACATCCT			
GAM201 FGF1	TCAGTATCATATGTTAGAGATGA	2908	CT _ TT I	
	GT TCATATGTTGG ATG			
	CA AGTATACAATC TAC			
	T_ T TC I			
GAM201 FGF1	TCAGTATCATATGTTAGAGATGA	2908	TGTCT _ TT I	
	GT TCATATGTTGG ATGA			

	CA AGTATACAATC TACT		
	T____ T TC T		
GAM201 FOXD2	TGTCTGTTCATGGGTCTGG 2914	AT	GII
	TGTCTGTTCAT GTT		
	ACAGACAAGTA CAG		
	CC ACC		
GAM201 FOXD2	TGTCTGTTCATGGGTCTGG 2914	ATG_	TTATG
	TGTCTGTTCAT TTGG		
	ACAGACAAGTA GACC		
	CCCA IIIAG		
GAM201 IDH1	CATTTACCCTTTTGAGCAATC 2904	AACGAA	AG
	CATTTA TGAGCAATC		
	GTAAAT ACTCGTTAG		
	GGGAAA II		
GAM201 IDH1	CATTTACCCTTTTGAGCAATC 2904	AACGAA	I
	ATTTA TGAGCAAT		
	TAAAT ACTCGTTA		
	GGGAAA I		
GAM201 NEB	TAATAAGCATTAGCAATCAG 2907	TAAACGAATG_	II
	AGCAATCA		
	TCGTTAGT		
	ATTATTCGTAA CI		
GAM201 PTPN7	TGTCTG--CATG-GATGGTTATGA 2916	TCAT	T_
	TGTCTGT ATG TGGTTATGA		
	ACAGACG TAC ACCAATACT		
	____ CT		
GAM201 PTPN7	TGTCTG--CATG-GATGGTTATGA 2916_	TCAT	T_
	GTCTGT ATG TGGTTATG		
	CAGACG TAC ACCAATAC		
	A ____ CT		
GAM201 RPL5	CTGTTTCATAAGTTTATTAT 2906	T G	II
	CTGTTTCATA GTT GTTA		
	GACAAGTAT CAA TAAT		
	T A AI		
GAM201 RPS19	TTTTTACGAATGAGGCAAT 2919	CATTTAA	_ CA
	ACGAATGAG CAAT		
	TGCTTACTC GTTA		
	AAA____ C AA		
GAM201 RPS19	TTTTTACGAATGAGGCAAT 2919	TTTAA	_ II
	ACGAATGAG CAA		

		TGCTTACTC GTT			
		AAAAA C AI			
GAM201 SAR1		TCTGTTTCATA-ATT--TTATGA	2910	TGTTGGTTAI	
		TCTGTTTCATA			
		AGACAAGTAT			
		TAAAATACTI			
GAM201 SAR1		TCTGTTTCATA-ATT--TTATGA	2910 TGTC	TGTTGG	
		TGTTTCATA TTATG			
		ACAAGTAT AATAC			
		____ TAA____			
GAM201 TDG		ATTATAAAGAGAA-GAGCAATCA	2900 CATTTAAAC T	GI	
		GAA GAGCAATCA			
		CTT CTCGTTAGT			
		AATATTTCT _ AI			
GAM201 TDG		ATTATAAAGAGAA-GAGCAATCA	2900 TTTAAAC_ T	I	
		GAA GAGCAATC			
		CTT CTCGTTAG			
		ATATTTCT _ I			
GAM201 TNFSF10		TTCACTATGTTGGTCACTATG	2918 _	IIIC	
		TTCAT ATGTTGGTTAT			
		AAGTG TACAACCAGTG			
		A ATAC			
GAM201 TRIM9		TGTCTAGGTCCTTTGTTGGTTA	2912 _ ATA	TGA	
		TGTCT GTTC TGTTGGTTA			
		ACAGA CAGG ACAACCAAT			
		TC AA_ III			
GAM201 TRIM9		TGTCTAGGTCCTTTGTTGGTTA	2912 G _ ATA	I	
		TCT GTTC TGTTGGTT			
		AGA CAGG ACAACCAA			
		_ TC AA_ I			
GAM201 ZNF124		TTCAAA--AATGAGCAACCA	2920 CATTTAAAC		
		GAATGAGCAATCA			
		TTTACTCGTTGGT			
		GTT_____			
GAM201 ZNF124		TTCAAA--AATGAGCAACCA	2920 TTAAAC	I	
		GAATGAGCAATC			
		TTTACTCGTTGG			
		AAGTT_ I			
GAM202 ADSL		AACAGGAAAGCACCATGGGAAGA	2923 ACA _	I	
		GAGAG GCCATGGGAAG			

	CTTTC TGGTACCCTTC		
	TC_ G I		
GAM202 ADSL	AACAGGAAAGCACCATGGGAAGA	2923	TGAACA _ TI
	GAGAG GCCATGGGAAGA		
	CTTTC TGGTACCCTTCT		
	GTC_ G TC		
GAM202 BAALC	TGTACAGAGAGGCCAAGGGGAAG	2939	A T_ ATI
	TG ACAGAGAGGCCA GGGGAAG		
	AC TGTCTCTCCGGT CCCTTC		
	A TC		
GAM202 BAALC	TGTACAGAGAGGCCAAGGGGAAG	2939	GA T_ I
	ACAGAGAGGCCA GGGAA		
	TGTCTCTCCGGT CCCTT		
	A_ TC I		
GAM202 BRS3	GAACAGAACAGA-ATGGGAAGA	2935	_ A CC I
	AACAGAG GG ATGGGAAG		
	TTGTCTT TC TACCCTTC		
	C G T_ I		
GAM202 BRS3	GAACAGAACAGA-ATGGGAAGA	2935	T_ GAGGCC T
	GAACAGA ATGGGAAGA		
	CTTGTCT TACCCTTCT		
	TTGT _ T		
GAM202 CARPX	AGGGAATCCCTGGGAAGAT	2930	A G A II
	AG GAG CC TGGGAAGA		
	TC CTT GG ACCCTTCT		
	C A G AI		
GAM202 CBFA2T2	TGCACAGAGAGGCTGTGGG	2940	A CA AAGA
	TG ACAGAGAGGC TGGG		
	AC TGTCTCTCCG ACCC		
	G AC IIIT		
GAM202 CBFA2T2	TGCACAGAGAGGCTGTGGG	2940	A CA II
	TG ACAGAGAGGC TGG		
	AC TGTCTCTCCG ACC		
	G AC CI		
GAM202 HIP1	GAACAGAGATGACCATGGG	2932	_ II
	GAACAGAGA GGCCATGG		
	CTTGTCTCT CTGGTACC		
	A CI		
GAM202 HIP1	GAACAGAGATGACCATGGG	2932	TG _ AAGA
	AACAGAGA GGCCATGGG		

	TTGTCTCT CTGGTACCC		
	___ A AIII		
GAM202 HOXA7	ACA-AGATGCC-TGGGAAGAT 2928	CA G A I	
	GAGA GCC TGGGAAGA		
	TTCT CGG ACCCTTCT		
	TG A _ I		
GAM202 HOXA7	ACA-AGATGCC-TGGGAAGAT 2928	TGAACAG G A	
	AGA GCC TGGGAAGA		
	TCT CGG ACCCTTCT		
	_____ A _		
GAM202 HSD17B2	TGAACAGAGAGTCAA---GAAG 2943	GC T AI	
	TGAACAGAGAG CA GGG		
	ACTTGTCTCTC GT CTT		
	A_ T CI		
GAM202 HSD17B2	TGAACAGAGAGTCAA---GAAG 2943	GC TG A	
	TGAACAGAGAG CA GGAAG		
	ACTTGTCTCTC GT TCTTC		
	A_ _ I		
GAM202 IL1R1	AGAGCGGCATCATGGGAAG 2929	A _ III	
	AGAG GGC CATGGGAA		
	TCTC CCG GTACCCTT		
	G TA CII		
GAM202 MAGP2	TGAACAGAGCCACTCCCTGGAAAG 2937	AGG_ A ATI	
	TGAACAGAG CC TGGGAAG		
	ACTTGTCTC GG ACCTTTC		
	GGTGA G III		
GAM202 MAGP2	TGAACAGAGCCACTCCCTGGAAAG 2937	GA AGG_ A I	
	ACAGAG CC TGGGAA		
	TGTCTC GG ACCTTT		
	_ GGTGA G I		
GAM202 MAP2K1	TGAACAGAGACAGGCATGGGAAG 2938	_ C ATI	
	TGAACAGAGA GGC ATGGGAAG		
	ACTTGTCTCT CCG TACCCTTC		
	GT _ III		
GAM202 MAP2K1	TGAACAGAGACAGGCATGGGAAG 2938	G _ C I	
	AACAGAGA GGC ATGGGAA		
	TTGTCTCT CCG TACCCTT		
	_ GT _ I		
GAM202 MPP3	TGGACAGAGAGG--ATGGGAA 2942	A CC GA	
	TG ACAGAGAGG ATGGGAA		

	AC TGTCTCTCC TACCCTT		
	C _ _ II		
GAM202 MPP3	TGGACAGAGAGG--ATGGGAA	2942 _ A	CC I
	G ACAGAGAGG ATGGGA		
	I		
	C TGTCTCTCC TACCCT		
	A C _ _ I		
GAM202 MYL3	ACAGAGAGG-GATGTGGAGA	2927 _	CC _ AGI
	CAGAGAGG ATG GGA		
	GTCTCTCC TAC CCT		
	T C_ A CII		
GAM202 MYL3	ACAGAGAGG-GATGTGGAGA	2927 TGAACA	CCA_ GA
	GAGAGG TGG AGA		
	CTCTCC ACC TCT		
	_____ CTAC TC		
GAM202 PKP1	GAGCAGAGAGGCGAGGCGA	2934 A	CAT GII
	GA CAGAGAGGC GG		
	CT GTCTCTCCG CC		
	C CT_ GCT		
GAM202 PKP1	GAGCAGAGAGGCGAGGCGA	2934 TGAA	CAT _ AGA
	CAGAGAGGC GG GA		
	GTCTCTCCG CC CT		
	TC_ CT_ G CII		
GAM202 PODXL	GAACATAGAGGG--TGGGAAGAT	2936 G	CCA I
	GAACA AGAGG TGGGAAG		
	CTTGT TCTCC ACCCTTC		
	A C_ T		
GAM202 PODXL	GAACATAGAGGG--TGGGAAGAT	2936 TG G	CCA
	AACA AGAGG TGGGAAGAT		
	TTGT TCTCC ACCCTTCTA		
	_ A C_		
GAM202 PTPRA	AACTGAG-GGCCATGGGCTGAT	2925 ACA_ A	AA I
	GAG GGCCATGGG GA		
	CTC CCGGTACCC CT		
	TTGA _ GA I		
GAM202 PTPRA	AACTGAG-GGCCATGGGCTGAT	2925 TGAACA A	AA
	GAG GGCCATGGG GAT		
	CTC CCGGTACCC CTA		
	GA_ _ GA		
GAM202 RAB38	AACATTCAGGCCATGGCAAG	2924 GAG	G I
	ACA AGGCCATGG AA		

	TGT TCCGGTACC TT			
	AAG G I			
GAM202 RAB38	AACATTCAGGCCATGGCAAG	2924	TGAACAGAG	G A
	AGGCCATGG AAG			
	TCCGGTACC TTC			
	GTAAG____ G A			
GAM202 RGS5	TGAGCAAAGCTGCTGTGGGAAGAT	2945	A AG CA	I
	TGA CAGAG GC TGGGAAGAT			
	ACT GTTTC CG ACCCTTCTA			
	C GA AC I			
GAM202 RGS5	TGAGCAAAGCTGCTGTGGGAAGAT	2945	A AG CA	I
	GA CAGAG GC TGGGAAGA			
	CT GTTTC CG ACCCTTCT			
	C GA AC I			
GAM202 RNF4	GAACAGAGATGGCC-TGGGA	2933	_ A II	
	GAACAGAGA GGCC TGGG			
	CTTGTCTCT CCGG ACCC			
	A _ TI			
GAM202 RNF4	GAACAGAGATGGCC-TGGGA	2933	TG _ A AGA	
	AACAGAGA GGCC TGGGA			
	TTGTCTCT CCGG ACCCT			
	_ A _ CII			
GAM202 SNAI1	ACAGAAATGGCCATGGGAAG	2926	_ II	
	ACAGAGA GGCCATGGGA			
	TGTCTTT CCGGTACCCTT			
	A CI			
GAM202 SNAI1	ACAGAAATGGCCATGGGAAG	2926	TGAACA _ A	
	GAGA GGCCATGGGAAG			
	CTTT CCGGTACCCTTC			
	_____ A C			
GAM202 TMEPAI	TGAACAGAG----CTTGGGA	2941	AGGCCA G	
	TGAACAGAG TGGGA			
	ACTTGTCTC ACCCTT			
	GA____ I			
GAM202 TMEPAI	TGAACAGAG----CTTGGGA	2941	_ AGGCCA	
	GAACAGAG TGGGA			
	CTTGTCTC ACCCT			
	A GA____			
GAM202 TNFSF4	AGAGGCCAACATGGGAAGA	2931	____ III	
	AGAGGCCA TGGGAAG			

	TCTCCGGT ACCCTTC	
	TGT TII	
GAM202 TP63	TGACCAGA-ATGC-ATGGGAAGAT 2944 A AG C	
	TGA CAGAG GC ATGGGAAGAT	
	ACT GTCTT CG TACCCTTCTA	
	G A_ _	
GAM202 TP63	TGACCAGA-ATGC-ATGGGAAGAT 2944 _ A AG C I	
	GA CAGAG GC ATGGGAAGA	
	CT GTCTT CG TACCCTTCT	
	A G A_ _ I	
GAM203 CHGB	TGTGATGGCTGCTTCTTAAC 2950 _ AA_ GTTTC	
	TGTGATGGC GC TTAAC	
	ACACTACCG CG AATTG	
	A AAG IIIC	
GAM203 LZTFL1	TGTGATGGC-C-ATCAATGT 2951 G A C TT	
	TGTGATGGC CA TTAA GT	
	ACACTACCG GT AGTT CA	
	_ _ A II	
GAM203 MUCDHL	TGTGATGGCCGAGTTGAGGT 2952 GCAATTAACGTTTC	
	TGTGATGGC	
	ACACTACCG	
	GCTCAACTCCAI	
GAM203 PPL	TGGTGGCTGACAATTAACGT 2948 TGTGA _ C	
	TGGC GCAATTAACGTTT	
	ACCG TGTTAATTGCAGG	
	C_ _ AC I	
GAM203 STAT1	TGTGATGGCGATAGCAATTA 2949 _ ACGTTTC	
	TGTGATGGC GCAATTA	
	ACACTACCG CGTTAAT	
	CTAT IIICCTT	
GAM204 ABCC3	TGAGGATGACAGGGG-CCAG 2963 TGTGA A TCC	
	GTGACAGGGG CCAG	
	TACTGTCCCC GGTC	
	TCC_ _ TTI	
GAM204 FE65L2	GAGGGGCAGGGGACC--TCCT 2958 TGTGAGTGA AG	
	CAGGGGACC TCC	
	GTCCCCTGG AGG	
	CCC_ _ _	
GAM204 GLTSCR1	TGAGGTGACAGGGCAGCCA 2964 TGTGA GAC C	
	GTGACAGGG CAGTC	

		CACTGTCCC GTCGG			
		TC_____T			
GAM204	GPC1	GTGAGTGACAGGAGGTCACCAG	2960 TG	_____	TCCT
		TGAGTGACAGGGG ACCAG			
		ACTCACTGTCCTC TGGTC			
		_____CAG CIII			
GAM204	GUK1	AGGGACAGGGGA-CAGCCC	2955 TGTGAGTG		C
		ACAGGGGAC AGTC			
		TGTCCCCTG TCGG			

GAM204	HTR4	GTGAGTGAC-GGGAACATGTC	2962 TG	A	CA C
		TGAGTGAC GGGGAC GTC			
		ACTCACTG CCCTTG CAG			
		_____TA T			
GAM204	KRT4	AGTGACA-GGGCCCAGGCC	2956 TGTGAGTG	GA	T
		ACAGGG CCAG C			
		TGTCCC GGTC G			
		_____G_ C			
GAM204	NDST1	GTGAC-GACAGGGGA-CAGTC	2961 TG G		C C
		TGA TGACAGGGGAC AGTC			
		ACT GCTGTCCCCTG TCAG			
		_____C			
GAM204	PIGR	TGTCAGTGAGGAGGGGACCAG	2966 TG_____	T CA	TCCT
		TGAG GA GGGGACCAG			
		ACTC CT CCCCTGGTC			
		ACAGTG _ _ IIIT			
GAM204	SEPN1	GAGTGACAGGG---CAGCCC	2957 TGTGAG		GAC
		TGACAGGG CAGTC			
		ACTGTCCC GTCGG			

GAM204	SH3BP2	GTGAGTGTGATGGGGGGACCAGT	2959 TG	ACA_____	CCTI
		TGAGTG GGGGACCAGT			
		ACTCAC CCCCTGGTCA			
		_____ACTACC CIII			
GAM204	ZNF43	TGGGTG-CAG-GGACCAGT	2965 TGTGA	A G	C
		GTG CAGGG ACCAGT			
		CAC GTCCC TGGTCA			
		C_____C			
GAM205	BCL2L2	GTTCTGGCGAGCACAACTACGTTGC	2970 T	_ CCC _	AGI
		CTGGCG GC ATT CGT			

	GACCGC CG TGA GCA		
	— T TGT T AII		
GAM205 BCL2L2	GTTCTGGCGAGCACAACTACGTTGC 2970 TG	— CCC — A II	
	TTCTGGCG GC ATT CGT GC		
	AAGACCGC CG TGA GCA CG		
	— T TGT T A GI		
GAM205 EEF1A1	TGTTCTGGCGGCAAACCC--TCGT 2972	— AT AGC	
	TGTTCTGGCGGC CCC TCGT		
	ACAAGACCGCCG GGG AGCA		
	TTT — III		
GAM205 EEF1A1	TGTTCTGGCGGCAAACCC--TCGT 2972	— ATTCGI	
	TTCTGGCGGC CCC		
	AAGACCGCCG GGG		
	TTT AGIIIG		
GAM205 GPR56	TCTGCCCTGGGCCCCATTCTG 2971	— CG III	
	TCTGG GCCCATTC		
	GGACC CGGGGTAAG		
	AGACG — CII		
GAM205 GPR56	TCTGCCCTGGGCCCCATTCTG 2971 T	CG AG	
	GTTCTGG GCCCATTCGT		
	CGGGACC CGGGGTAAGCG		
	— — GG		
GAM205 RAB38	CTGGCGGCCGCGCCAGACGT 2969	— TT III	
	CTGGCGGCC CCA CG		
	GACCGCCGG GGT GC		
	CC CT AII		
GAM205 RAB38	CTGGCGGCCGCGCCAGACGT 2969 TGTTCT	— CCATT A	
	GGC GGCC CGT G		
	CCG CCGG GCA C		
	G — G TCT —		
GAM206 ADCY7	TGTCTCTAAACAGACTCCAT 2996 GCA TT	GGA	
	TG CT ACAGACTCCAT		
	AC GA TGTCTGAGGTA		
	AGA TT III		
GAM206 ADCY7	TGTCTCTAAACAGACTCCAT 2996 GGCA TT	I	
	CT ACAGACTCCA		
	GA TGTCTGAGGT		
	CAGA TT I		
GAM206 AS3	CACTTTCACAAGACTCCAT 2977	— — III	
	CACTT TACA GACTCCA		

	GTGAA GTGT CTGAGGT			
	A T AII			
GAM206 AS3	CACTTTCACAAGACTCCAT	2977	TGGCAC _	A
	TTTACA GACTCCATGG			
	AAGTGT CTGAGGTATC			
	A_____ T A			
GAM206 B3GALT5	GCCCTTCTAT-GACTCCATG	2986	A ACA	II
	GC CTTT GACTCCAT			
	CG GAAG CTGAGGTA			
	G ATA CI			
GAM206 B3GALT5	GCCCTTCTAT-GACTCCATG	2986	TGGCA ACA	A
	CTTT GACTCCATGG			
	GAAG CTGAGGTACT			
	G_____ ATA A			
GAM206 CDR2	TGGCACTTTGGCAGAACCCTCC	2993	A_ _	IIIG
	TGGCACTTT CAGA CTC			
	ACCGTGAAA GTCT GGG			
	CC T AGGI			
GAM206 CDR2	TGGCACTTTGGCAGAACCCTCC	2993	A_ ____	ATGGAG
	TGGCACTTT CAGA CTCC			
	ACCGTGAAA GTCT GAGG			
	CC TGG IIIGAG			
GAM206 COL4A1	GGCACTTTACGGTTTTTCAT	2989		AGACTCCAII
	GGCACTTTAC			
	CCGTGAAATG			
	CCAAAAGTAI			
GAM206 CRACC	TGTCAGGTGCATCTGCTTCT	3001	GAC T	AGG
	TGTCAGGTG CATCT CT			
	ACAGTCCAC GTAGA GA			
	_____ C AGA			
GAM206 CRACC	TGTCAGGTGCATCTGCTTCT	3001	GAC	TCI
	GTCAGGTG CATCT			
	CAGTCCAC GTAGA			
	_____ CGA			
GAM206 CSHL1	GTCAGGTGGCTGCCGTCTTCCAG	2991	TC A__ A	I
	AGGTGG CC TCTTCTA			
	TCCACC GG AGAAGGT			
	_____ GAC C I			
GAM206 CSHL1	GTCAGGTGGCTGCCGTCTTCCAG	2991	TG A__ A	GGI
	TCAGGTGG CC TCTTCTAG			

	AGTCCACC GG AGAAGGTC		
	— GAC C GII		
GAM206 CSPG4	GCACTGTTTATCCAGGCTCCATGGA 2985 CACTTTA A I		
	CAG CTCCATGG		
	GTC GAGGTACC		
	CAAATAG C I		
GAM206 CSPG4	GCACTGTTTATCCAGGCTCCATGGA 2985 TGGCACTTTA A II		
	CAG CTCCATGGAG		
	GTC GAGGTACCTT		
	TGACAAATAG C GI		
GAM206 EIF2C1	CAGGTGGA-CATC-TCTGGG 2983 C CTAI		
	CAGGTGGAC ATCTT		
	GTCCACCTG TAGAG		
	— ACCC		
GAM206 EIF2C1	CAGGTGGA-CATC-TCTGGG 2983 TGTCAG C T A		
	GTGGAC ATCT CT G		
	CACCTG TAGA GA C		
	— — —		
GAM206 EVC	CTTTGCACAACCTCCATGGA 2984 A _ II		
	CTTT CA GACTCCATGG		
	GAAA GT TTGAGGTACC		
	C G TI		
GAM206 EVC	CTTTGCACAACCTCCATGGA 2984 TGGCACTT A		
	TACAG CTCCATGGA		
	GTGTT GAGGTACCT		
	— —		
GAM206 HKE4	CACTTTACAGACTCTCTGG 2979 CA II		
	CACTTTACAGACTC TG		
	GTGAAATGTCTGAG AC		
	AG CI		
GAM206 HKE4	CACTTTACAGACTCTCTGG 2979 TGGCAC CA A		
	TTTACAGACTC TGG		
	AAATGTCTGAG ACC		
	AG C		
GAM206 MEPE	TGTCAGGTGG-CTCTCCTCTA 3002 ACCA GG		
	TGTCAGGTGG TCTTCTA		
	ACAGTCCACC AGGAGAT		
	GAG_ II		
GAM206 MEPE	TGTCAGGTGG-CTCTCCTCTA 3002_ ACCA I		
	GTCAGGTGG TCTTCT		

	CAGTCCACC AGGAGA		
	A GAG_ I		
GAM206 MYO15A	CACTTAGCA-ACTCCATGGAG 2980 _ CTTTACAG		
	TGGCA ACTCCATGGA		
	ATCGT TGAGGTACCT		
	A _____		
GAM206 MYO15A	CACTTAGCA-ACTCCATGGAG 2980 _ TACA I		
	ACTT GACTCCATGGA		
	TGAA TTGAGGTACCT		
	G TCG_ I		
GAM206 NOC4	TTACAAATTCCTCCATGGAG 3003 _ III		
	TTACAGA CTCCATGGA		
	AATGTTT GAGGTACCT		
	AAG CII		
GAM206 NRXN3	ACATTACAGACTCACTTGGAG 2975 CT CA_ I		
	TTACAGACTC TGGAG		
	AATGTCTGAG ACCT		
	T_ TGA I		
GAM206 NRXN3	ACATTACAGACTCACTTGGAG 2975 TGGCACTT CA_		
	TACAGACTC TGGAG		
	ATGTCTGAG ACCTC		
	_____ TGA		
GAM206 PAP	GTCACATCCATCATCTTCTA 2992 G GGAC I		
	TCA GT CATCTTCT		
	AGT TA GTAGAAGA		
	G GGTA I		
GAM206 PHYH	CACTTTATTTGGACTCCATG 2978 CA_ III		
	CACTTTA GACTCCAT		
	GTGAAAT CTGAGGTA		
	AAAC CII		
GAM206 PML	TGG-ACTTGAGAGGCCTCCATGGAG 2994 C TAC A_ I		
	TGG ACTT AG CTCCATGGAG		
	ACC TGAA TC GAGGTACCTC		
	_ CTC CG I		
GAM206 PML	TGG-ACTTGAGAGGCCTCCATGGAG 2994 C TAC A_ I		
	GG ACTT AG CTCCATGGA		
	CC TGAA TC GAGGTACCT		
	_ CTC CG I		
GAM206 PPP1R3C	TGTACAGAGTGGACCATCTTATGAGG 2998 _ _ CT_ GII		
	TGT CAG GTGGACCATCTT AGG		

	ACA GTC CACCTGGTAGAA TCC		
	T T TAC III		
GAM206 PPP1R3C	TGTACAGAGTGGACCATCTTATGAGG 2998 T _		CTAGI
	CAG GTGGACCATCTT		
	III		
	GTC CACCTGGTAGAA		
	_ T TACTI		
GAM206 PTPRD	TGGCTCAGAAGAGACTCCATGGA 2997	ACTTTAC	GI
	TGGC AGACTCCATGGA		
	III		
	ACCG TCTGAGGTACCT		
	AGTCTTC II		
GAM206 PTPRD	TGGCTCAGAAGAGACTCCATGGA 2997	ACTTTAC	I
	GGC AGACTCCATGG		
	III		
	CCG TCTGAGGTACC		
	AGTCTTC I		
GAM206 SFRP1	CACTTTACAGCCTCACTGCAG 2982	A CA GAI	
	ACTTTACAG CTC TG		
	III II		
	TGAAATGTC GAG AC		
	G TG GTI		
GAM206 SFRP1	CACTTTACAGCCTCACTGCAG 2982	TGGCAC A CA G	
	TTTACAG CTC TG AG		
	III II II		
	AAATGTC GAG AC TC		
	_____ G TG G		
GAM206 STS	GCACTTTAC--ATTCCATAGGAG 2987 _	GAC AI	
	CACTTTACA TCCATGG		
	GTGAAATGT AGGTATC		
	C A__ CT		
GAM206 STS	GCACTTTAC--ATTCCATAGGAG 2987	TGGC GAC _	
	ACTTTACA TCCAT GGAG		
	TGAAATGT AGGTA CCTC		
	_____ A__ T		
GAM206 TBL2	TGTCAGGTGGAAATCCATTTGCT 2999	_____ CTTCTAGGGI	
	TGTCAGGTGGA CCAT		
	ACAGTCCACCT GGTA		
	TTA AACGAIIGG		
GAM206 TBL2	TGTCAGGTGGAAATCCATTTGCT 2999	GTC _____ CTTCI	
	AGGTGGA CCAT		
	TCCACCT GGTA		
	_____ TTA AACGI		
GAM206 USP9Y	CACTTTACA-ATTTCA GTGAG 2981 _	AC CA AI	
	ACTTTACAG TC TGG		
	II		

		TGAAATGTT AG ACT			
		G AA TC II			
GAM206 XRCC3		GTCAGTCTGTGGCCACCATCTTC	2990	___	___ IIIG
		GTCAG GTGG ACCATCTT			
		CAGTC CACC TGGTAGAA			
		AGA GG GIII			
GAM206 XRCC3		GTCAGTCTGTGGCCACCATCTTC	2990	T___ AG ___	TAGGGI
		GTC GTGG ACCATCTTC			
		CAG CACC TGGTAGAAG			
		AGT A_ GG CIIIGG			
GAM206 ZNF2		AGGTGGACCTGTCTTCAAG	2976	A_ TAI	
		AGGTGGACC TCTTC			
		TCCACCTGG AGAAG			
		AC TTCI			
GAM206 ZNF2		AGGTGGACCTGTCTTCAAG	2976	TGTCAGGT A_ T	
		GGACC TCTTC AGG			
		CCTGG AGAAG TCT			
		_____ AC T			
GAM206 ZNF255		TGG-ACTATGCAGACTCCA	2995	C TTA TGG	
		TGG ACT CAGACTCCA			
		ACC TGA GTCTGAGGT			
		_ TAC III			
GAM206 ZNF255		TGG-ACTATGCAGACTCCA	2995	C TTA I	
		TGG ACT CAGACTCC			
		ACC TGA GTCTGAGG			
		_ TAC T			
GAM206 ZNF264		GGAATTTTACAAACATTCCATGGAG	2988	GCAC ___	I
		TTTACAGAC TCCATGGA			
		AAATGTTTG AGGTACCT			
		TA___ TA I			
GAM206 ZNF264		GGAATTTTACAAACATTCCATGGAG	2988	TGGCAC ___	II
		TTTACAGAC TCCATGGAG			
		AAATGTTTG AGGTACCTC			
		CTTA___ TA TI			
GAM206 ZNF266		TGT-AGATGG-CCATCTTCT	3000	C A AG	
		TGT AGGTGG CCATCTTCT			
		ACA TCTACC GGTAGAAGA			
		_____ II			
GAM206 ZNF266		TGT-AGATGG-CCATCTTCT	3000	_ C A I	
		GT AGGTGG CCATCTTC			

	CA TCTACC GGTAGAAG		
	A _ _ I		
GAM207 AQP6	GGAGGAAGGTACCGGGAGAGA	3012 G	_ TA I
	AGGAAGG AC GGAGGG		
	TCCTTCC TG CCTCTC		
	_ A GC I		
GAM207 AQP6	GGAGGAAGGTACCGGGAGAGA	3012 TTAGGGAG	_ TA
	GAAGG AC GGAGGGA		
	CTTCC TG CCTCTCT		
	_____ A GC		
GAM207 BIG1	AGGAGAGGAAGGAAGAGAAGAGA	3006	CT I
	GGGAGGAAGGA AGGAGGG		
	CTCTCCTTCCT TCTTCTC		
	TC I		
GAM207 BIG1	AGGAGAGGAAGGAAGAGAAGAGA	3006 TTA	CT I
	GGGAGGAAGGA AGGAGGGA		
	CTCTCCTTCCT TCTTCTCT		
	_____ TC C		
GAM207 CALM1	AGGGAGGAA-GAGCA-GAGGGA	3008 _	ACTA I
	GGGAGGAAGG GGAGGG		
	CCCTCCTTCT TCTCCC		
	T CG_ I		
GAM207 CALM1	AGGGAGGAA-GAGCA-GAGGGA	3008 TTAG	ACTA
	GGAGGAAGG GGAGGG		
	CCTCCTTCT TCTCCC		
	_____ CG_		
GAM207 JAM2	GGGAGGAAG---AGGAGGGA	3017 _	GA CT
	GGAGGAAG AGGAGGG		
	CCTCCTTC TCCTCCC		
	C _____		
GAM207 LTBR	GGGAGGAAGG-C-AGGAGG	3013	AC I
	GGGAGGAAGG TAGGAG		
	CCCTCCTTCC GTCCTC		
	_____ C		
GAM207 LTBR	GGGAGGAAGG-C-AGGAGG	3013 TTAGGG	AC
	AGGAAGG TAGGAGG		
	TCCTTCC GTCCTCC		

GAM207 NCF2	TTAGGTAG-AA--ACTAGGAGG	3020	GA AG G
	TTAGG GGA GACTAGGAGG		

	AATCC TCT TTGATCCTCC	
	A_ _ I	
GAM207 NCF2	TTAGGTAG-AA-ACTAGGAGG 3020_ GA AG	
	TAGG GGA GACTAGGAG	
	ATCC TCT TTGATCCTC	
	A A_ _	
GAM207 NDST2	GGGAGGAAG----GGAGGGA 3016_ ACTAG	
	GGAGGAAGG GAGG	
	CCTCCTTCC CTCC	
	C _	
GAM207 NDST2	GGGAGGAAG----GGAGGGA 3016 TTAGGG ACTA	
	AGGAAGG GGAG	
	TCCTTCC CCTC	
	_ CTC_	
GAM207 NHLH1	GGGAGGAAGGGGGAGGAAGG 3015 ACTA I	
	GGAGGAAGG GGAGG	
	CCTCCTTCC CCTCC	
	C_ T	
GAM207 NHLH1	GGGAGGAAGGGGGAGGAAGG 3015 TTAGGG ACT	
	AGGAAGG AGGAGGG	
	TCCTTCC TCCTTCC	
	_ CCC	
GAM207 PAFAH1B1	AGGGAGGAAGGA--GGGAGGGA 3010_ CTA I	
	GGGAGGAAGGA GGAGGG	
	CCCTCCTTCCT CCTCCC	
	T C_ I	
GAM207 PAFAH1B1	AGGGAGGAAGGA--GGGAGGGA 3010 TTAG CTA	
	GGAGGAAGGA GGAGGG	
	CCTCCTTCCT CCTCCC	
	_ C_	
GAM207 PMX1	AGGGAGGAA-GA--GGGAGGGA 3007_ ACTA	
	GGGAGGAAGG GGAGGG	
	CCCTCCTTCT CCTCCC	
	T C_	
GAM207 PMX1	AGGGAGGAA-GA--GGGAGGGA 3007 TTAG ACTA	
	GGAGGAAGG GGAGGG	
	CCTCCTTCT CCTCCC	
	_ C_	
GAM207 RAP1GA1	TTAGGGTAGAGTGAAGGAGTATAGGAGGGA3019 _ _ C_	
	TTAGGG AG GAAGGA TAGGAGGGA T	

	AATCCC TC CTTCTC ATCCTCCCT A
	ATC A CAT III
GAM207 RAP1GA1	TTAGGGTAGAGTGAAGGAGTATAGGAGGGA3019 TAG _ C_ I
	GGAG GAAGGA TAGGAGGG
	TCTC CTTCTC ATCCTCCC
	_ A CAT I
GAM207 TRPC5	AGGGAGGAAGGA-AGGGATGGA 3011 _ CTA _ GI
	GGGAGGAAGGA GGA GG
	CCCTCCTTCCT CCT CC
	T TC_ A II
GAM207 TRPC5	AGGGAGGAAGGA-AGGGATGGA 3011 TTAG CTA G
	GGAGGAAGGA GGA GGA
	CCTCCTTCCT CCT CCT
	_ TC_ A
GAM207 TSLP	GGGAGGAAGGTCAGGGAGG 3014 ACTA II
	GGGAGGAAGG GGAG
	CCCTCCTTCC CCTC
	AGTC CI
GAM207 TSLP	GGGAGGAAGGTCAGGGAGG 3014 TTAGGG ACTA
	AGGAAGG GGAGGG
	TCCTTCC CCTCCT
	_ AGTC
GAM207 ULBP2	TAGGGAGGAGAGACT-TGATGGA 3018 _ AG A GA GI
	AGGGAGGA GACT G GG
	I
	TCCCTCCT CTGA C CC
	A CT A TA II
GAM207 ULBP2	TAGGGAGGAGAGACT-TGATGGA 3018 TT AG A GA
	AGGGAGGA GACT G GGGA
	I
	TCCCTCCT CTGA C CCTT
	_ CT A TA
GAM207 WNT10B	GGGAGGAAG----GGAGGGA 3016 _ ACTAG
	GGAGGAAGG GAGG
	CCTCCTTCC CTCC
	C _
GAM207 WNT10B	GGGAGGAAG----GGAGGGA 3016 TTAGGG ACTA
	AGGAAGG GGAG
	TCCTTCC CCTC
	_ CTC_
GAM207 WNT10B	AGGGAGGAAG----GGAGGGA 3009 _ ACTAG
	GGGAGGAAGG GAGG

	CCCTCCTTCC CTCC		
	T _____		
GAM207 WNT10B	AGGGAGGAAG----GGAGGGA	3009 TTAG	ACTAG
	GGAGGAAGG GAGG		
	CCTCCTTCC CTCC		
GAM208 BACE	GTAGAATGATCTTGGGATG	3024 A	CC II
	GTA AATGATCTT GAT		
	CAT TTAGTAGAA CTA		
	C CC CI		
GAM208 CAPN11	TCAGTAAAAGTGGGC-TCCG	3027 _ AT	CII
	TCAGTAAAA TG CTTC		
	AGTCATTTT AC GAGG		
	C CC CII		
GAM208 CAPN11	TCAGTAAAAGTGGGC-TCCG	3027 TGTC	_ ATC AT
	AGTAAAA TG TTCCG		
	TCATTTT AC GAGGC		
	_____ C CC_ GT		
GAM208 CAV3	GTCACCTTAAACATGATCTTCC	3025 G_ _	III
	GTCA TAAA ATGATCTTC		
	CAGT ATTT TACTAGAAG		
	GA G GII		
GAM208 CAV3	GTCACCTTAAACATGATCTTCC	3025 TG G_ _	ATG
	TCA TAAA ATGATCTTCCG		
	AGT ATTT TACTAGAAGGT		
	_ GA G III		
GAM208 FOXO1A	TCAAAAAAATGATCATCACGGTG	3028 AGT	T _ AI
	AAAATGATC TC CG		
	TTTTACTAG AG GC		
	TT_ T T CI		
GAM208 FOXO1A	TCAAAAAAATGATCATCACGGTG	3028 TGTCAGT	T _ ATGI
	AAAATGATC TC CG		
	TTTTACTAG AG GC		
	TTT_____ T T CACC		
GAM208 GPR85	AGTAATAAATGATCTTCC-ATG	3023 AGTA	AI
	AAATGATCTTCCG		
	TTTACTAGAAGGT		
	TTA_ AC		
GAM208 GPR85	AGTAATAAATGATCTTCC-ATG	3023 TGTCAGTA	ATG
	AAATGATCTTCCG		

		TTTACTAGAAGGT			
		TA_____ACG			
GAM208 NRG1		TGTCAGT-AAATAATCTTC	3029	A	CGA
		TGTCAGTAAA TGATCTTC			
		ACAGTCATTT ATTAGAAG			
		_____III			
GAM208 NRG1		TGTCAGT-AAATAATCTTC	3029	A	I
		TGTCAGTAAA TGATCTT			
		ACAGTCATTT ATTAGAA			
		_____G			
GAM208 TCTE1L		GTCACTATTATGATCTTCC	3026	TG G AA	AT
		TCA TA ATGATCTTCCG			
		AGT AT TACTAGAAGGT			
		___ G AA _____II			
GAM208 TCTE1L		GTCACTATTATGATCTTCC	3026	G AA	II
		GTCA TA ATGATCTTC			
		CAGT AT TACTAGAAG			
		G AA GI			
GAM209 ARHGEF12		AAGAACATTCAAAAA--TTGTGA	3035	TA	TA
		AGAACATTC GAAGGTTGTGA			
		TCTTGTAAG TTTTAACT			

GAM209 EGLN3		TAAGAACA-TCTGGAA-ATTGT	3041	T A G G	
		TAAGAACAT CT GAAG TTGT			
		ATTCTTGTA GA CTTT AACA			
		_____C _____I			
GAM209 FOXE3		AAAAACATGAGAGAAGGTTGATGA	3033	TA	TCT _ I
		AGAACAT AGAAGGTTG TGA			
		TTTTGTA TCTTCCAAC ACT			
		_____CTC T T			
GAM209 GOCAP1		GAACATTCTAGTTTAAGATT	3038	TAAGAA	___ G
		CATTCTAG AAGGTTGT			
		GTAAGATC TTCTAATA			
		_____AAA G			
GAM209 GRAF		GAACATTCTAAGAAGCTGGT	3037	TAAGAA	GA TG
		CATTCTA AGGTTG			
		GTAAGAT TTCGAC			
		_____TC CA			
GAM209 HNRPD		AAGAACATTGTTCAAAGGTGTG	3034	TA	CTA_ T A
		AGAACATT GAAGGT GTG			

	TCTTGTAA TTTCCA CAC		
	___ CAAG _ C		
GAM209 MDM4	TAAGAACATTCTCTGACAGGTTG 3039	AGA___	TGAI
	TAAGAACATTCT AGGTTG		
	ATTCTTGTAAGA TCCAAC		
	GA CTG IIIA		
GAM209 PBX3	AAGAACATTG-AAAATGTT 3032 TA	T G GT	
	AGAACATTG AGAA GTT		
	TCTTGTAAG TTTT CAA		
	___ _ A AI		
GAM209 SH2D1A	AGAACACTAGGCAAGAAGGTTG 3036 TAAG	CT___	GA
	AACATT AGAAGGTTGT		
	TTGTGA TCTTCCAACG		
	___ TCCGT AI		
GAM209 THO2	TAAGAACAT--TAGATGCCTGT 3042	TC AGG G	
	TAAGAACAT TAGA TTGT		
	ATTCTTGTA ATCT GACA		
	___ ACG I		
GAM209 TRIM9	TAAGAACATTCTAGCAGGT 3040	A TGTG	
	TAAGAACATTCTAG AGGT		
	ATTCTTGTAAGATC TCCA		
	G IIIA		
GAM210 B4GALT5	AGGTCGGGTTATTTTGTCTT 3046	TATATGCACTI	
	GGTCGGGTT		
	CCAGCCCAA		
	TAAAACAAGAI		
GAM210 B4GALT5	AGGTCGGGTTATTTTGTCTT 3046 TGAG	TATA CA A	
	GTCGGGTT TG CTT		
	CAGCCCAA AC GAA		
	___ TAAA AA A		
GAM210 SAR1	TGAAGTAGGACATATATGCACT 3048	C TT	TA
	TGAGGT GGG TATATGCACT		
	ACTTCA CCT ATATACGTGA		
	T GT II		
GAM210 SAR1	TGAAGTAGGACATATATGCACT 3048	C TT	I
	GAGGT GGG TATATGCAC		
	CTTCA CCT ATATACGTG		
	T GT I		
GAM210 WEE1	AGATCGG-TTTATATACAC 3045	G	I
	AGGTCGG TTTATATGCA		

	TCTAGCC AAATATATGT			
	— G			
GAM210 WEE1	AGATCGG-TTTATATACAC 3045 TGAG G T			
	GTCGG TTTATATGCAC			
	TAGCC AAATATATGTG			
	— — T			
GAM210 ZNF184	TGAGTTAGGCTATTATATGCAATT 3047 GTC — CTTAI			
	TGAG GGGT TTATATGCA			
	ACTC TCCG AATATACGT			
	AA_ AT TAAII			
GAM210 ZNF184	TGAGTTAGGCTATTATATGCAATT 3047 A CG — CTI			
	GGT GGT TTATATGCA			
	TCA CCG AATATACGT			
	_ AT AT TII			
GAM211 ADORA3	TGGCAGCCTCCTAACCTTAG 3063 — AACAC			
	TGGCAGCCTTTT CCTTAG			
	ACCGTCGGAGGA GGAATC			
	TT IIIC			
GAM211 ARHGEF12	CCCTTTCCTTAGCAACCCC 3053 — TT AGAACAC			
	TGGCAGCCTT CCTT			
	ATCGTTGGGG GGGG			
	GGA GT IIICAC			
GAM211 CARKL	TGGGAGACGTTTTTCTGGTAGAACACC3062 C _C_ CT_ III			
	TGG AG C TTTTC TAGAACACC			
	ACC TC G AAAAG ATCTTGTGG			
	C T CA ACC III			
GAM211 CYP1B1	CAACCTTTTCCT--GAACA 3052 TGGCAG TA			
	CCTTTTCCT GAACA			
	GGAAAAGGA CTTGT			
	— —			
GAM211 DCT	CAGACTTAATTTTCCTTAGAA 3051 TGGCAGCCT CAC			
	TTTCCTTAGAA			
	AAAGGAATCTT			
	TGAATT— CGC			
GAM211 DMD	TGGCAG---TTTCCTTAGTAAC 3065 CCT _ AC			
	TGGCAG TTTCCTTAG AAC			
	ACCGTC AAAGGAATC TTG			
	— A II			
GAM211 DMRT2	GCAGCCTTTCCTGAGAGACAC 3057 TGGC TC T _ C			
	AGCCTTT CT AGA ACAC			

	TCGGAAA GA TCT TGTG	
	_____ GT C C C	
GAM211 EDG8	GCTGCATTT--CTTAGAACAC 3058 TGGCA CT C	
	GC TTTC TTAGAACAC	
	CG AAAG AATCTTGTG	
	A_____ T_ _	
GAM211 FUT3	TGGCAGCC-TCTCCTAGGAGACA 3067 T TA _ CC	
	TGGCAGCCTTT CCT GA ACA	
	ACCGTCGGAGA GGA CT TGT	
	_ TC C	
GAM211 GAB2	CCTTTTCC-TAGAATCCACC 3054__ CAG _ AGAACAC	
	TGG CC TTTCCTT	
	ATC GG GGAAGGGA	
	GG TTA T CCAC	
GAM211 GRF2	TGGCAGCCTGGGTAGCTTAGAA 3064 TTTC__ CACC	
	TGGCAGCCT CTTAGAA	
	ACCGTCGGA GAATCTT	
	CCCATC C	
GAM211 INPP1	GCAGCCTTTCCCTCGAGAA 3056 TGGC _ CAC	
	AGCCTTTTCCTT AGAA	
	TCGGAAAGGGAG TCTT	
	_____ C TGI	
GAM211 MASP1	TGG-AGCCTTTTCCCTATACCAC 3068 C GAA C	
	TGG AGCCTTTTCCTTA CAC	
	ACC TCGGAAAAGGGAT GTG	
	_ ATG I	
GAM211 MEF2C	GGCAGCCTTTTACAATGAGAAACAC 3060 TG CCTT__ _ CII	
	GCAGCCTTTT AGAA CAC	
	CGTCGGAAAA TCTT GTG	
	_ TGTTAC T TII	
GAM211 MYCL2	TGTCAGCCTTTTCTTTGGA 3066 G C A ACAC	
	TG CAGCCTTTTC TT GA	
	AC GTCGGAAAAG AA CT	
	A A C C	
GAM211 NBS1	GGCAGTCTT--CCTTAGAA 3061 TG CC CA	
	GCAG TTTCCTTAGAA	
	CGTC AGAAGGAATCTT	
	_ _ TI	
GAM211 SRGAP2	GCACCTCTTTTCCTTTGCACA 3055 TGGCAGC AGA CC	
	CTTTTCCTT ACA	

	GAAAAGGAA TGT	
	TGGA___ ACG CC	
GAM211 ZNF8	GGAAGCATCATTTCTTAGAA 3059 T_ GCCT CACC	
	GGCA TTTCCTTAGAA	
	TCGT AAAGGAATCTT	
	CT AGT_ T	
GAM212 MGAT5	GTCAGCCAGCTATGTGGCA 3073 T__ C ATT TCGG	
	GTC GC TATGTGGCA	
	CGG CG ATACACCGT	
	AGT T ___ C	
GAM212 PCDHGA8	GTCCAGCAGTTAGTTTGTGGCATC 3072 TG _ T ___ GGTI	
	TCC GCA TTA TGTGGCATC	
	AGG CGT AAT ACACCGTAG	
	___ T C CAA A	
GAM212 SUFU	TGTGGGCACTCCTGTGGCATC 3074 CC A GGT	
	TGT GCATTT TGTGGCATC	
	ACA CGTGAG ACACCGTAG	
	CC G	
GAM212 SUV39H2	CCCCTTTTCAGAGGCATCGGT 3071 TGTCCGCA TGT	
	TTTA GGCATCGGT	
	AAGT CCGTAGCCA	
	GAA___ CT_	
GAM213 FBXL2	TGGCATGGTCCTAGCTGCATTGAGAC 3080 ___ C _ TAI	
	TGGCATGGTT GCT TATTG GAC	
	ACCGTACCAG CGA GTAAC CTG	
	GAT C T A	
GAM213 GSTM5	GGCATGGTTCAGGCTTTACTGG 3079 TG ___ C ACTA	
	GCATGGTT GCT TATTGG	
	CGTACCAA CGA ATGACC	
	___ GTC A C	
GAM213 LANGERIN	GCTTGTTGCTC---TGGAGTA 3077 TGGCA ATT CT	
	TGTTGCTCT GGA	
	ACCAACGAGA CCT	
	A___ ___ CA	
GAM213 LENG4	GGCTATGGTTGCTAAGCTAT 3078 TG _ ___ TGGACT	
	GC ATGGTTGCT CTAT	
	CG TACCAACGA GATA	
	___ A TTC C AT	
GAM214 ADCY4	TGAGCTGCTCAATGACCTGGAAGA 3096 AAAT___ _ TGAI	
	TGAGCTGCT CCTG AAGA	

	ACTCGACGA	GGAC TTCT	
	GTTACT	C IIIA	
GAM214 AP1G1	AGATGTTAAAAGTGCCTGAAGATG	3083 TGAGCTGCTAAAT	AI
	CCTGAAGATG		
	GGACTTCTAC		
	TACAATTTTCAC_	CA	
GAM214 AQP8	TGAGCTGCTGGGAAACCTG	3095 AAAT_ AAGATG	
	TGAGCTGCT	CCTG	
	ACTCGACGA	GGAC	
	CCCTTT	IIIAGT	
GAM214 ASTN	CTGTTATA-CCTGAAGATG	3088 TGAGCTGCTAAAT	
	CCTGAAGAT		
	GGACTTCTA		
	ATAT_____		
GAM214 BLAME	TGAGCTGCT-TTCTTGAAGTTG	3099 AAA C A A	
	TGAGCTGCT	TC TGAAG TG	
	ACTCGACGA	AG ACTTC AC	
	AA_ A A I		
GAM214 CAPN7	CTGCTTACTGTCCTGAAGAT	3087 TGA CTAAA G	
	GCTG	TCCTGAAGAT	
	TGAC	AGGACTTCTA	
	AA_ _____	A	
GAM214 CTSL	GCTGGTAGA--CTGAAGATGA	3094 TGAGCTGCTAAATC	
	CTGAAGATG		
	GACTTCTAC		
	CCATCT_____		
GAM214 HLA-DRA	GCTGGAAAACGCTGAAGATGA	3092 TGAGCTGCT C	
	AAAT CTGAAGATGA		
	TTTG	GACTTCTACT	
	CCT_____	C	
GAM214 HLA-DRA	GCTGGAAAATGCTGAAGATGA	3093 TGAGCTGCT C	
	AAAT CTGAAGATGA		
	TTTA	GACTTCTACT	
	CCT_____	C	
GAM214 MAP1A	TGAGCTGCTAA----GAAGATGA	3100 ATCCT	
	TGAGCTGCTAA	GAAGATG	
	ACTCGACGATT	CTTCTAC	

GAM214 MKKS	AGCTGCTTCTTTACCTGAAGAT	3084 TGAG AAAT_ GA	
	CTGCT	CCTGAAGAT	

	GACGA GGACTTCTA		
	____ AGAAAT AC		
GAM214 MLLT2	GCTTCTAAAAATTACTGAAGATGA	3090	TGAGCTG TC____ I
	CTAAA CTGAAGATGA		
	GATTT GACTTCTACT		
	A_____ TTAAT T		
GAM214 PPARBP	TGAGCT--TTCATCCTGAAG	3098	GCTAA AT
	TGAGCT ATCCTGAAG		
	ACTCGA TAGGACTTC		
	AAG__ II		
GAM214 SMARCC1	TGAGAAGAAAAATCCTGAA	3097	CTGCT GATG
	TGAG AAATCCTGAA		
	ACTC TTTAGGACTT		
	TTCTT IIIA		
GAM214 TBL2	GCTGCTAAAGTCCATGCAAGAT	3091	TGAGCT _ _ _ A
	GCTAAA TCC TG AAGATG		
	CGATTT AGG AC TTCTAT		
	_____ C T G A		
GAM214 TDRD1	CTGCCAATATGCCTGAAGATG	3086	TGAGCTGCTAAAT A
	CCTGAAGATG		
	GGACTTCTAC		
	GTTATAC_____ A		
GAM214 TSN	CTTCTAAATCCTCAA-ATG	3089	TGAGCTGC GA
	TAAATCCT AGAT		
	ATTTAGGA TTTA		
	_____ G_		
GAM214 TYRP1	AGCT-CACAATCCTGAAGGATG	3085	TGAGCTGCTA _ A
	AATCCTGAAG ATG		
	TTAGGACTTC TAC		
	GAGTG_____ C A		
GAM215 FCER1A	ACCAGTTTCACTCAG--TTTA	3104	CA GATTI
	ACCAGTTTC TCAG		
	TGGTCAAAG AGTC		
	TG AAATI		
GAM215 FCER1A	ACCAGTTTCACTCAG--TTTA	3104	TA CA GATTTAT
	CCAGTTTC TCAG		
	GGTCAAAG AGTC		
	_____ TG AAATTII		
GAM215 FCGR2A	GTTTGC-TCAGGATTTTTC	3112	CCA ATI
	GTTT TCAGGATTT		

	CAAA AGTCCTAAA			
	CG_ AAG			
GAM215 IFRD1	ACCAGTTTCAAT-AGTATT	3103	C C GATI	
	ACCAGTTTC AT AG			
	TGGTCAAAG TA TC			
	T _ ATAA			
GAM215 IFRD1	ACCAGTTTCAAT-AGTATT	3103 TA	C C GATTTA	
	CCAGTTTC AT AG			
	GGTCAAAG TA TC			
	_ T _ ATAACI			
GAM215 LIFR	TAGCAGTTAAAATCAGGATTCAT	3116 AC	TCC	I
	CAGTT ATCAGGATTTA			
	GTCAA TAGTCCTAAGT			
	TC TTT I			
GAM215 LIFR	TAGCAGTTAAAATCAGGATTCAT	3116 TAC	TCC	CI
	CAGTT ATCAGGATTTAT			
	GTCAA TAGTCCTAAGTA			
	ATC TTT II			
GAM215 PSMA2	TAACAGTTT--ATTAGGATTTAT	3115 AC_	CC C	I
	CAGTTT AT AGGATTTA			
	GTCAAA TA TCCTAAAT			
	ATT _ A I			
GAM215 PSMA2	TAACAGTTT--ATTAGGATTTAT	3115 TAC	CC C	C
	CAGTTT AT AGGATTTAT			
	GTCAAA TA TCCTAAATA			
	ATT _ A I			
GAM215 PSME3	CCAGTTTCCCCATCACGAT	3108	_ G III	
	CCAGTTTCC ATCA GA			
	GGTCAAAGG TAGT CT			
	GG G All			
GAM215 PSME3	CCAGTTTCCCCATCACGAT	3108 TACCAG TT	G TTAT	
	T CCATCA GAT			
	I			
	A GG TAGT CTA			
	TCAA_ GG G TCII			
GAM215 RARG	AGTTTCCATCA--CTTTAT	3107	GGATTTAI	
	AGTTTCCATCA			
	TCAAAGGTAGT			
	GAAATAII			
GAM215 RCN1	TACCACTTTCACCTTAATCAGGATTT	3113	G C_	ATCII
	TACCA TTTC ATCAGGATTT			

	ATGGT AAAG TAGTCCTAAA	
	G TGAAT IICT	
GAM215 RCN1	TACCACTTTCACTTAATCAGGATTT 3113 AC__ G TCC I	
	CA TT ATCAGGATT	
	II II IIIIIII	
	GT AA TAGTCCTAA	
	GAAA G T__ I	
GAM215 SCA1	CCAGTTTCCACTGTCCGGCTTGAT 3109 TACC CA__ ATTTATCI	
	AGTTTCCAT GG	
	IIIIII II	
	TCAAAGGTG CC	
	__ ACAGG GAACTAAA	
GAM215 SLBP	AGTTTCCATAAAGATATTA 3106 C TTII	
	AGTTTCCAT AGGAT	
	IIIIII IIII	
	TCAAAGGTA TTCTA	
	T TAAT	
GAM215 SPON1	AGTCTCCAAAATCAGGATTT 3105 __ III	
	AGTTTCCA TCAGGATT	
	IIIIII IIIIIII	
	TCAGAGGT AGTCCTAA	
	TTT AII	
GAM215 SPON1	AGTCTCCAAAATCAGGATTT 3105 TA TTTCC AT	
	CCAG ATCAGGATTT	
	III IIIIIII	
	GGTT TAGTCCTAAA	
	A_ T__ AT	
GAM215 SRGAP2	TACCAGTTTTGATCAGTTGGATT 3114 CC GATTTATCI	
	TACCAGTTT ATCAG	
	IIIIII IIII	
	ATGGTCAAA TAGTC	
	AC AACCTAAII	
GAM215 TCEB1L	CCAGTTTCCAACATCATGAT 3110 __ G III	
	CCAGTTTCCA TCA GA	
	IIIIII III II	
	GGTCAAAGGT AGT CT	
	TG A AII	
GAM215 TCEB1L	CCAGTTTCCAACATCATGAT 3110 TACC __ G TTAT	
	AGTTTCCA TCA GAT	
	IIIIII III III	
	TCAAAGGT AGT CTA	
	__ TG A TTII	
GAM215 WNT8B	CCAGTTTCC-TCAGTTTTT 3111 A GATTI	
	CCAGTTTCC TCAG	
	IIIIII IIII	
	GGTCAAAGG AGTC	
	_ AAAAA	
GAM215 WNT8B	CCAGTTTCC-TCAGTTTTT 3111 TACC A GA A	
	AGTTTCC TCAG TTT	
	IIIIII IIII III	

	TCAAAGG AGTC AAA	
	____ _ AA G	
GAM215 ZNF124	TTTACATTTACAGGATTTAT 3117 TACCAGTTTCCAT	
	CAGGATTTAT	
	GTCCTAAATA	
	AAAT_____	
GAM215 ZNF124	TTTACATTTACAGGATTTAT 3117 TTTCCAT____ III	
	CAGGATTTA	
	GTCCTAAAT	
	AAATGTAAAT AII	
GAM216 ABCC5	AACTCCC-CGGCTCGGAGGA 3121 AAG A AI	
	TCCC CGGCTCGGA	
	AGGG GCCGAGCCT	
	TG_ _ CC	
GAM216 ABCC5	AACTCCC-CGGCTCGGAGGA 3121 TCCAAG A A	
	TCCC CGGCTCGGA GA	
	AGGG GCCGAGCCT CT	
	____ _ C	
GAM216 ATOX1	CCAAGTCCCAGGTCTGTCTGGAAG 3128 CAA C _ C____ I	
	GTCCCA GG CT GGAA	
	CAGGGT CC GA CCTT	
	____ _ A CAGA I	
GAM216 ATOX1	CCAAGTCCCAGGTCTGTCTGGAAG 3128 TC C _ C____ AGI	
	CAAGTCCCA GG CT GGAAG	
	GTTCAGGGT CC GA CCTTC	
	____ _ A CAGA GII	
GAM216 CHST7	CAAGTCCCA-GACTCTG-AGAG 3125 C G AGI	
	CAAGTCCCA GGCTC GA	
	GTTCAGGGT CTGAG CT	
	____ _ A CTC	
GAM216 CHST7	CAAGTCCCA-GACTCTG-AGAG 3125 TCCA C G A	
	AGTCCCA GGCTC GA GA	
	TCAGGGT CTGAG CT CT	
	____ _ A _	
GAM216 CNGB3	TCCAAGTCCCTTGAGC-CAGATGAG 3130 AC_ T A I	
	TCCAAGTCCC GGC CGGA GAG	
	AGGTTCAGGG TCG GTCT CTC	
	AAC _ A I	
GAM216 CNGB3	TCCAAGTCCCTTGAGC-CAGATGAG 3130 AC_ T A I	
	CCAAGTCCC GGC CGGA GA	

	GGTTCAGGG TCG GTCT CT		
	AAC _ A I		
GAM216 ESRRA	TCCAAGTCCCCTCTGCTTTGAAGAG 3129	G__ CG	II
	TCCAAGTCCCAC GCT GAAGAG		
	AGGTTCAGGGTG CGA CTTCTC		
	AGA AA II		
GAM216 ESRRA	TCCAAGTCCCCTCTGCTTTGAAGAG 3129 CC	G__ CG	I
	AAGTCCCAC GCT GAAGA		
	TTCAGGGTG CGA CTTCT		
	_ AGA AA I		
GAM216 IGHMBP2	CAAGTCCCA-GACATTGGAGGAG 3123	C TC_ A I	
	AAGTCCCA GGC GGA GA		
	II		
	TTCAGGGT CTG CCT CT		
	_ TAA C I		
GAM216 IGHMBP2	CAAGTCCCA-GACATTGGAGGAG 3123 TCCA	C TC_ A	
	AGTCCCA GGC GGA GAG		
	TCAGGGT CTG CCT CTC		
	_____ _ TAA C		
GAM216 IRS1	CCAAGTCCCAACGTTGCACGG 3126	_ _ T III	
	CCAAGTCCCA CG GC CG		
	GGTTCAGGGT GC CG GC		
	T AA T CII		
GAM216 IRS1	CCAAGTCCCAACGTTGCACGG 3126 TC	_ _ T AAGAG	
	CAAGTCCCA CG GC CGG		
	GTTTCAGGGT GC CG GCC		
	_ T AA T CIIIG		
GAM216 MAT1A	CAATTGCCACGGCTCAACAAGAG 3122 AA T	_ I	
	G CCCACGGCTCGG AAGA		
	I		
	C GGGTGCCGAGTT TTCT		
	AA_ G I		
GAM216 MAT1A	CAATTGCCACGGCTCAACAAGAG 3122 TCCAA T	_ I	
	G CCCACGGCTCGG AAGAG		
	I		
	C GGGTGCCGAGTT TTCTC		
	TAA__ G G		
GAM216 PAEP	AAGTCCCCTCTGCTGGAG 3120	G _ AII	
	AAGTCCCAC GCTC GGA		
	TTCAGGGTG CGAG CCT		
	A A CII		
GAM216 PAEP	AAGTCCCCTCTGCTGGAG 3120 TCCAAG	G _ AGA	
	TCCCAC GCTC GGA		

		AGGGTG CGAG CCT		
		_____ A A CCA		
GAM216 RGL	CCAAGTCCCAGCCAGC-CGGA	3127	___ T II	
	CCAAGTCCCA CGGC CGG			
	GGTTCAGGGT GTCG GCC			
	CG _ TI			
GAM216 RGL	CCAAGTCCCAGCCAGC-CGGA	3127 TC	___ T AGA	
	CAAGTCCCA CGGC CGGA			
	GTTTCAGGGT GTCG GCCT			
	CG _ GII			
GAM216 SOST	CAAGTCCCACG--T-GGAAGA	3124 _	GCTC	
	AAGTCCCACG GGAAG			
	TTCAGGGTGC CCTTC			
	G A__			
GAM216 SOST	CAAGTCCCACG--T-GGAAGA	3124 TCCA	GCTC	
	AGTCCCACG GGAAG			
	TCAGGGTGC CCTTC			
	_____ A__			
GAM216 WHSC1L1	TCCTCGGCGCTCGGCTCGGAA	3131	AAGTCCCA GAG	
	TCC CGGCTCGGAA			
	AGG GCCGAGCCTT			
	AGCCGCGA			
GAM216 WHSC1L1	TCCTCGGCGCTCGGCTCGGAA	3131	CCAAGTCCCA I	
	CGGCTCGGA			
	GCCGAGCCT			
	GGAGCCGCGA I			
GAM217 ACCN2	CCCTGAGCTGGACGCTAACC	3153 AC G	C TC	
	CC GGGCTGGACGC AGCC			
	GG CTCGACCTGCG TTGG			
	__ A A TI			
GAM217 ADRA2A	CCCGGGGCTGGGGCG-CGGA	CTCT 3146 AC	A_ CAGC I	
	CCGGGGCTGG CGC CTCT			
	GGCCCCGACC GCG GAGA			
	__ CC CCT_ C			
GAM217 ATRN	CCCGGGGCTGAGACGGC-GCC	3147 AC	_ CCA C	
	CCGGGGCTG GACG GCCT			
	GGCCCCGAC CTGC CGGG			
	__ T CG_ I			
GAM217 BTEB1	TGGCCG-GTCCGGGCCTCCTGGCTC	3170	T AC _ I	
	TGGCTG GTCC GC TCCTGGCTC			

	ACCGGC CAGG CG AGGACCGAG		
	_ CC G I		
GAM217 CCND1	CGGGGCCGGCCCCCGCCAGCCT 3162 ACCCGG A__ CT		
	GGCTGG CGCCAGCCT		
	CCGGCC GCGGTCGGA		
	_____ GGGG CA		
GAM217 CENTD2	ACCCGGGGCTGCCACGCC-CCCTCT 3140 G_ AG I		
	ACCCGGGGCTG ACGCC CCTCT		
	TGGGCCCCGAC TGCGG GGAGA		
	GG G_ I		
GAM217 CRYBA2	ACCCGGGGGGCTGGAC-CCGGCCT 3135 _ G A CT		
	ACCCGGGG CTGGAC CC GCCT		
	TGGGCCCC GACCTG GG CGGA		
	C _ C II		
GAM217 DRP2	CCGGGGCTGG--G-CTGCCTCT 3160 ACCC AC CA		
	GGGGCTGG GC GCCTC		
	CCCCGACC CG CGGAG		
	_____ _ A_		
GAM217 DUSP4	CCCGGGTTTGACGCCAGC 3151 AC GC CTC		
	CCGGG TGGACGCCAGC		
	GGCCC ACCTGCGGTCG		
	_ AA CII		
GAM217 EMX2	CTGGGCTCCCAGCTCCTGGC 3163 T GTG C T		
	GGCT TCCA GCTCCTGGC		
	CCGA GGGT CGAGGACCG		
	_ _ _ C		
GAM217 EXTL1	CCCGGGGCTCGCAAGCCAGTCCT 3145 AC GGAC_ _ CTI		
	CCGGGGCT GCCAG CCT		
	GGCCCCGA CGGTC GGA		
	_ GCGTT A CII		
GAM217 EXTL1	GGCCGTGTCCCCCTGCCCTCCTGGCT 3168 TG ACG_____ CII		
	GCTGTGTCC CTCCTGGCT		
	CGGCACAGG GAGGACCGA		
	_ GGGACGG CII		
GAM217 FE65L2	ACCCCGGCTGCTCCCCGCCAGCCTCT 3136 A_ G_ GGA II		
	CCCGG GCT CGCCAGCCTCT		
	GGGCC CGA GCGGTCGGAGA		
	TG GA GGG II		
GAM217 FGFR2	CCCGGGGCTCGCGGCCCGGCC 3152 AC GGAC A C		
	CCGGGGCT GCC GCCT		

	GGCCCCGA CGG CGGG		
	___ GCGC C I		
GAM217 GAK	ACCCGGGGGCTCGGAGCCCCACCCT 3138	_ C A_ CTI	
	ACCCGGGGGCT GGA GCC GCCT		
	TGGGCCCCGA CCT CGG TGGG		
	G _ GG AII		
GAM217 GRB10	ACCCGGGGGCTGCAGGGACGCC 3137	___ AGCCTCT	
	ACCCGGGGGCT GGACGCC		
	TGGGCCCCGA CCTGCGG		
	CGTC IIITCTC		
GAM217 HPS3	CCGGGTCACGTGAACGCCAGCC 3155	ACCC _ _ TCT	
	GGG GC TGGACGCCAGCC		
	CCC TG ACTTGCGGTCGG		
	___ AG C CCI		
GAM217 IKBKB	ACCCGGGGGCTATGACACCCCCCT 3139	_ AG I	
	ACCCGGGGGCTG GACGCC CCTCT		
	TGGGCCCCGAT CTGTGG GGGGA		
	A _ I		
GAM217 KIP2	CCCGGGGCTGGACCACAGC 3150	AC GC CTC	
	CCCGGGGCTGGAC CAGC		
	GGCCCCGACCTG GTCG		
	___ GT CII		
GAM217 KRT16	ACCCGGGCACAGGCCATTGACGCCAGCCTC3134	___ G_ TIII	
	ACCCGG GGCT GACGCCAGCCTC G		
	TGGGCC CCGG CTGCGGTCGGAG C		
	GTGT TAA IIIT		
GAM217 LZTS1	CCGGGGGCTGG--GACAGCC 3159	ACCC ACGC	
	GGGGCTGG CAGCCT		
	CCCCGACC GTCGGG		
	___ CT_		
GAM217 MAP3K8	CTGAGTC-AGACTCCTGGCT 3165	TGGCTGT CAC	
	GTC GTCCTGGCT		
	CAG TGAGGACCGA		
	T_ TC_		
GAM217 MATN1	CCAGGGGCTGGA-GCCCGC 3149	ACCC C A CT	
	GGGGCTGGA GCC GC		
	CCCCGACCT CGG CG		
	GT_ _ G CI		
GAM217 NDUFV3	TGGCTGGG-CCACGCTCCT 3171	T T GGC	
	TGGCTG G CCACGCTCCT		

	ACCGAC C GGTGCGAGGA		
	C _ III		
GAM217 NFRKB	GGCTGTGTCACCACACTCCT 3167 TG _ GGCT		
	GCTGTGT CCACGCTCCT		
	CGACACA GGTGTGAGGA		
	_ GT GIII		
GAM217 PABPC1	CCGGGGGCTGGGGGCCGGAGCC 3158 ACCC AC _ TCT		
	GGGGCTGG GCC AGCC		
	CCCCGACC CGG TCGG		
	_ CC CC CCI		
GAM217 PCSK1	GGCTCTAGACCAC--TCCTGGCTC 3166 TG G TCCA		
	GCT TG CGCTCCTGGCTC		
	CGA AT GTGAGGACCGAG		
	_ G CTG_		
GAM217 POU2F2	CCCGGGGCTGCACCGGCTGCC 3148 AC G _ CA CT		
	CCGGGGGCTG AC GC GCCT		
	GGCCCCGAC TG CG CGGG		
	_ G GC A_		
GAM217 POU3F1	CCCGGGGCTCGGGCGACGCAGCCT 3144 AC _ A _ CTI		
	CCGGGGGCT GG CG C CAGCCT		
	GGCCCCGA CC GC G GTCGGA		
	_ G C T C TII		
GAM217 PPP3CB	CCCGGGGCTCG--GCTAGGCTCT 3154 AC GGAC C C		
	CCGGGGGCT GC AG CTCT		
	GGCCCCGA CG TC GAGA		
	_ GC_ A C		
GAM217 PRKACA	ACCCGGGGGCCCCACCCAGGCCT 3141 GG G _ CTI		
	ACCCGGGGGCT AC CCAG CCT		
	TGGGCCCGG TG GGTC GGA		
	GG G C III		
GAM217 PXN	GGGGTGGAGCCCCAGCCTCT 3169 ACCC GGACG		
	GGGGCT CCAGCCTCT		
	CCTCGG GGTCGGAGA		
	_ G_		
GAM217 SET7	CGGGGCTGGCTCGCACTGCCTC 3161 ACCCGG A_ CA_		
	GGCTGG CGC GCCTCT		
	CCGACC GCG CGGAGG		
	_ GA TGA		
GAM217 SHOX	CCGGGGGCTGG-CGAGCAGCC 3156 ACCC A C_ TC		
	GGGGCTGG CG CAGCC		

	CCCCGACC GC GTCGG	
	_____ TC CC	
GAM217 SHOX	CCCGGGGCTGGACGCACGGCCGCT 3157 ACCCG	CA_ T I
	GGGCTGGACGC GCC CT	
	CCCGACCTGCG CGG GA	
	G_____ TGC C G	
GAM217 SORL1	CCCGGGGCTCCAGGCCGCCGC 3143 AC	___ A A CTCT
	CCGGGGCT GG CGCC GC	
	GGCCCCGA CC GCGG CG	
	___ GGT G G CII	
GAM217 STC1	CTCTTTCC-CTCTCCTGGCT 3164 TGGCTGTG ACG	
	TCC CTCCTGGCT	
	AGG GAGGACCGA	
	AA_____ GA_	
GAM217 WHSC1	ACACGGGCCTC-AC-CCAGCCTCT 3142 ACCCG	GG G
	GGGCT AC CCAGCCTCT	
	CCCGG TG GGTCGGAGA	
	TGTG_ AG _	
GAM218 ADAM19	GGCAAGGAC---ATGGGGAA 3194	C AT I
	GGCAAGGAC TG GGAG	
	CCGTTCTG AC CCTT	
	T C_ I	
GAM218 ADAM19	GGCAAGGAC---ATGGGGAA 3194 TG	CTG A G
	GCAAGGAC ATGG GAA	
	CGTTCCTG TACC CTT	
	___ ___ C G	
GAM218 AOC3	GGAAAGGACCTGGAT-GAGAGGG 3190 GC	_ _ AAI
	AAGGACCTG ATG GAG	
	TTCCTGGAC TAC CTC	
	T_ C T CII	
GAM218 AOC3	GGAAAGGACCTGGAT-GAGAGGG 3190 TGGC	ATG A T
	AAGGACCTG GAGA GG	
	TTCCTGGAC CTCT CC	
	CT___ CTA C T	
GAM218 ARPC2	GGCAAGGA-CGAGAGGGAGA 3192	CT T I
	GGCAAGGAC GA GGAG	
	CCGTTCTG CT CCTC	
	C_ C T	
GAM218 ARPC2	GGCAAGGA-CGAGAGGGAGA 3192 TG	CT T AG
	GCAAGGAC GA GGAGA	

	CGTTCCTG CT CCTCT		
	___ C_ C CI		
GAM218 BSN	TGGCAAAGGACCTGCCTGGAAAA 3199	_ A_ GGTI	
	TGGCAA GGACCTG TGGAGAA		
	ACCGTT CCTGGAC ACCTTTT		
	T GG IIIT		
GAM218 BSN	TGGCAAAGGACCTGCCTGGAAAA 3199 G C	A_ I	
	G AAGGACCTG TGGAGA		
	G TTCCTGGAC ACCTTT		
	_T GG I		
GAM218 CAPON	GCAAGGGCCT---GGAGAAGG 3185	A AT AI	
	GCAAGG CCTG GGAG		
	CGTTCC GGAC CTTC		
	C CT CI		
GAM218 CAPON	GCAAGGGCCT---GGAGAAGG 3185 TGGC	A GAT	
	AAGG CCT GGAGAAG		
	TTCC GGA CCTCTTC		
	___ C ___		
GAM218 CNTN2	AAGGACCTGGGGCGAGAGAAGG 3175	AT___ III	
	AAGGACCTG GGAGAAG		
	TTCCTGGAC TCTCTTC		
	CCCGC CII		
GAM218 CSF3	GCAAGGACCCAGATGGGGAA 3181	_ A II	
	GCAAGGACCT GATGG GA		
	II		
	CGTTCCTGGG CTACC CT		
	T C TI		
GAM218 CSF3	GCAAGGACCCAGATGGGGAA 3181 TGGC	_ A GG	
	AAGGACCT GATGG GAA		
	TTCCTGGG CTACC CTT		
	___ T C GT		
GAM218 DCX	CAAGGTGAACTGATGGAGAA 3179	AC___ III	
	CAAGG CTGATGGAGA		
	GTTCC GACTACCTCT		
	ACTT TII		
GAM218 DCX	CAAGGTGAACTGATGGAGAA 3179 TGGCAA	C	
	GGAC TGATGGAGAAGG		
	CTTG ACTACCTCTTTT		
	CCA___ _		
GAM218 EIF2AK3	GGCAAGGACGTGCTAGGGA 3193	C AT_ AGII	
	GGCAAGGAC TG GG		

	CCG TTCCTG AC CC			
	C GAT CTII			
GAM218 EIF2AK3	GGCAAGGACGTGCTAGGGA	3193 TG	C AT_ A AGG	
	GCAAGGAC TG GG GA			
	CGTTCCTG AC CC CT			
	___ C GAT _ GII			
GAM218 ESRRG	GGAAAGAAGATGATGGAGAAAGT	3198 GC CC	I	
	AAGGA TGATGGAGAAGG			
	TTCTT ACTACCTCTTTC			
	CT CT I			
GAM218 ESRRG	GGAAAGAAGATGATGGAGAAAGT	3198 TGGC CC	I	
	AAGGA TGATGGAGAAGGT			
	TTCTT ACTACCTCTTTCA			
	CT__ CT T			
GAM218 FXR2	GCAAG--CGAGATGGAGAAGG	3184 _ CCT	I	
	GCAAG GA GATGGAGAA			
	CGTTC CT CTACCTCTT			
	G _ C			
GAM218 GLUL	TGGGAGAGGGC--GATGGAGAAGG	3200 __ CA ACC	I	
	GG AGG TGATGGAGAAG			
	CC TCC GCTACCTCTTC			
	AC TC C__ I			
GAM218 GLUL	TGGGAGAGGGC--GATGGAGAAGG	3200 T_ CA ACC	T	
	GG AGG TGATGGAGAAGG			
	CC TCC GCTACCTCTTCC			
	AC TC C__ I			
GAM218 GNRH1	TGGCAAGGACAGTGAAGGA	3201 C_ T II		
	TGGCAAGGAC TGA GG			
	ACCGTTCCTG ACT CC			
	TC T TI			
GAM218 GNRH1	TGGCAAGGACAGTGAAGGA	3201 CTGAT A		
	TGGCAAGGAC GG GAAGG			
	ACCGTTCCTG TC CTTCC			
	___ A			
GAM218 GPR4	AAGGTCACCAGTAAGGAGAAGGT	3174 AGG TGAT_	I	
	ACC GGAGAAGG			
	TGG CCTCTTCC			
	AG_ TCATT I			
GAM218 GPR4	AAGGTCACCAGTAAGGAGAAGGT	3174 TGGCAAGG TGAT_	I	
	ACC GGAGAAGGT			

	TGG CCTCTTCCA	
	AG_____ TCATT A	
GAM218 HMGCR	TGGCA-GGAG-TGAGGGAGAAGGT 3203	A CC T
	TGGCA GGA TGA GGAGAAGGT	
	ACCGT CCT ACT CCTCTTCCA	
	_ C_ C	
GAM218 HMGCR	TGGCA-GGAG-TGAGGGAGAAGGT 3203_	A CC T I
	GGCA GGA TGA GGAGAAGG	
	CCGT CCT ACT CCTCTTCC	
	A _ C_ C I	
GAM218 HOXC13	GGCTAGTGCCCTGATGGA-AAGGT 3188	A GA_ A I
	GC AG CCTGATGGAGA GG	
	CG TC GGA CTACCTTT CC	
	A ACG _ I	
GAM218 HOXC13	GGCTAGTGCCCTGATGGA-AAGGT 3188 TG	A GA_ A I
	GC AG CCTGATGGAGA GGT	
	CG TC GGA CTACCTTT CCA	
	_ A ACG _ C	
GAM218 IGF2	GGGATGGAACCTGATGGA-AACGT 3189	CAA AI
	GGACCTGATGGAGA	
	CTTGGA CTACCTTT	
	TAC GI	
GAM218 IGF2	GGGATGGAACCTGATGGA-AACGT 3189 T	CAA AGGTI
	GG GGACCTGATGGAGA	
	CC CTTGGA CTACCTTT	
	_ TAC GCAGI	
GAM218 IL1F5	GCCAGGACCTGA-GGAGGAG 3182	GCA T AI
	AGGACCTGA GGAG	
	TCCTGGACT CCTC	
	GG_ _ CT	
GAM218 IL1F5	GCCAGGACCTGA-GGAGGAG 3182 TGGCA	T A G
	AGGACCTGA GGAG AG	
	TCCTGGACT CCTC TC	
	G_ _ C G	
GAM218 ITGA2B	GGCAA---CTTGTTGGAGAAGG 3196	AGG C A I
	GGCA AC TG TGGAGAA	
	CCGT TG AC ACCTCTT	
	_ A A C	
GAM218 ITGA2B	GGCAA---CTTGTTGGAGAAGG 3196 TGGCAAG	C A
	GAC TG TGGAGAAGG	

	TTG AC ACCTCTTCC			
	CG_____ A A			
GAM218 LHX3	AAGGATCTGATGGAGGAGG	3176	TGGCAAGGAC	A
	CTGATGGAG AGG			
	GACTACCTC TCC			
	TA_____ C			
GAM218 LHX3	AAGGATCTGATGGAGGAGG	3176	C AAGII	
	AAGGA CTGATGGAG			
	TTCCT GACTACCTC			
	A CTCCI			
GAM218 LRP1	GGCAGGGAGGGGATGGAGAA	3195	A CCT I	
	GCA GGA GATGGAGA			
	CGT CCT CTACCTCT			
	C CCC I			
GAM218 LRP1	GGCAGGGAGGGGATGGAGAA	3195	TG A CCT G	
	GCA GGA GATGGAGAAG			
	CGT CCT CTACCTCTTT			
	__ C CCC I			
GAM218 NEK2	CAGGGACCTGGATGGAGAAG	3180	A _ II	
	CA GGACCTG ATGGAGAA			
	GT CCTGGAC TACCTCTT			
	C C CI			
GAM218 NEK2	CAGGGACCTGGATGGAGAAG	3180	TGGCAA _ G	
	GGACCTG ATGGAGAAG			
	CCTGGAC TACCTCTTC			
	_____ C G			
GAM218 NXF5	GGACACTGGGATGGAGAAGG	3186	_ _ III	
	GGAC CT GATGGAGAAG			
	CCTG GA CTACCTCTTC			
	T CC CII			
GAM218 RECQL5	GCAAATATCTGGTGGAGAAGG	3183	GAC A I	
	CAAG CTG TGGAGAAG			
	GTTT GAC ACCTCTTC			
	ATA C I			
GAM218 RECQL5	GCAAATATCTGGTGGAGAAGG	3183	TGGCAAGGAC A T	
	CTG TGGAGAAGG			
	GAC ACCTCTTCC			
	TTTATA__ C C			
GAM218 RNGTT	AAGGACCTGGTGGTGTATGT	3177	A AGAAGGI	
	AGGACCTG TGG			

	TCCTGGAC ACC			
	C ACATACI			
GAM218 RNGTT	AAGGACCTGGTGGTGTATGT	3177	TGGCAAGG	A AGAAGG
	ACCTG TGG			
	TGGAC ACC			
	_____ C ACATAC			
GAM218 RXRA	GGGAAAGAC-T-ATGGAGAAGG	3197	_ C CTG	I
	GG AAGGAC ATGGAGAA			
	CC TTTCTG TACCTCTT			
	C _ A _ C			
GAM218 RXRA	GGGAAAGAC-T-ATGGAGAAGG	3197	T C CTG	
	GG AAGGAC ATGGAGAAGG			
	CC TTTCTG TACCTCTTCC			
	_ _ A _			
GAM218 SCAP2	GGAAAGGACCTGCGCTGAAAAGGT	3191	GC ATG_	I
	AAGGACCTG GAGAAGG			
	TTCCTGGAC CTTTTCC			
	T_ GCGA I			
GAM218 SCAP2	GGAAAGGACCTGCGCTGAAAAGGT	3191	TGGC ATG_	I
	AAGGACCTG GAGAAGGT			
	TTCCTGGAC CTTTTCCA			
	CT_ GCGA C			
GAM218 THRA	GGCAGAGG-CCTG--GGAGAAGGT	3187	_ _ A AT	I
	GCA AGG CCTG GGAGAAGG			
	CGT TCC GGAC CCTCTTCC			
	C C _ _ I			
GAM218 THRA	GGCAGAGG-CCTG--GGAGAAGGT	3187	TG _ A AT	
	GCA AGG CCTG GGAGAAGGT			
	CGT TCC GGAC CCTCTTCCA			
	_ C _ _			
GAM218 ZNF192	TGGCAAGAAACAGATGGAGAA	3202	CCT GGT	
	TGGCAAGGA GATGGAGAA			
	ACCGTTCTT CTACCTCTT			
	TGT			
GAM218 ZNF192	TGGCAAGAAACAGATGGAGAA	3202	CCT I	
	GGCAAGGA GATGGAGA			
	CCGTTCTT CTACCTCT			
	TGT I			
GAM218 ZNFN2A1	AGGAAGCCCTGCTGGAGAAGG	3178	_ A	
	AGGA CCTG TGGAGAAG			

	TCCT GGAC ACCTCTTC			
	TCG G CII			
GAM218 ZNFN2A1	AGGAAGCCCTGCTGGAGAAGG	3178	TGGCAAGGA	A
	CCTG TGGAGAAGGT			
	GGAC ACCTCTTCCG			
	CG_____ G			
GAM219 DUT	ATCAGTCCCATATCTGCAATG	3208	T CG TI	
	TCAGTCCC TATC GTA			
	AGTCAGGG ATAG CGT			
	T A_ TA			
GAM219 DUT	ATCAGTCCCATATCTGCAATG	3208	TA T CG TGTG	
	TCAGTCCC TATC GTA			
	AGTCAGGG ATAG CGT			
	___ T A_ TACT			
GAM219 FACL4	ATCAAGTCCCTTATCAAGTA	3206	_ C II	
	ATCA GTCCCTTATC GGT			
	TAGT CAGGGAATAG TCA			
	T T TI			
GAM219 FACL4	ATCAAGTCCCTTATCAAGTA	3206	TA _ C TGT	
	TCA GTCCCTTATC GGTA			
	AGT CAGGGAATAG TCAT			
	___ T T TII			
GAM219 GABPA	ATCAGTCCC-ACTCCGGAAT	3207	_ TTA TAI	
	TCAGTCCC TCCGG			
	AGTCAGGG AGGCC			
	T TG_ TTI			
GAM219 GABPA	ATCAGTCCC-ACTCCGGAAT	3207	TA TTA T GT	
	TCAGTCCC TCCGG AT			
	AGTCAGGG AGGCC TA			
	___ TG_ T GI			
GAM219 PPP1R12B	GTCCCTTATTCAGGAATAGTG	3209	C TATGTIII	
	GTCCCTTAT CGG			
	CAGGGAATA GTC			
	A CTTATCAC			
GAM220 C4orf1	TAACATTAGAAAAATTAAACCAAAT	3239	C _ GII	
	TAACAT AGAGAA TAAACCAAAT			
	ATTGTA TCTTTT ATTTGGTTTA			
	A TA III			
GAM220 C4orf1	TAACATTAGAAAAATTAAACCAAAT	3239	AA C _ I	
	CAT AGAGAA TAAACCAA			

		GTA TCTTTT ATTTGGTTT		
		__ A TA I		
GAM220 CHAC		AACTACTGAGAATAAAC--AATG 3221 AACATCA	CI	
		GAGAATAAAC		
		CTCTTATTTG		
		ATGA__ TT		
GAM220 CHAC		AACTACTGAGAATAAAC--AATG 3221 TAACATCA	CA	
		GAGAATAAAC AATG		
		CTCTTATTTG TTAC		
		TGATGA__ __		
GAM220 COG3		TAACATCAGCGGCAAAACCAA 3243	AGAAT	ATG
		TAACATCAG AAACCAA		
		ATTGTAGTC TTTGGTT		
		GCCGT III		
GAM220 COG3		TAACATCAGCGGCAAAACCAA 3243	AGAAT	I
		AACATCAG AAACCA		
		TTGTAGTC TTTGGT		
		GCCGT I		
GAM220 DUOX2		CAACAGAAGAATAAAACAACTG 3230 T _ C I		
		CAGA GAATAAAC AAAT		
		GTCT CTTATTTG TTTG		
		T T _ I		
GAM220 DUOX2		CAACAGAAGAATAAAACAACTG 3230 TAACAT _ C G		
		CAGA GAATAAAC AAAT		
		GTCT CTTATTTG TTTG		
		_____ T _ A		
GAM220 EFNB2		ACAGCACCGCATAAACCAAA 3227 ____ AGAGA	I	
		CATC ATAAACCAA		
		GTGG TATTTGGTT		
		GTC CG__ I		
GAM220 EFNB2		ACAGCACCGCATAAACCAAA 3227 TAA AGAGA	T	
		CATC ATAAACCAAA		
		GTGG TATTTGGTTT		
		TC_ CG__ C		
GAM220 FAFL4		CATCA-AGAATAAACACAAA 3231 G _ II		
		CATCA AGAATAAAC CAA		
		GTAGT TCTTATTTG GTT		
		_ T TI		
GAM220 FAFL4		CATCA-AGAATAAACACAAA 3231 TAACATCA	_ T	
		GAGAATAAAC CAAA		

	TTCTTATTTG GTTT	
	G_____ T T	
GAM220 FIGF	AACTTCACACAGAAAACCAAAT 3220 A___ T G TA I	
	CA CA AGAA AACCAAA	
	GT GT TCTT TTGGTTT	
	TGAA _ G _ I	
GAM220 FIGF	AACTTCACACAGAAAACCAAAT 3220 TA___ T ATAA	
	ACA CAGAGA ACCAAATG	
	TGT GTCTTT TGGTTTAT	
	TGAAG _ _	
GAM220 FXVD7	CAGAGGAAAAAACCAAATG 3229 _ T II	
	CAGAG AA AAACCAAAT	
	GTCTC TT TTTGGTTTA	
	C T CI	
GAM220 GALNT3	AACATTTGACAGACAAGTAAACCAAA 3212 ACAT G _ I	
	CAGA AA TAAACCAA	
	GTCT TT ATTTGGTT	
	ACT_ G C I	
GAM220 GALNT3	AACATTTGACAGACAAGTAAACCAAA 3212 TA ____ G _ GII	
	ACAT CAGA AA TAAACCAAAT	
	TGTA GTCT TT ATTTGGTTTG	
	_ AACT G C III	
GAM220 GEMIN5	ACATGAAAGAATAAAACCAAAT 3225 CATC _ I	
	AGAGAATAAA CCAA	
	TTTCTTATTT GGTTT	
	TAC_ T I	
GAM220 GEMIN5	ACATGAAAGAATAAAACCAAAT 3225 TAACATC _ G	
	AGAGAATAAA CCAAAT	
	TTTCTTATTT GGTTTA	
	TAC_____ T A	
GAM220 HIRA	AACATTTAAAAATTAAAACCAAATG 3215 ACATCA _ I	
	GAGAAT AAACCAAAT	
	TTTTTA TTTGGTTTA	
	TAAA_ AT I	
GAM220 HIRA	AACATTTAAAAATTAAAACCAAATG 3215 TA CA _ II	
	ACAT GAGAAT AAACCAAATG	
	TGTA TTTTTA TTTGGTTTAC	
	_ AA AT TI	
GAM220 HOXA3	TAAATTCAGAGAAT--GCCAAAT 3245 AACA_ AAA I	
	TCAGAGAAT CCAA	

	AGTCTCTTA GGTTT			
	ATTTA C__ I			
GAM220 HOXA3	TAAATTCAGAGAAT--GCCAAAT 3245 TAACA AAA G			
	TCAGAGAAT CCAAAT			
	AGTCTCTTA GGTTTA			
	ATTTA C__ I			
GAM220 HPSE	TAAC-TCAG-GAATGGAAAACCAAAT 3240 A A ____ GI			
	TAAC TCAG GAAT AAACCAAAT			
	ATTG AGTC CTTA TTTGGTTTA			
	_ _ CCT II			
GAM220 HPSE	TAAC-TCAG-GAATGGAAAACCAAAT 3240 AACA A ____ I			
	TCAG GAAT AAACCAAA			
	AGTC CTTA TTTGGTTT			
	TG__ _ CCT I			
GAM220 INPP4A	AAGAACACAAAATAAACCAA 3219 ACAT G I			
	CA AGAATAAACCA			
	GT TTTTATTTGGT			
	TCTT G I			
GAM220 INPP4A	AAGAACACAAAATAAACCAA 3219 TAACAT G AT			
	CA AGAATAAACCAA			
	GT TTTTATTTGGTT			
	TCTT__ G AI			
GAM220 MTMR8	TATCATCTGAGAATAAATGTAAATG 3241 A A CCAAATI			
	CATC GAGAATAAA			
	GTAG CTCTTATTT			
	A A ACATTTI			
GAM220 MTMR8	TATCATCTGAGAATAAATGTAAATG 3241 TAA A CC_ II			
	CATC GAGAATAAA AAATG			
	GTAG CTCTTATTT TTTAC			
	ATA A ACA II			
GAM220 MYO15A	AACATCAGACCCTGAGTAAACCAAA 3213 ACAT ____ A I			
	CAGA GA TAAACCAA			
	GTCT CT ATTTGGTT			
	____ GGG A C I			
GAM220 MYO15A	AACATCAGACCCTGAGTAAACCAAA 3213 TA ____ A TGII			
	ACATCAGA GA TAAACCAAA			
	TGTAGTCT CT ATTTGGTTT			
	____ GGG A C CII			
GAM220 NOTCH2	TAACAATAAA-AATAAACCAAA 3244 TCA TG			
	TAACA GAGAATAAACCAAA			

	ATTGT TTTTATTTGGTTT	
	TA_ II	
GAM220 NOTCH2	TAACAATAAA-AATAAACCAA 3244 _ TCA I	
	AACA GAGAATAAACCAA	
	TTGT TTTTATTTGGTT	
	A TA_ I	
GAM220 NOTCH2	ACATGGAGAGAATAAAGCAGAGAATG 3222 TAACATC C AATGII	
	AGAGAATAAA CA	
	II	
	TCTCTTATTT GT	
	TACC_ C CTCTTA	
GAM220 NOTCH2	ACATGGAGAGAATAAAGCAGAGAATG 3222 TC C AATI	
	AGAGAATAAA CA	
	II	
	TCTCTTATTT GT	
	C_ C CTCT	
GAM220 OPHN1	TAAC-TCACC-AATAAACCA 3242 A GAG AA	
	TAAC TCA AATAAACCA	
	ATTG AGT TTATTTGGT	
	_ GG_ II	
GAM220 OSCAR	AACATCAGA----AAACCA 3218 AAACC	
	AACATCAGAGAAT	
	TTGTAGTCTTTTG	
	GTIII	
GAM220 OSCAR	AACATCAGA----AAACCA 3218 TA ATAA A	
	ACATCAGAGA ACCA	
	TGTAGTCTTT TGGT	
	_ _ C	
GAM220 PCDHB16	TAACAATCAGAGAAAAATACC 3234 _ TAA_ AAATG	
	TAACA TCAGAGAA ACC	
	ATTGT AGTCTCTT TGG	
	T TTTA GT	
GAM220 PCDHB16	TAACAATCAGAGAAAAATACC 3234 _ TAAACIII	
	TAACA TCAGAGAA	
	ATTGT AGTCTCTT	
	T TTTATGGI	
GAM220 PHKA1	TAACAGATCTAGAGAATAAAAACACATG3233 _ _ CCAAATGIII	
	TAACA TC AGAGAATAAA	
	ATTGT AG TCTCTTATTT	
	CT A TTGTGTACII	
GAM220 PHKA1	TAACAGATCTAGAGAATAAAAACACATG3233 _ CCAAAI	
	ATC AGAGAATAAA	

	TAG TCTCTTATTT A TTGTII ACATTAAAGAATAAACCAAA 3228 C I CAT AGAGAATAAACCAA GTA TTTCTTATTTGGTT A I
GAM220 PIGK	ACATTAAAGAATAAACCAAA 3228 TAACATC T AGAGAATAAACCAAA TTTCTTATTTGGTTT TAA____ C
GAM220 PKP2	AAAATCAGAGAAAAACAACCAA 3216 AC TA__ I ATCAGAGAA AACCA TAGTCTCTT TTGGT __ TTTG I
GAM220 PKP2	AAAATCAGAGAAAAACAACCAA 3216 TAAC TA__ ATG ATCAGAGAA AACCAA TAGTCTCTT TTGGTT TT__ TTTG CII
GAM220 PPARGC1	ACATCAGAGAATGTAGCAA 3226 AAACCAII ACATCAGAGAAT TGTAGTCTCTTA CATCGTTI
GAM220 PPARGC1	ACATCAGAGAATGTAGCAA 3226 TAAC AAACCAAAT ATCAGAGAAT TAGTCTCTTA ____ CATCGTTAA
GAM220 PX19	ACATCAGAGAACAAAACCAAA 3224 C _ I ATCAGAGAATAAAA CCAA TAGTCTCTTGTTT GGTT _ T I
GAM220 PX19	ACATCAGAGAACAAAACCAAA 3224 TAAC _ TG ATCAGAGAATAAAA CCAA TAGTCTCTTGTTT GGTTT ____ T TC
GAM220 RBBP5	TCAGAGAATTTCAAACACCAAATG 3246 AA____ IIIC TCAGAGAAT ACCAAAT AGTCTCTTA TGGTTTA AAGTTTG CII
GAM220 RDX	TAAAATAAGAATTAACAAACCAAAT 3237 AACATC _ I AGAG AATAAACCAAA

	TCTT TTGTTTGTTT		
	TTAT__ AA I		
GAM220 RDX	TAAAATAAGAATTAACAAACCAAAT 3237 TAACATC __		GII
	AGAG AATAAACCAAAT		
	TCTT TTGTTTGTTTA		
	ATTTTAT AA III		
GAM220 SOX11	TAAATTCTGAAGTAAAAACCAAATG 3236 TAACA A AAT_ II		
	TC GAG AAACCAAATG		
	AG CTT TTTGGTTTAC		
	ATTTA A CATT II		
GAM220 SPG4	AACATCAGAAGACAAACAAACAAATG 3217 ACA GA __ I		
	TCAGA ATAAAC CAAAT		
	AGTCT TGTTTG GTTTA		
	__ TC TTT I		
GAM220 SPG4	AACATCAGAAGACAAACAAACAAATG 3217 TA GA __ II		
	ACATCAGA ATAAAC CAAATG		
	TGTAGTCT TGTTTG GTTTAC		
	__ TC TTT AI		
GAM220 SPP1	CATGAGAGAATAA--CAAAT 3232 C ACCAAI		
	CAT AGAGAATAA		
	GTA TCTCTTATT		
	C GTTTAI		
GAM220 SPP1	CATGAGAGAATAA--CAAAT 3232 TAACATC AC		
	AGAGAATAA CAAA		
	TCTCTTATT GTTT		
	C_____		
GAM220 STX7	AACATCAGACTTAAATAGACCATATG 3214 A __ A AATI		
	TCAGA GAATA ACCA		
	AGTCT TTTAT TGGT		
	_ GAA C AIII		
GAM220 STX7	AACATCAGACTTAAATAGACCATATG 3214 TA __ A A II		
	ACATCAGA GAATA ACCA ATG		
	TGTAGTCT TTTAT TGGT TAC		
	__ GAA C A AI		
GAM220 TBX5	TAA-ATAA-AGACATAAACCAA 3238 AACATC _ I		
	AGAGA ATAAACCA		
	TTTCT TATTTGGT		
	ATTTA_ G I		
GAM220 TBX5	TAA-ATAA-AGACATAAACCAA 3238 TAACATC _ AT		
	AGAGA ATAAACCAA		

	TTTCT TATTTGGTT		
	ATTTA__ G II		
GAM220 TEM7R	ACATCAGAGAACATTTGAACCAA 3223 CATC	_____	I
	AGAGAATA AACCAA		
	TCTCTTGT TTGGTT		
	_____ AAAC I		
GAM220 TEM7R	ACATCAGAGAACATTTGAACCAA 3223 TAAC	_____	TGI
	ATCAGAGAATA AACCAA		
	TAGTCTCTTGT TTGGTTT		
	_____ AAAC CCI		
GAM220 TRAM	TAA-ATATGATGAATAAACCAAATG 3235 AACATCA	_	I
	GA GAATAAACCAAAT		
	CT CTTATTTGGTTTA		
	TTTATA_ A I		
GAM220 TRAM	TAA-ATATGATGAATAAACCAAATG 3235 TAACATCA	_	I
	GA GAATAAACCAAATG		
	CT CTTATTTGGTTTAC		
	ATTTATA_ A I		
GAM220 ZNF255	TAAC-TCAG-GAATGGAAAACCAAAT 3240 A A	_____	GI
	TAAC TCAG GAAT AAACCAAAT		
	ATTG AGTC CTTA TTTGGTTTA		
	_ _ CCT II		
GAM220 ZNF255	TAAC-TCAG-GAATGGAAAACCAAAT 3240 AACA A	_____	I
	TCAG GAAT AAACCAA		
	AGTC CTTA TTTGGTTT		
	TG_ _ CCT I		
GAM221 AKAP1	TGCTTCCGGTGAAACTGG 3260 ACTTTGCT	AC A	
	TCCGGT AAAC GG		
	AGGCCA TTTG CC		
	_____ CT A		
GAM221 CD5	TTTTCT-CAGG-ACAAACAGG 3263 ACTTTGC	C T	
	TTC GG ACAAACAGG		
	GAG CC TGTTTGTC		
	AA_____ T _		
GAM221 EIF4EBP2	ACTTTGCTTTCTTGAAGTACAA 3251	_C_____	ACAGGC
	ACTTTGCTT C GGTACAA		
	TGAAACGAA G TCATGTT		
	A AACT CGG		
GAM221 EN2	ACTTTGCTTCCTGCTA-AAA-AGGC 3252	G AC C I	
	ACTTTGCTTCC GT AAA AGGC		

	TGAAACGAAGG CG TTT TCCG		
	A A_ T I		
GAM221 ESRRBL1	ACTTTGCTTCTGATTGAAA 3254	C	ACAAACAGG
	ACTTTGCTTC GGT		
	TGAAACGAAG CTA		
	A ACTTTIIC		
GAM221 FUT4	ACTTTGCTTCCATTACAGGACAGG 3253	G_ A_ CII	
	ACTTTGCTTCCG TACA ACAGG		
	TGAAACGAAGGT GTGT TGTCC		
	AA CC III		
GAM221 INSR	ACTTTTGTTC--ACAAACAGG 3257	GC	GGT
	ACTTT TTCC ACAAACAGG		
	TGAAA AAGG TGTTTGTCC		
	AC _		
GAM221 KIF3B	TTTG-TTCTTATTCAAACAGGC 3265	ACTT C CG A	
	TG TTC GT CAAACAGGC		
	AC AAG TA GTTTGTCCG		
	_ _ AA A		
GAM221 MCL1	ACTTTGCTTC--TTTCAGACAG 3255	CGGTA A G	
	ACTTTGCTTC CA ACAG		
	TGAAACGAAG GT TGTC		
	AAA_ C I		
GAM221 NCOA4	ACTTTGCTTTACTAGTTCAAA 3250	CC_ A CAGGC	
	ACTTTGCTT GGT CAAA		
	TGAAACGAA TCA GTTT		
	ATGA A IIICG		
GAM221 PIGA	TTTGCATTTTAGTACAAACA 3261	ACTT TTCC_	
	TGC GGTACAAACAGG		
	ACG TCATGTTTGTTT		
	_ TAAAA		
GAM221 PRKG1	CTTTGCTTCAGG-ACCACCA 3258	AC C T AAA GG	
	TTTGCTTC GG AC CA		
	AAACGAAG CC TG GT		
	_ T _ GTG AI		
GAM221 RAPSIN	TTTTTTTCCAGGTACAAACAG 3262	ACTTTGC _ GC	
	TTCC GGTACAAACAG		
	AAGG CCATGTTTGTC		
	AAA_ T AA		
GAM221 SP3	ACTATTGATT--GGTACAAAC 3249	ACTTTGCTTCC	AGG
	GGTACAAAC		

	CCATGTTTG			
	TGATAACTAA_ III			
GAM221 STK38	TTTTCTGGAGG-ACAAACAGG	3264	ACTTTGCTTCC T	
	GG ACAAACAGG			
	II IIIIIII			
	CC TGTTTGTCC			
	AAGACCT____ _			
GAM221 ZIC1	CTTGCCATTTCAGTACAAACAG	3259	ACT TC_ GC	
	TTGCT CGGTACAAACAG			
	IIII IIIIIIIII			
	AACGG GTCATGTTTGTG			
	____ TAA AI			
GAM221 ZNF289	ACTTTGTTTCAA-TACAAACAG	3256	C C GC	
	ACTTTG TTC GGTACAAACAG			
	IIII III IIIIIIIII			
	TGAAAC AAG TTATGTTTGTG			
	A _ II			
GAM222 ADCY2	TGACCAGGAATAATGCTCT	3277	T C_ II	
	TG CCAG ATAATGCTC			
	II III IIIIIII			
	AC GGTC TATTACGAG			
	T CT AI			
GAM222 ADCY2	TGACCAGGAATAATGCTCT	3277	CAGTGTGTCCAGC	
	ATAATGCTCT			
	IIIIIIII			
	TATTACGAGA			
	TCCT_____			
GAM222 BIN3	AGTGTGTCCTCCACA--GCTCT	3268	_ AG AT I	
	GTGTGTCC CATA GCTC			
	IIIIII III III			
	CACACAGG GTGT CGAG			
	T AG _ I			
GAM222 BIN3	AGTGTGTCCTCCACA--GCTCT	3268	CA AG AT	
	GTGTGTCC CATA GCTCT			
	IIIIII III III			
	CACACAGG GTGT CGAGA			
	_ AG _			
GAM222 BLMH	CAGTGATACTGTCCAGCAGCATGC	3269	____ TA TCTCI	
	CAGTG TGTCCAGCA ATGC			
	IIII IIIIIII III			
	GTCAC ACAGGTCGT TACG			
	TATG CG IICT			
GAM222 BLMH	CAGTGATACTGTCCAGCAGCATGC	3269	AGTG TAATGI	
	TGTCCAGCA			
	IIIIII			
	ACAGGTCGT			
	TATG CGTACI			
GAM222 GGT2	CAGTGTGTCCCTCCCAAT-CTC	3274	AGCA G TC	
	CAGTGTGTCC TAAT CTC			
	IIIIII III III			

	GTCACACAGG GTTA GAG	
	GAGG _ II	
GAM222 GGT2	CAGTGTGTCCCTCCCAAT-CTC 3274_ AGCA GCTI	
	AGTGTGTCC TAAT	
	TCACACAGG GTTA	
	G GAGG GAI	
GAM222 HLCS	CACTTTGTACC-CA-AATGCTCTC 3275 AG__ GT GCAT I	
	TGT CCA AATGCTCT	
	ACA GGT TTACGAGA	
	GTGAA TG ____ I	
GAM222 HLCS	CACTTTGTACC-CA-AATGCTCTC 3275 CAG__ GT GCAT	
	TGT CCA AATGCTCTC	
	ACA GGT TTACGAGAG	
	GTGAA TG ____	
GAM222 KLK3	GTGTCCAGCA-CATGTCACTCTC 3276 TG A__ I	
	TCCAGCATA TGCTCT	
	AGGTCGTGT GTGAGA	
	_ ACA I	
GAM222 MYLK	CAGTGTGT-CAG-AAGATGTTC 3273 C CATA C T	
	CAGTGTGTC AG ATG TC	
	GTCACACAG TC TAC AG	
	_ TTC_ A I	
GAM222 MYLK	CAGTGTGT-CAG-AAGATGTTC 3273 C CATA CI	
	CAGTGTGTC AG ATG	
	GTCACACAG TC TAC	
	_ TTC_ AA	
GAM222 OCRL	TGTCAAACATGAATGCTCTC 3278 C _ II	
	TGTC AGCAT AATGCTCT	
	ACAG TTGTA TTACGAGA	
	T C GI	
GAM222 RBM8A	CAGTGTGT-CACCA-AAGGC 3271 C G TAAT TC	
	CAGTGTGTC A CA GC	
	GTCACACAG T GT CG	
	_ G TTC_ II	
GAM222 RBM8A	CAGTGTGT-CACCA-AAGGC 3271 C G TAATI	
	CAGTGTGTC A CA	
	GTCACACAG T GT	
	_ G TTCCG	
GAM222 SNX2	CACTGTGGAATCCAGCATAA 3270 G ____ TGCTCT	
	CA TGTG TCCAGCATAA	

	GT ACAC AGGTCGTATT			
	G CTT IIICTC			
GAM222 SNX2	CACTGTGGAATCCAGCATAA 3270 G ____ III			
	CA TGTG TCCAGCATA			
	II IIII IIIIIII			
	GT ACAC AGGTCGTAT			
	G CTT TII			
GAM222 ZNF36	CACTATGTCCAGCACTGTGCT 3272 G AA CTC			
	CA TGTGTCCAGCAT TGCT			
	II IIIIIIIII III			
	GT ATACAGGTCGTG ACGA			
	G AC III			
GAM222 ZNF36	CACTATGTCCAGCACTGTGCT 3272 AG AA I			
	TGTGTCCAGCAT TGC			
	IIIIIIII III			
	ATACAGGTCGTG ACG			
	TG AC I			
GAM223 APPBP2	CCACTCATGCTATAGATACCT 3283 CC ATC AT G CT			
	CACTCATG TA TA CT			
	IIIIII II III			
	GTGAGTAC AT AT GA			
	____ GAT CT G TI			
GAM223 APPL	CCCACTCATAACTTCTATTTAGC 3285 ____ A TCTI			
	CCCACTCATGA TCTA TTAGC			
	IIIIIIII III IIII			
	GGGTGAGTATT AGAT AATCG			
	GA A IIIT			
GAM223 DISC1	ACTC-TGAGGTTAATTAGCTCT 3281 CCCACTCA TC_			
	TGA TAATTAGCTCT			
	III IIIIIIIII			
	ACT ATTAATCGAGA			
	G_____ CCA			
GAM223 EFG1	ACACAT--TC-AATTAGCTC 3282 CCCACTCATGATC			
	TAATTAGCT			
	IIIIII			
	GTTAATCGA			
	GTAA_____			
GAM223 MICB	CCCA-TGATAATCTAATTA 3286 CTC GCT			
	CCCA ATGATCTAATTA			
	III IIIIIIIII			
	GGGT TATTAGATTAAT			
	AC_ III			
GAM223 NRCAM	CCCATTCACTGCAT-TAATTAGCT 3284 C GATC_ CTI			
	CCCA TCAT TAATTAGCT			
	III III IIIIIII			
	GGGT AGTG ATTAATCGA			
	A ACGTA III			
GAM224 BCL9	TGATCTGTTTTTCTTCTGACT 3299 AA A GTG			
	TGA TGTTTT CTTCTGACT			
	III IIII IIIIIII			

	ACT ACAAAA GAAGACTGA	
	AG A III	
GAM224 BCL9	TGATCTGTTTTCTTCTGACT 3299 AA A I	
	GA TGTTTT CTTCTGAC	
	II IIIII IIIIIII	
	CT ACAAAA GAAGACTG	
	AG A I	
GAM224 CGTHBA	AAATGTTTTATTTCTAGAAAAGTGTG 3289 TGAA C ____ II	
	ATGTTTTA TTCT GACTGTG	
	IIIIII III IIIII	
	TACAAAAT AAGA TTGACAC	
	____ A TCTT GG	
GAM224 CHN2	GAAATGTTTTA-TCCTTAGCTGTG 3294 C GA_ I	
	AAATGTTTTA TTCT CTGT	
	IIIIIIII III III	
	TTTACAAAAT AGGA GACA	
	_ ATC I	
GAM224 CHN2	GAAATGTTTTA-TCCTTAGCTGTG 3294 TG C GA_ I	
	AAATGTTTTA TTCT CTGTG	
	IIIIIIII III IIII	
	TTTACAAAAT AGGA GACAC	
	_ _ ATC A	
GAM224 CPB2	GAAATCTTTAATGTACTTCTGAC 3293 G ____ IIIG	
	GAAAT TTT TACTTCTGA	
	IIII III IIIIIII	
	CTTTA AAA ATGAAGACT	
	G TTAC GIII	
GAM224 CPB2	GAAATCTTTAATGTACTTCTGAC 3293 TGA____ TTT GTGI	
	AATGT ACTTCTGACT	
	IIII IIIIIII	
	TTACA TGAAGACTGG	
	TTTAGAAA ____ IIIG	
GAM224 DAZL	TGAAATGTTTGTA-TTCAGAC 3295 TAC T TGT	
	TGAAATGTTT TTC GAC	
	IIIIIIII III III	
	ACTTTACAAA AAG CTG	
	CAT T III	
GAM224 FBP2	GAAACCTTGCTTACTTCTGA 3292 G ____ III	
	GAAAT TT TTA CTCTG	
	IIII II IIIIIII	
	CTTTG AA AATGAAGAC	
	G CG TII	
GAM224 FBP2	GAAACCTTGCTTACTTCTGA 3292 TGAAA_ T CTGT	
	TGTTT ACTTCTGA	
	IIII IIIIIII	
	ACGAA TGAAGACT	
	TTTGGA _ CIII	
GAM224 GPR85	TGAAATGTTTTAAAGTCTTCAAAGT 3296 ____ T GTGII	
	TGAAATGTTTTA CTTC GACT	
	IIIIIIIIII III IIII	

	ACTTTACAAAAT GAAG TTGA	
	TTCA T IIIGT	
GAM224 HAO2	TGAGATCTTTTACTTCAGA 3298 A G T CTGT	
	TGA AT TTTTACTTC GA	
	ACT TA AAAATGAAG CT	
	C G T IIIG	
GAM224 HAO2	TGAGATCTTTTACTTCAGA 3298 A G TGII	
	TGA AT TTTTACTTC	
	ACT TA AAAATGAAG	
	C G TCTI	
GAM224 HOXB3	TGTTCTGAAACTTCTGACTG 3304 ____ III	
	TGTTTT ACTTCTGACT	
	ACAAGA TGAAGACTGA	
	CTT CII	
GAM224 HOXB3	TGTTCTGAAACTTCTGACTG 3304 TGAAATGTTTT	
	ACTTCTGACTGT	
	TGAAGACTGACG	
	ACTT_____	
GAM224 HSPA8	TGAAATGTTTGTCTTTT--CTGT 3302 TAC__ ACTI	
	TGAAATGTTT TTCTG	
	ACTTTACAAA AAGAC	
	CAGAA AIII	
GAM224 HSPA8	TGAAATGTTTGTCTTTT--CTGT 3302 TACT GA_ G	
	TGAAATGTTT TCT CTGT	
	ACTTTACAAA AGA GACA	
	C__ AAA I	
GAM224 JUN	TGAAATGTTTGACTTCTCAGTG 3301 T GACT	
	TGAAATGTTT ACTTCT GTG	
	ACTTTACAAA TGAAGA CAC	
	C GT__	
GAM224 JUN	TGAAATGTTTGACTTCTCAGTG 3301 T GACTI	
	GAAATGTTT ACTTCT	
	CTTTACAAA TGAAGA	
	C GTCAl	
GAM224 LANCL1	TGAAATGTT--CTTCTCCCTG 3300 TTA GA T	
	TGAAATGTT CTTCT CTG	
	ACTTTACAA GAAGA GAC	
	__ GG I	
GAM224 LANCL1	TGAAATGTT--CTTCTCCCTG 3300 A GAl	
	TGAAATGTTTT CTTCT	

	ACTTTACAAGA GAGGG		
	A ACI		
GAM224 NDUFA9	TGAAATGTTTAAATAGTGGAACGTGTG 3297	CTTCT__	II
	TGAAATGTTTAA GACTGTG		
	ACTTTACAAAAT TTGACAC		
	TATCACC II		
GAM224 NDUFA9	TGAAATGTTTAAATAGTGGAACGTGTG 3297 GA	CTTCT__	I
	AATGTTTAA GACTGT		
	TTACAAAAT TTGACA		
	__ TATCACC I		
GAM224 TGFA	TGTCTTACTTCTGCAATGTG 3305	AC_ II	
	TGTTTTACTTCTG TGT		
	ACAGAATGAAGAC ACA		
	GTT CI		
GAM224 UGT2A1	AAATGTTTTTC-TCTG-CTG 3291	A T ACI	
	AAATGTTTT CT CTG		
	TTTACAAAA GA GAC		
	A _ GAC		
GAM224 UGT2A1	AAATGTTTTTC-TCTG-CTG 3291 TGAA	A T A	
	ATGTTTT CT CTG CTG		
	TACAAAA GA GAC GAC		
	__ A _ _		
GAM224 UVRAG	AAATGCTGACCTTCTGACTG 3290	TTA I	
	AATGTT CTTCTGACT		
	TTACGA GAAGACTGA		
	CTG I		
GAM224 UVRAG	AAATGCTGACCTTCTGACTG 3290 TGAA	TTA T	
	ATGTT CTTCTGACTG		
	TACGA GAAGACTGAC		
	__ CTG T		
GAM224 ZNF200	TGAAATGTTTT-CTTC--CCTGTG 3303	A GA	
	TGAAATGTTTT CTTCT CTGTG		
	ACTTTACAAAA GAAGG GACAC		
	__ __		
GAM224 ZNF200	TGAAATGTTTT-CTTC--CCTGTG 3303 _	A GA	
	GAAATGTTTT CTTCT CTGT		
	CTTTACAAAA GAAGG GACA		
	A _ _		
GAM225 BUB1B	TGAGACTTGATTGCCTAGC 3314	ATT_ TGATG	
	TGAGAC TTGCCTAGC		

	ACTCTG AACGGATCG			
	AACT IIIAG			
GAM225 HOXB5	AGACATTTTGC--A-CTGAGGA 3312 TGAG	CTA	T	
	ACATTTTGC GCTGA G			
	TGTAAAACG TGA CT C			
	_____ C			
GAM225 LNK	ACCTTTTGCCTA--TAATGA 3309 TGAGACAT	GC_		
	TTTGCCTA TGAT			
	AAACGGAT ACTA			
	_____ ATT			
GAM225 SET	ACACTTTTGCCTA-TTGATG 3308 TGAGACA	GC		
	TTTTGCCTA TGATG			
	AAAACGGAT ACTAC			
	_____ A_			
GAM225 TRPS1	AGACATTTTG-AGAGCTGAT 3310 TGAG	CCT	G	
	ACATTTTG AGCTGAT			
	TGTAAAAC TCGACTA			
	_____ TC_ G			
GAM225 TRPS1	AGACATTTT--CT-GCTGGTGA 3311 TGAG	GC A A		
	ACATTTT CT GCTG TG			
	TGTAAAA GA CGAC AC			
	_____ _ _ C			
GAM225 XYLB	TGAGAATCACTTTTC--AGCTGATGA 3313	___ GCC	I	
	TGAGA CATT TT TAGCTGATGA			
	ACTCT GTGAAA GTCGACTACT			
	TA A_ I			
GAM226 ALDH8A1	TCCTGAACTCAAGTGATCCACCCA 3332	C		I
	TCTTGA CTCAAGTGATCCACCCA			
	AGGACT GAGTTCAGGTGGGT			
	T I			
GAM226 ANKH	TCCTGACCTTAAGTGATCCACCC 3326	C		AI
	TCTTGACCT AAGTGATCCACCC			
	AGGACTGGA TTCAGGTGGG			
	A II			
GAM226 BCAS1	TCCTGACCTCAGGTGATCCACC 3320	A		CA
	TCTTGACCTCA GTGATCCACC			
	AGGACTGGAGT CACTAGGTGG			
	C II			
GAM226 C5R1	TCTTGACCTCAGGTGATCCACCCA 3338	A		I
	TCTTGACCTCA GTGATCCACCCA			

		AGAACTGGAGT CACTAGGTGGGT			
		C I			
GAM226 CD68	TCCTGACCTCCAGTGATCCACC	3321	A	CA	
	TCTTGACCTC AGTGATCCACC				
	AGGACTGGAG TCACTAGGTGG				
	G II				
GAM226 CHST5	TCCTGACCTCAGGTGATCCACCC	3325	A	AI	
	TCTTGACCTCA GTGATCCACCC				
	AGGACTGGAGT CACTAGGTGGG				
	C II				
GAM226 CPT2	TCCTGACCTCAAGTGATCCACCC	3323		AI	
	TCTTGACCTCAAGTGATCCACCC				
	AGGACTGGAGTTCACTAGGTGGG				
	II				
GAM226 DMC1	TCCTGACCTCAAGTGATCCACC	3319		CA	
	TCTTGACCTCAAGTGATCCACC				
	AGGACTGGAGTTCACTAGGTGG				
	II				
GAM226 DNASE2	TCCTGAGTTCAAGTGATCCTCCC	3327	CC	A AI	
	TCTTGA TCAAGTGATCC CCC				
	AGGACT AGTTCACTAGG GGG				
	CA A II				
GAM226 DNASE2	TCCTGACCTCAAGTGATCTGCCCA	3334		CA I	
	TCTTGACCTCAAGTGATC CCCA				
	AGGACTGGAGTTCACTAG GGGT				
	AC I				
GAM226 HIP1	TCCTGACCTCAGGTGATCCACCC	3325	A	AI	
	TCTTGACCTCA GTGATCCACCC				
	AGGACTGGAGT CACTAGGTGGG				
	C II				
GAM226 HTR2A	TCTTGGCCTCAAGTGATCCTCCCA	3340	A	A I	
	TCTTG CCTCAAGTGATCC CCCA				
	AGAAC GGAGTTCACTAGG GGGT				
	C A I				
GAM226 IL10	TCCTGACCTCAAGTGATCCACCC	3323		AI	
	TCTTGACCTCAAGTGATCCACCC				
	AGGACTGGAGTTCACTAGGTGGG				
	II				
GAM226 IL4R	TCCTGATCTCAAGTGATCTGCCC	3328	C	CA AI	
	TCTTGA CTCAAGTGATC CCC				

	AGGACT GAGTTCACTAG GGG			
	A AC II			
GAM226 ITGAL	TCCTGACCTCAGGTGATCCACCC 3325	A	AI	
	TCTTGACCTCA GTGATCCACCC			
	AGGACTGGAGT CACTAGGTGGG			
	C II			
GAM226 LAMP2	TCCTGGCCTCAAGTGATCCACCCA 3336	A	I	
	TCTTG CCTCAAGTGATCCACCCA			
	AGGAC GGAGTTCACTAGGTGGGT			
	C I			
GAM226 LRRC2	TCCTGGGCTCAAGTGATTTTCCCA 3337	AC	CCA I	
	TCTTG CTCAAGTGAT CCA			
	AGGAC GAGTTCACTA GGGT			
	CC AAA I			
GAM226 LRRC2	GACCTCAGGTGATCCACCCA 3317	TCTTGACC A		
	TCA GTGATCCACCC			
	AGT CACTAGGTGGG			
	C			
GAM226 NPHP1	TCCTGACCTCAGGTGATCCACCCA 3335	A	I	
	TCTTGACCTCA GTGATCCACCCA			
	AGGACTGGAGT CACTAGGTGGGT			
	C I			
GAM226 NPHS1	TCCTGACCTCAGGTGATCCACCC 3325	A	AI	
	TCTTGACCTCA GTGATCCACCC			
	AGGACTGGAGT CACTAGGTGGG			
	C II			
GAM226 OPA3	TCCTGACCTCAAGTGATCCGCC 3324	A AI		
	TCTTGACCTCAAGTGATCC CCC			
	AGGACTGGAGTTCACTAGG GGG			
	C II			
GAM226 OPTN	TGACCCCAAGTGATCCACCCA 3342	TCTTGA		
	CCTCAAGTGATCCACCCA			
	GGGGTTCACTAGGTGGGT			
	C			
GAM226 PA2G4	TCGTGACCTCAGGTGATCCACCC 3330	T A AI		
	TC TGACCTCA GTGATCCACCC			
	AG ACTGGAGT CACTAGGTGGG			
	C C II			
GAM226 PCDH11X	TCCTGACCTC--GTGATCCACCC 3322	AA A		
	TCTTGACCTC GTGATCCACCC			

	AGGACTGGAG CACTAGGTGGG			
	— I			
GAM226 PCDH11X	TCCTGACCTCAGGTGATCCACCCA 3335	A	I	
	TCTTGACCTCA GTGATCCACCCA			
	AGGACTGGAGT CACTAGGTGGGT			
	C I			
GAM226 PCDH11Y	TCCTGACCTC--GTGATCCACCC 3322	AA	A	
	TCTTGACCTC GTGATCCACCC			
	AGGACTGGAG CACTAGGTGGG			
	— I			
GAM226 PCDH11Y	TCCTGACCTCAGGTGATCCACCC 3325	A	AI	
	TCTTGACCTCA GTGATCCACCC			
	AGGACTGGAGT CACTAGGTGGG			
	C II			
GAM226 PRY	TCTTGACCTC-ACTGCATCC 3318	AG _	ACCC	
	TCTTGACCTCA TG ATCC			
	AGAACTGGAGT AC TAGG			
	G_ G IIIA			
GAM226 PSD	TCTTGACCT--TGTGATCCGCC 3331	CAA	A A	
	TCTTGACCT GTGATCC CCC			
	AGAACTGGA CACTAGG GGG			
	A_ C I			
GAM226 SUDD	TCCTGACCTCAAGTGATCCACCC 3323		AI	
	TCTTGACCTCAAGTGATCCACCC			
	AGGACTGGAGTTCAGGTGGG			
	II			
GAM226 SWAP70	TCCTGACCTCAGGTGATCCACCC 3325	A	AI	
	TCTTGACCTCA GTGATCCACCC			
	AGGACTGGAGT CACTAGGTGGG			
	C II			
GAM226 TIRAP	TCTTGACCTCATG-GA-GCAGCCA 3339	AGT TC	C	
	TCTTGACCTCA GA CA CCA			
	AGAACTGGAGT CT GT GGT			
	AC_ C_ C			
GAM226 TNFRSF10A	TGACCTCAAGTGATCCACCC 3341	A	CA	
	TCTTGACCTCA GTGATCCACC			
	AGGACTGGAGT CACTAGGTGG			
	G II			
GAM226 XT3	TCCTGACCTCAAGTGATCCACCCA 3333		I	
	TCTTGACCTCAAGTGATCCACCCA			

AGGACTGGAGTTCAGTGGGT

I

GAM226	ZNF264	TCCTGGCCTCAGGTGATCCACCC	3329	A	A	AI
		TCTTG CCTCA GTGATCCACCC				
		AGGAC GGAGT CACTAGGTGGG				
		C C II				
GAM227	BRCA1	GGAGTTTCACCACGTTGGTCAGG	3345		C	I
		GGGTTTCACCATGTTGG CAG				
		CTCAAAGTGGTGCAACC GTC				
		A I				
GAM227	BRCA1	GGAGTTTCACCACGTTGGTCAGG	3345	TG		C I
		GGGTTTCACCATGTTGG CAGG				
		CTCAAAGTGGTGCAACC GTCC				
		A G				
GAM227	MAN2C1	GGCTTTCACCCCATGTTGGCCA	3348	GGT_	A	I
		TTC CCATGTTGGCC				
		GGG GGTACAACCGG				
		AAGT _ I				
GAM227	MAN2C1	GGCTTTCACCCCATGTTGGCCA	3348	TGGGG	___	I
		TTTCACC ATGTTGGCCAGG				
		AAAGTGG TACAACCGTTT				
		G___ GGG I				
GAM227	PSD	TGGGGTTTCACTACGTTGGCCAGG	3349		C	I
		TGGGGTTTCACTACGTTGGCCAGG				
		ACCCCAAAGTG TGCAACCGGTCC				
		A I				
GAM227	PSD	TGGGGTTTCACTACGTTGGCCAGG	3349		C	I
		GGGGTTTCACTACGTTGGCCAGG				
		CCCAAAGTG TGCAACCGGTC				
		A I				
GAM227	SLC22A1LS	GGGGTTT---CATGCT-GCCAGG	3346		CCA	G
		GGGGTTTCA TGTTG CCA				
		CCCAAAGT ACGAC GGT				
		___ -				
GAM227	SLC22A1LS	GGGGTTT---CATGCT-GCCAGG	3346	TG	CCA	G
		GGGGTTTCA TGTTG CCAG				
		CCCAAAGT ACGAC GGTC				
		___ -				
GAM227	TRIM9	GGTGTTTTCCATGTTGGTCAGG	3347	GG	CA	C I
		GTTT CCATGTTGG CAG				

	CAAA GGTACAACC GTC	
	CA AA A I	
GAM227 TRIM9	GGTGT TTTTCCATGTTGGTCAGG 3347 TGGG CA C I	
	GTTT CCATGTTGG CAGG	
	CAAA GGTACAACC GTCC	
	CA__ AA A G	
GAM228 ACAT2	CTTCTCCTGCCGCCGTCTGC 3356 _ _ _ CGTCT	
	TGCCGCC TGCTC GTG GC G	
	ACGGCGG ACGGG CGC CG C	
	G CAG A TCTGC	
GAM228 AP2M1	GCCCCCTGCTCGTCTGCCCGCTGC 3362 TG G _ G T I	
	CC CCGTCTCGT G CCG CTGC	
	GG GGACGAGCA C GGC GACG	
	_ G GA G _ G	
GAM228 CALM1	GCCGCCTG--CGCCGCCGCCTG 3365 TG TC G	
	CCGCCTGC GT GCCGTCTG	
	GGCGGACG CG CGGCGGAC	
	_ _ G	
GAM228 CDC34	GCCGCCTGCCTCCT--CC-TCTGC 3360 TG CGTGG G	
	CCGCCTGCT CC TCTGC	
	GGCGGACGG GG AGACG	
	_ AGGA _	
GAM228 DPP4	GCCTGCTCGTGTGGTATGC 3369 TGCCGCCT GCC C	
	GCTCGTG GT TG	
	CGAGCAC CA AC	
	_ AAC T	
GAM228 DVL3	GCGGCCTGCTCGGGCGGCCG 3361 TGCC _ TCTG	
	GCCTGCTC GTGGCCG	
	CGGACGAG CGCCGGC	
	GC__ CC C	
GAM228 EDN3	GCCGACGCCTCGTGGCCCTC 3363 _ C TGC G TG	
	TG CGCC TCGTGGCC TC	
	GC GCGG AGCACCGG AG	
	G T _ G TI	
GAM228 EIF2B1	GCCGCCTG--CGAGCCAGTCTG 3364 TG TCGT _	
	CCGCCTGC GGCC GTCTG	
	GGCGGACG TCGG CAGAC	
	_ C__ T	
GAM228 ESR2	GCCGCCTGCTCTTCGCC--CTGC 3367 TG GTG GT	
	CCGCCTGCTC GCC CTGC	

		GGCGGACGAG CGG GACG		
		___ AAG ___		
GAM228 GNA15		TGCCGCCTGCCCCAGGTGG 3371	___	CCGTCTG
		TGCCGCCTGCTC GTGG		
		ACGGCGGACGGG CACC		
		GTC CGTC		
GAM228 GRB14		GCCGCCTGCGCTCGGGGCC 3358 TG	___ T	GTCTG
		CCGCCTGC TCG GGCC		
		GGCGGACG AGC CCGG		
		___ CG C G C		
GAM228 HS2ST1		CCGCCTGCT--TGCCCGCCT 3352 TGCC	CG G	
		GCCTGCT TG CCGTCT		
		CGGACGA AC GGCGGA		
		___ ___ G		
GAM228 ICA1		TGGCTCCTTCACTTGGCCGTCT 3374 T_ CG	GCTCG	GC
		GC CCT TGGCCGTCT		
		CG GGA ACCGGCAGA		
		AC A_ AGTGA		
GAM228 MAGOH		GCCGCACTGC-CG---CCGTCTGC 3357 TG	_	CGTG
		CCGC CTGCT GCCGTCTG		
		GGCG GACGG CGGCAGAC		
		___ T ___		
GAM228 MDFI		TGCGCGCCTGCTCCGGGCGCCCCTGC 3370	_	G C GCII
		TGC CGCCTGCTC TGG CGTCT		
		ACG GCGGACGAG GCC GCGGG		
		C _ C GACG		
GAM228 PDGFB		CCGCCTGCTCGCCGC--TCTG 3353 TGCC	G CG	
		GCCTGCTCGT GC TCTG		
		CGGACGAGCG CG AGAC		
		___ G ___		
GAM228 RGS6		GCCGCCTGCCTGTGG-GGTCCGC 3366 TG	TC CC	
		CCGCCTGC GTGG GTCTGC		
		GGCGGACG CACC CAGGCG		
		___ GA C_		
GAM228 RNF12		CGCCTGCTCGGAGACGT-TGC 3355 TGCCGC	TG C C	
		CTGCTCG G CGT TG		
		GACGAGC C GCA AC		
		___ CT T _		
GAM228 SLC9A5		TGCCGCCTGCCCAGCCGCCCTC 3372	GT GC	
		TGCCGCCTGCTC GGCCGTCT		

ACGGCGGACGGG TCGGCGGG
 — AG
 GAM228 TIMP3 GCCGCCTGCCTGCTGCCCGCTCTGC 3359 TG TC _ G _ II
 CCGCCTGC G TG CCG TCTGC
 ||||| | || ||||
 GGCGGACG C AC GGC AGACG
 — GA G G G CI
 GAM228 TRPS1 TGCCTC-TGCCCTTGCCCGTCT 3373 GC G GC
 TGCC CTGCTC TGGCCGTCT
 ||| |||| |||||
 ACGG GACGGG ACCGGCAGA
 A_ A II
 GAM228 WNT6 CGCCTTTTCGGGGCCGTCTG 3354 TGCCGC GC T
 CT TCG GGCCGTCTG
 || ||| |||||
 GA AGC CCGGCAGAC
 — AA C
 GAM228 WNT7A GCGTCCCCGGGGCCGTCTG 3368 TGCCGCCTG T
 CTCG GGCCGTCTG
 ||| |||||
 GGGC CCGGCAGAC
 G_____ C
 GAM229 ABR ATGCGGTGGTGAGGCTGGGGCTGG 3380 TA C _ _ AAI
 TGCGGTGG G GG TGGGG TGG
 ||||| | || ||||
 ACGCCACC C CC ACCCC ACC
 — AT G G CII
 GAM229 ADD2 TATGGGTTTGGGGGGTGGGGTG 3394 C _ C GAA
 TATG GGT GG GGGTGGGGTG
 ||| ||| || |||||
 ATAC CCA CC CCCACCCAC
 _ AA C III
 GAM229 ALOX12B TGAGGTGGCGAGGTGGGGTG 3401 TATGC _ A
 GGTGGCG GGTGGGGTGG
 ||||| |||||
 CCACCGC CCACCCCACT
 T_____ T G
 GAM229 ANXA11 TATACGG-GTCAGGAGGGGTGGAA 3395 TGG T I
 TATGCGG CGGG GGGGTGGAA
 ||||| ||| |||||
 ATATGCC GTCC CCCACCTT
 CA_ T I
 GAM229 ARF3 TATGTCAGGGGTGGGTGGGGTG 3393 _ T C GAA
 TATG CGG GG GGGTGGGGTG
 ||| ||| || |||||
 ATAC GTC CC CCCACCCAC
 A C A III
 GAM229 CD7 CGGTGGCGGCGTGGGCTGG 3381 TAT GC G TG A
 GCGGTG GGGT GGG G
 ||||| ||| ||| |

CGCCGC CCCG CCC C
C__ A_ A GT I
GAM229 COPE ATGCAGGTGGATGCCGGGTGGGGAGG 3377 TA _ ____ T AAI
TGC GGTGG CGGGTGGGG GG
||| |||| ||||| ||
ACG CCACC GCCACCCC CC
_ T TACG T C||
GAM229 CTNNB1 TGCGGTGGCGGCTCGGCGGGGA 3403 TATG G_ _ T A
CGGTGGCGG TGG GG GGA
||||||| ||| |||
GCCACCGCC GCC CC CCT
____ GA G _ G
GAM229 ENIGMA GGTGGAGGGAGTGGGGTGG 3390 TATGCGGT C A
GG GGGTGGGGTGG
|| |||||
CC CTCACCCCACC
T_____ C
GAM229 ENO2 GCGGTGGC-GGTGGCGGTGG 3386 TAT GTGG A
GCGGTGGCGG GGTGG
||||||| ||||
CGCCACCGCC CCGCC
CAC A__ I
GAM229 EXTL1 ATG-GGTGGCGGGGTGGGGCGG 3379 TA C _ AA
TG GGTGGCGGG TGGGGTGG
|| ||||| |||||
AC CCACCGCCC ACCCGCC
_ _ C CI
GAM229 FASN GCGGGGGTGGGGTGGGGTGG 3385 TATGC CG A
GGTGG GGTGGGGTGG
|||| |||||
CCACC CCACCCCACC
CC__ _ C
GAM229 FASN TGGGGTGG--GGTGGGGTGG 3406 TATGC CG
GGTGG GGTGGGGTGG
|||| |||||
CCACC CCACCCCACC
C__ _
GAM229 FLT1 TGAGGTGGCGG--GGGTTGGA 3407 TATGC T GG
GGTGGCGGG GG TGGA
||||||| || |||
CCACCGCCC CC ACCT
T_____ A_
GAM229 GAL TGCGGTGGCGGGTCTGGGCGG 3402 TATG G_ AA
CGGTGGCGGGT GGGTGG
||||||| |||||
GCCACGCCCCA CCCGCC
____ GA GT
GAM229 GRM7 TGCGGTGGCGGCGGCGGCGCTGGA 3400 TATG _ G_ AI
CGGTGGCGG GTGG G TGGA
||||||| |||| | |||

	GCCACCGCC CGCC C ACCT		
	_____ GC G G CC		
GAM229 HSF4	TGGGGTGGAGTGGGGTGGGGTGG 3399 TATGC C_____	AAI	
	GGTGG GGGTGGGGTGG		
	CCACC CCCACCCCACC		
	C_____ TCAC CCI		
GAM229 HSF4	TGGGGTGG--GGTGGGGTGG 3404 TATGC CG		
	GGTGG GGTGGGGTGG		
	CCACC CCACCCCCT		
	C_____ _		
GAM229 INSR	TGCTGGGGGCGGGTGGGG-GGAA 3396 TA C T T		
	TG GG GCGGGTGGGG GGAA		
	AC CC CCGCCCACCCC CCTT		
	G_ _ _ _		
GAM229 MADH4	GCGGTGGCGAGGGGAGTGG 3388 TATGCG T A		
	GTGGCGGG GGGGTGG		
	CACCGCTC CCTCACC		
	_____ C C		
GAM229 MAF	TGCGGTGGCGGCGGTGGTGG 3405 TATG G _ A		
	CGGTGGCGG TGG GGTGG		
	GCCACCGCC GCC CCACC		
	_____ _ A G		
GAM229 MLLT7	TGCTTTGGGGGCTGGGGTGGGA 3408 TATGCGG C _ A		
	TGG GGG TGGGGTGGGA		
	ACC CCC ACCCCACCT		
	GAA_____ _ G C		
GAM229 PKP1	GGTGGCGGGAGGCGGGTGG 3392 TATGC T G GA		
	GG GCGGGTGG GTG		
	CC CCGCCCACC CGC		
	GC_____ T G GI		
GAM229 PPT2	CGGTGGCGGGGGGAAGGGTGG 3382 TATGC C T A		
	GGTGG GGG GGGGTGG		
	CCGCC CCC TCCCACT		
	_____ C T C		
GAM229 RANBP3	GGGGGCGGGTGGGCGGGTGGGA 3391 TATGC _ G A		
	GGTGG CGGGTGGG TGGA		
	CCACC GCCCACCT ATCT		
	GC_____ C _ G		
GAM229 RFX1	GCGGGGGCGGGTGGGGCGG 3387 TATGC T A		
	GG GCGGGTGGGGTGG		

		CC CCGCCCACCCCGCC		
		_____ C		
GAM229 RNH	ATGCGGGGAGGGGTGGGTGGGGTGG	3378 TA	T_____ C	AAII
	TGCGG GG GGGTGGGGTGG			
	ACGCC CC CCCACCCCACC			
	___ CCTCC A CII			
GAM229 S100A1	TGGGGTGGGCAAGGGTGGGGT	3398 TATGC	___	GGAA
	GGTGG C GGGTGGGGT			
	CCACC G CCCACCCCA			
	C_____ C TT ATII			
GAM229 SLC12A7	TGGGGTGG--GGTGGGGTGG	3406 TATGC	CG	
	GGTGG GGTGGGGTGG			
	CCACC CCACCCCACC			
	C_____			
GAM229 SMURF1	TGCAGATGGCGGGTGGGG-GGA	3397 TATGC	T A	
	GGTGGCGGGTGGGG GGA			
	CTACCGCCCACCCC CCT			
	GT_____ G			
GAM229 STAU	GCGGTGGCGGCGAGGAGGGGAA	3384 TATGC	_ T T_ A	
	GGTGGCG GG GGGG GGA			
	CCGCCGC CC CCCC CCT			
	CA_____ T T TT I			
GAM229 ZNF278	GCGGTGGCGCGGGCCGGGT	3383 TATGC	G G GGA	
	GGTG CGGGT GGGT			
	CCGC GCCCG CCCA			
	CA_____ G GGG			
GAM229 ZNF278	GCGGTGGCGGCGGCGGCGG	3389 TATGC	G _ A	
	GGTGGCGG TGG GGTGG			
	CCGCCGCC GCC CCGCC			
	CA_____ G I			
GAM230 AF5Q31	CGGTGACAGGCTGCCAAGGGC	3411	C _ III	
	CGGTGACAG CT CAAGGG			
	GCCACTGTC GA GTTCCC			
	C CG GII			
GAM230 AF5Q31	CGGTGACAGGCTGCCAAGGGC	3411 GTCG	C _ TTC	
	GTGACAG CT CAAGGGC			
	CACTGTC GA GTTCCCG			
	_____ C CG CTI			
GAM230 ATP8B2	TGACAGCCTCCAGCAGGCT	3416	AA_ III	
	TGACAGCCTC GGGC			

	ACTGTCGGAG TCCG			
	GTCG AII			
GAM230 FA4L4	TGGCAGAGCCAG-CCGAATC 3418	A	CTCI	
	TGGCAGAGCCAG CCGA			
	ACCGTCTCGGTC GGCT			
	_ TAGI			
GAM230 FA4L4	TGGCAGAGCCAG-CCGAATC 3418 _	A	CTI	
	GGCAGAGCCAG CCGA			
	CCGTCTCGGTC GGCT			
	A _ TAI			
GAM230 GNA11	TCGGTGCCTCAGTGCCTCAAGGG 3415	ACA_____	IIIC	
	TCGGTG GCCTCAAGG			
	AGCCAC CGGAGTTCC			
	GGAGTCA CIII			
GAM230 GNA11	TCGGTGCCTCAGTGCCTCAAGGG 3415 GT	ACA_____	CTTCI	
	CGGTG GCCTCAAGGG			
	GCCAC CGGAGTTCCC			
	_ GGAGTCA CIIIC			
GAM230 MAP3K5	CGGTG-CAGC-TCAAGGGC 3413	A C I		
	CGGTG CAGC TCAAGGG			
	GCCAC GTCG AGTTCCC			
	_ _ G			
GAM230 MAP3K5	CGGTG-CAGC-TCAAGGGC 3413	GTCG A C T		
	GTG CAGC TCAAGGGC			
	CAC GTCG AGTTCCCG			
	_ _ _ C			
GAM230 MTMR6	CGGTGACAGCGACAGAGAGC 3412	CT _ II		
	CGGTGACAGC CA AGGG			
	GCCACTGTCG GT TCTC			
	CT C GI			
GAM230 MTMR6	CGGTGACAGCGACAGAGAGC 3412	GTCG CT _ TT		
	GTGACAGC CA AGGGC			
	CACTGTCG GT TCTCG			
	_ CT C TT			
GAM230 NPR2L	GTCAGAGACAGCCTCGAGGCCT 3414	T A G TC		
	GTCGG GACAGCCTC AGG CT			
	CAGTC CTGTCGGAG TCC GA			
	T C G II			
GAM230 NPR2L	GTCAGAGACAGCCTCGAGGCCT 3414	T A GCI		
	TCGG GACAGCCTC AGG			

	AGTC CTGTCGGAG TCC		
	T C GGI		
GAM230 TAZ	TGGCAGTCT-AAGGGCTTC	3417	A C C I
	TG CAG CT AAGGGCTT		
	II III II IIIIIII		
	AC GTC GA TTCCCGAA		
	C A _ G		
GAM231 CTF1	ACAGGGCCACGAGAAGGCAG	3423	TAACAG C TTGG
	CACGAGAAG CAG		
	IIIIIIII III		
	GTGCTCTTC GTC		
	TCCCG_ C CTII		
GAM231 GATA6	TAAAGGCACGAGAATCACGTT	3430	TAACA GCCA GGG
	GCACGAGAA GTT		
	IIIIIIII III		
	CGTGCTCTT CAA		
	ATTTC AGTG III		
GAM231 GRB10	ACAGCACGAAGACAACCAGGTG	3424	TAAC _ _ T GG
	AGCACGA GA AGCCAG TG		
	IIIIII II IIIII II		
	TCGTGCT CT TTGGTC AC		
	_ _ T G C GG		
GAM231 HNF4G	TAACAGCACCAATGAAGAAGCC--TTGG3428		_ _ AG GII
	TAACAGCAC GAGAAGCC TTGG		
	IIIIII IIIII III		
	ATTGTGCTG TTCTTCGG AACC		
	GTTAC _ III		
GAM231 IL1R1	AACACCAGACTAGAAGCCAG	3421	TAA_ C G TTGG
	CAG AC AGAAGCCAG		
	III II IIIIIII		
	GTC TG TCTTCGGTC		
	TGTG _ A TIII		
GAM231 ITPKB	TAACAGCACTGGCCGCCAG	3429	GAGAA TTGG
	TAACAGCAC GCCAG		
	IIIIII III		
	ATTGTGCTG CGGTC		
	ACCGG IIIG		
GAM231 MKKS	CAGCTACAAGAAGCCAGTT	3425	TAACAGC GG
	ACGAGAAGCCAGTT		
	IIIIIIIIII		
	TGTTCTTCGGTCAA		
	GA_ GA		
GAM231 RAB36	AACAGCACGAGA---CGGGTG	3422	TA AGCCAGT
	ACAGCACGAGA TGG		
	IIIIIIII III		
	TGTCGTGCTCT ACC		
	_ GCCC_		
GAM231 SH3BP2	TAACGAGCCAAAGAAGCCAGCTG	3427	_ AC GGI
	TAAC AGC GAGAAGCCAGTTG		
	III III IIIIIIIII		

	ATTG TCG TTCTTCGGTCGAC	
	C GT III	
GAM231 SLC22A1LS	CAGCCCCGGGAGAAGCCA--TGGG 3426 TAACAGCAC GT	
	GAGAAGCCA TGGG	
	CTCTTCGGT ACCC	
	GGGGCC__ _	
GAM232 ADCY8	GCGGATATCTG-AGGCTGAG 3435 TGGC TTC G T	
	GG TCTG AGGCTGAG	
	CC AGAC TCCGACTC	
	__ TAT _ T	
GAM232 ATP7B	GCAGTTCTCTGGAAAGGCCAGTG 3434 TGGC _ G I	
	GGTTCTCTGGA GGCT AGTG	
	TCAAGAGACCT CCGG TCAC	
	__ TT G T	
GAM232 CLECSF11	CGGCTACTCAGGAGGCTGAG 3433 TGGCGGTT T T	
	CTC GGAGGCTGAG	
	GAG CCTCCGACTC	
	GAT__ T C	
GAM232 DEFB1	TGGC--TCCTTTGGAGGCTGAG 3447 TGGC C_ T	
	GGTTCT TGGAGGCTGAG	
	CCGAGG ACCTCCGACTC	
	A__ AA I	
GAM232 EBAG9	GGCGG--CTTTGGAGGCTGCGTG 3441 TG CTC A	
	GCGGTT TGGAGGCTG GTG	
	CGCCGA ACCTCCGAC CAC	
	_ A_ G	
GAM232 F2RL3	GGCTGGTTCCCTCTGGAGGCTG 3436 _ CGG AGTG	
	TGG TTCTCTGGAGGCTG	
	ACC GGGAGACCTCCGAC	
	CG AA_ A	
GAM232 GJB3	GGCGGCTCCTCTGGAGG--GAGT 3438 TG _ CT	
	GCGGTTCTCTGGAGG GAGTG	
	CGCCGAG AGACCTCC CTCAT	
	_ G _	
GAM232 GPC1	GGGGCTTCTCTGGAGGCTG 3439 T GG AGT	
	GGC TTCTCTGGAGGCTG	
	CCG AAGAGACCTCCGAC	
	C _ C	
GAM232 HGF	TGGCGGATCCCTCTGGAGG 3443 _ CTGAGT	
	TGGCGG TTCTCTGGAGG	

	ACCGCC GGGAGACCTCC	
	TA III GTG	
GAM232 HSPA1L	GGTTCTCT-GAGGCCTAGT 3442 TGGCGGTT G G	
	CTCTG AGGCT AG	
	GAGAC TCCGG TC	
	_____ _ A	
GAM232 ITGA11	TGG-GTTTCTCTGGAGGATG 3445 CGG C AGT	
	TGG TTCTCTGGAGG TG	
	ACC AAGAGACCTCC AC	
	CA_ T	
GAM232 PTGIS	TGGGGGTGC-CTGGAGGCTGAG 3448 C T T TG	
	TGG GGT C CTGGAGGCTGAG	
	ACC CCA G GACCTCCGACTC	
	C C_	
GAM232 RET	TGGCTGTGCTCCCA GTGCAGGCTGAGTG3444 G_ _ G	
	TGGC GTTCTC TG AGGCTGAGTG	
	ACCG CGAGGG AC TCCGACTCAC	
	ACA TC G	
GAM232 RNPEP	GGCAGGTTCTCTGTCTCGGGGCTCAGTG3437 TG _ GA_____ G	
	GC GGTTCTCTG GGCT AGTG	
	CG CCAAGAGAC CCGA TCAC	
	_ T AGAGCC G C	
GAM232 SLA2	TGG-GGTGCCCAGGAGGCTGA 3446 C T T GT	
	TGG GGT CTC GGAGGCTGA	
	ACC CCA GGG CCTCCGACT	
	_ C T	
GAM232 XPNPEP1	GGTGGCTTTCTGGAGGCTG 3440 TGGC C AGT	
	GGTT TCTGGAGGCTG	
	CCGA AGACCTCCGAC	
	CA_ A G	
GAM233 ATF5	GAAAGAAGG--TGGGAGCGG 3457 TG ACC C	
	AAAGAGG TGGGAGCGG	
	TTTCTTC ACCCTCGCC	
	_ C_ T	
GAM233 ATP6V1G2	AAAGGGGCCGCTGGGAGCAGCA 3451 TGAA A A_ AI	
	AG GG CCTGGGAGCGGCA	
	TC CC GGACCCTCGTCGT	
	_ C GGC CT	
GAM233 CENPB	GAAAGAGGATTCTGAGAAAGAGGCAA 3454 TG C_ C_	
	AAAGAGGA CTGGGAG GGCAA	

	TTTCTCCT GACTCTT CCGTT		
	— AA TCT AI		
GAM233 CHST2	GAAAGAGGACAAGAGA-AGGCAA 3459 TG	CT	C
	AAAGAGGAC GGGAG GGCAA		
	TTTCTCCTG CTCTT CCGTT		
	— TT —		
GAM233 CNTN2	TGAGAAAGGACCTGGG-GCG 3463 A	A	GCA
	TGA AGAGGACCTGGG GCG		
	ACT TTTCTGACCC CGC		
	C —		
GAM233 CYLN2	TGAATGAAGGACCTGGGGAGGGG 3460 A_	_	C CAAI
	TGAA GAGGACCTGGG AG GG		
	ACTT TTCCTGGACCC TC CC		
	AC C _ C		
GAM233 DDX26	GAAAGAGGAGATGGTAGAGG 3458 TG	CC	G C CA
	AAAGAGGA TGG AG GG		
	TTTCTCCT ACC TC CC		
	— CT A T AI		
GAM233 EMD	AAAGAGGACCATGGAG-GGC 3452 TGAA	TG	C A
	AGAGGACC GGAG GGC		
	TCTCCTGG CCTC CCG		
	— TA _ G		
GAM233 FZD4	TGAGACAGTGACCTGGGAGAGGAAA 3461 T_	A AG	C CAAII
	GA AG GACCTGGGAG GG		
	CT TC CTGGACCCTC CC		
	ACT G A_ T TTTII		
GAM233 HAGH	AGACGGGCCTGGGAGCGGC 3453 TGAAAGA A		A
	GG CCTGGGAGCGGC		
	CC GGACCCTCGCCG		
	C — C		
GAM233 MAFF	GAAATGGGACCTGGGCACAGAGGC 3456 TG	GA	— C AAI
	AAA GGACCTGGG AG GGC		
	TTT CCTGGACCC TC CCG		
	— AC GTG T CII		
GAM233 MBNL	TGAAAGAGGCCCTTGACCCGG 3464	A	GGGAG CAA
	TGAAAGAGG CCT CGG		
	ACTTTCTCC GGA GCC		
	G ACGTG		
GAM233 MPHOSPH6	TGACA-ATGACCTGGGAGC 3462	AAGAG	GGC
	TGA GACCTGGGAGC		

	ACT CTGGACCCTCG		
	GTTA_ III		
GAM233 PCDHGA1	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C _	C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	_ T AA A CII		
GAM233 PCDHGA10	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C _	C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	_ T AA A CII		
GAM233 PCDHGA11	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C _	C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	_ T AA A CII		
GAM233 PCDHGA12	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C _	C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	_ T AA A CII		
GAM233 PCDHGA2	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C _	C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	_ T AA A CII		
GAM233 PCDHGA3	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C _	C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	_ T AA A CII		
GAM233 PCDHGA4	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C _	C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	_ T AA A CII		
GAM233 PCDHGA5	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C _	C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	_ T AA A CII		
GAM233 PCDHGA6	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C _	C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	_ T AA A CII		
GAM233 PCDHGA7	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C _	C CAA
	AAAGAGGA CTG GGAG GG		

	TTTCTCCT GAC CCTC CC		
	— T AA A CII		
GAM233 PCDHGA8	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C	— C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	— T AA A CII		
GAM233 PCDHGA9	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C	— C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	— T AA A CII		
GAM233 PCDHGB1	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C	— C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	— T AA A CII		
GAM233 PCDHGB2	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C	— C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	— T AA A CII		
GAM233 PCDHGB3	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C	— C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	— T AA A CII		
GAM233 PCDHGB4	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C	— C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	— T AA A CII		
GAM233 PCDHGB5	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C	— C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	— T AA A CII		
GAM233 PCDHGB6	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C	— C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	— T AA A CII		
GAM233 PCDHGB7	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C	— C CAA
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	— T AA A CII		
GAM233 PCDHGC3	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C	— C CAA
	AAAGAGGA CTG GGAG GG		

	TTTCTCCT GAC CCTC CC		
	___ T AA A CII		
GAM233 PCDHGC4	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C ___ C CAA	
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	___ T AA A CII		
GAM233 PCDHGC5	GAAAGAGGAACTGTTGGAGTGG 3455 TG	C ___ C CAA	
	AAAGAGGA CTG GGAG GG		
	TTTCTCCT GAC CCTC CC		
	___ T AA A CII		
GAM234 DAB2	TCAA-ATA-AACATAACCTC 3467 ATA I		
	TCAAG AACATAACT		
	AGTTT TTTGTATTGG		
	A___ A		
GAM234 DAB2	TCAA-ATA-AACATAACCTC 3467 TTCA A		
	AGATAAA CATAACTTCT		
	TTTATTT GTATTGGAGG		
	G___ _		
GAM234 SLC26A3	TTCAAGATAAAGTTCTAAGTTCTA 3468	ACA_ C CI	
	TTCAAGATAAA TAA TTCTA		
	AAGTTCTATTT ATT AAGAT		
	CAAG C II		
GAM234 SLC26A3	TTCAAGATAAAGTTCTAAGTTCTA 3468 T	ACA_ C I	
	CAAGATAAA TAA TTCT		
	GTTCTATTT ATT AAGA		
	___ CAAG C I		
GAM235 APOL1	TGGCCAACATGGTGAAACCCCATC 3489 A	A I	
	TG CCAACATGG GAAACCCCATC		
	AC GGTGTACC CTTTGGGGTAG		
	C A I		
GAM235 BRIP1	TGGCCAACATGGTGAAACCCCATC 3489 A	A I	
	TG CCAACATGG GAAACCCCATC		
	AC GGTGTACC CTTTGGGGTAG		
	C A I		
GAM235 CAMLG	TGACCAACATGGAGAAACCC 3473 A	A I	
	TG CCAACATGG GAAACCCCATC		
	AC GGTGTACC CTTTGGGGTAG		
	C A I		
GAM235 CBFA2T2	TGACCAACAAGGAGAAACCCCGTC 3476	T ATCI	
	TGACCAACA GGAGAAACCC		

	ACTGGTTGT CCTCTTTGGGG			
	T CAGI			
GAM235 CLECSF11	TGGCCAACATAGTGAAACCCCATC 3483	A	A	I
	TG CCAACATGG GAAACCCCATC			
	II			
	AC GGTGTATC CTTTGGGGTAG			
	C A I			
GAM235 CNGA1	TGGCCAACATGGTGAAATCCCATC 3492	A	A C	I
	TG CCAACATGG GAAA CCCATC			
	II			
	AC GGTGTACC CTTT GGGTAG			
	C A A I			
GAM235 CNN2	TGGCCAACATGGGGAAACCCCATC 3486	A	A	I
	TG CCAACATGG GAAACCCCATC			
	II			
	AC GGTGTACC CTTTGGGGTAG			
	C C I			
GAM235 CYP1A2	TGGCCAACATGGTGAAACCCCATC 3489	A	A	I
	TG CCAACATGG GAAACCCCATC			
	II			
	AC GGTGTACC CTTTGGGGTAG			
	C A I			
GAM235 CYP1A2	TGACCAACATGGTGAAACCC 3474	A	CAT	
	TGACCAACATGG GAAACCC			
	ACTGGTTGTACC CTTTGGG			
	A III			
GAM235 DHFR	ACCAACATGTGAAAAGCCC 3471	TGAC	— A	CAT
	CAACATG GAGAA CCC			
	GTTGTAC CTTTT GGG			
	— A C CTI			
GAM235 DHFR	TGACCAACATGGTGAAACCCCATC 3479	A	I	
	TGACCAACATGG GAAACCCCATC			
	ACTGGTTGTACC CTTTGGGGTAG			
	A I			
GAM235 GM2A	TGGCCAACATGGTGAAACCCCATC 3489	A	A	I
	TG CCAACATGG GAAACCCCATC			
	II			
	AC GGTGTACC CTTTGGGGTAG			
	C A I			
GAM235 GRM7	TGGCCAACATGGTGAAACCCAATC 3488	A	A C	I
	TG CCAACATGG GAAACCC ATC			
	II			
	AC GGTGTACC CTTTGGG TAG			
	C A T I			
GAM235 HTR1E	TGGCCAACATGGTGAAATCCCGTC 3493	A	A C	ATCI
	TG CCAACATGG GAAA CCC			
	II			

	AC GGTGTGACC CTTT GGG C A A CAGI			
GAM235 HYAL4	TGGCCAACACGGTGAAACCCCATC 3482 A TG CCAACATGG GAAACCCCATC AC GGTGTGCC CTTTGGGGTAG C A I	A	I	
GAM235 LTB4R	TGGCCAACATGGTGAAACCCCGTC 3490 A TG CCAACATGG GAAACCCC AC GGTGTACC CTTTGGGG C A CAGI	A	ATCI	
GAM235 MEF2A	TGGCCAACATGGTGAAACTCCATC 3491 A TG CCAACATGG GAAAC CCATC AC GGTGTACC CTTTG GGTAG C A A I	A	C I	
GAM235 MLANA	TGACCAACATGGAGAAACCCCGTC 3477 TGACCAACATGGAGAAACCCC ACTGGTTGTACCTCTTTGGGG CAGI		ATCI	
GAM235 MRPL49	TGGCCAACATGGTGAAACCCCATC 3489 A TG CCAACATGG GAAACCCCATC AC GGTGTACC CTTTGGGGTAG C A I	A	I	
GAM235 NCOA6	TGGCCAACATGATGAAACCCCATC 3484 A TG CCAACATG GAAACCCCATC AC GGTGTAC CTTTGGGGTAG C TA I	GA	I	
GAM235 PPEF2	TGACCAACATGGAGAAACCC 3473 A TG CCAACATGG GAAACCCCATC AC GGTGTACC CTTTGGGGTAG C A I	A	I	
GAM235 PPID	TGACCAATATGGTGAAACCCCATC 3481 TGACCAA ATGG GAAACCCCATC ACTGGTT TACC CTTTGGGGTAG A A I	C A	I	
GAM235 PTGIS	TGACCAACATGGGGAAACCCCGTC 3478 TGACCAACATGG GAAACCCC ACTGGTTGTACC CTTTGGGG C CAGI	A	ATCI	
GAM235 RHD	TGGCCAACATGGTGAAACCCCATC 3489 A TG CCAACATGG GAAACCCCATC 	A	I	

	AC GGTGTACC CTTTGGGGTAG			
	C A I			
GAM235 RPH3AL	TGGCCAACATGGAGAAACCCCATC 3485	A		I
	TG CCAACATGGAGAAACCCCATC			
	II			
	AC GGTGTACCTCTTTGGGGTAG			
	C I			
GAM235 SCML2	TGACCAACATGGAGAAACCCCATC 3470	TGACCAAC	A	
	ATGG GAAACCCCAT			
	TACC CTTTGGGGTA			
	_____ A			
GAM235 SH3GL3	TGGCCAACATGGTGAAA-CCCATC 3487	A	A	C I
	TG CCAACATGG GAAACCC ATC			
	II			
	AC GGTGTACC CTTTGGG TAG			
	C A _ I			
GAM235 SIL	GACCAACATGGTGAAACCCCGTC 3472	TG	A	ATCI
	ACCAACATGG GAAACCCC			
	TGGTTGTACC CTTTGGGG			
	_____ A CAGA			
GAM235 SMAC	TGACCAACATGGTGAAACCCCATC 3479		A	I
	TGACCAACATGG GAAACCCCATC			
	ACTGGTTGTACC CTTTGGGGTAG			
	A I			
GAM235 SULT2B1	TGGCCAACATGGTGAAACCCC 3475	A	A	ATC
	TG CCAACATGG GAAACCCC			
	II			
	AC GGTGTACC CTTTGGGG			
	C A III			
GAM235 TNFRSF10B	TGACCAACATGGTGAAACCCCGTC 3480		A	ATCI
	TGACCAACATGG GAAACCCC			
	ACTGGTTGTACC CTTTGGGG			
	A CAGI			
GAM235 TPMT	TGACCAACATGGTGAAACCCCGTC 3480		A	ATCI
	TGACCAACATGG GAAACCCC			
	ACTGGTTGTACC CTTTGGGG			
	A CAGI			
GAM235 TRPM6	TGGCCAACATGGTGAAACCCCATC 3489	A	A	I
	TG CCAACATGG GAAACCCCATC			
	II			
	AC GGTGTACC CTTTGGGGTAG			
	C A I			
GAM236 APP	CTA-TTCATGCACTAGTTT 3499	TCACTACTTC		CT
	GCACTAGTTT			

	CGTGATCAAA	
	AAGTA_____CT	
GAM236 CACNA1A	GGGATAGCAGCTCG--GGAC 3502 AG _ AA TC	
	GGATAGCA TTCG GGAC	
	CCTATCGT GAGC CCTG	
	_ C _ TI	
GAM236 CORO2B	GGAAGAACATTTCGAAGGAGCTC 3503 AG T _ G	
	GGA AGCATTTCGAAGGA CTCG	
	CTT TTGTAAGCTTCCT GAGT	
	_ C C I	
GAM236 CYP24	GGGACAGGCAGCAGAAGGACTCGG 3501 A__ A TTC I	
	GGG TAGCA GAAGGACTCGG	
	TCC GTCGT CTCCTGAGCC	
	CCTG _ _ G	
GAM236 GPC3	AGCGAGAGCAGTCCCAGGACTCGG 3497 G T T GA I	
	AG GA AGCA TC AGGACTCGG	
	TC CT TCGT AG TCCTGAGCC	
	G C C GG I	
GAM236 IL10RA	CACATACCCTGCACTAGTT 3498 TC _ TC CT	
	AC TACT GCACTAGTTT	
	TG ATGG CGTGATCAAG	
	_ T GA II	
GAM236 PAX2	AGGGACAGG--CGAAGGACT 3496 CATT C	
	AGGGATAG CGAAGGACT	
	TCCCTGTC GCTTCCTGA	
	C__ I	
GAM236 PRKG1	GGCATGCCAGT-GAAGGACTC 3504 AGGGATA ATTC	
	GC GAAGGACTCG	
	CG CTCCTGAGT	
	CGTA__ GTCA	
GAM236 WBSCR5	TCACTACTT--CTCTAGACTCTC 3505 GCA T	
	TCACTACTTC CTAG TTCTC	
	AGTGATGAAG GATC GAGAG	
	A__ T	
GAM236 ZNF146	CTACCTT-CACTAGTTTCTC 3500 TCACTA GC	
	CTTC ACTAGTTTCT	
	GAAG TGATCAAAGA	
	G_____	
GAM237 ABCA4	CAATATGGAGGCCAAAGCTG 3516 AGAT I	
	AATATGGAGG AGGT	

	TTATACCTCC	TTCG		
	GGT_ A			
GAM237 ABCA4	CAATATGGAGGCCAAAGCTG	3516 ATCA	AGAT G G	
	ATATGGAGG AG TG			
	TATACCTCC TC AC			
	_____ GGTT G G			
GAM237 AFM	TCAATATGGAGTAAAATAG	3520	_ II	
	TCAATATGGAG GAGATA			
	AGTTATACCTC TTTTAT			
	A CI			
GAM237 AFM	TCAATATGGAGTAAAATAG	3520 AT	_ TGG	
	CAATATGGAG GAGATAGG			
	GTTATACCTC TTTTATCT			
	_____ A III			
GAM237 AP2B1	ATCAATATGGA---ATATGTG	3514	GAGATAG	
	ATCAATATGGAG GTG			
	TAGTTATACCTT CAC			
	ATA_____			
GAM237 AP2B1	ATCAATATGGA---ATATGTG	3514	GAGATAI	
	ATCAATATGGAG			
	TAGTTATACCTT			
	ATACACI			
GAM237 ARAF1	AATGATGGAGGAGACAGGGGG	3508 T	TGI	
	A ATGGAGGAGATAGG			
	I			
	A TACCTCCTCTGTCC			
	C CCI			
GAM237 ARAF1	AATGATGGAGGAGACAGGGGG	3508 ATCAAT	T A	
	ATGGAGGAGATAGG GG			
	TACCTCCTCTGTCC CC			
	C_____ _ C			
GAM237 CLCA2	TCAATATGGATGCAGAT-GGT	3519	GG_ A I	
	CAATATGGA AGAT GG			
	GTTATACCT TCTA CC			
	ACG _ I			
GAM237 CLCA2	TCAATATGGATGCAGAT-GGT	3519 AT	GGAGA	
	CAATATGGA TAGGTGG			
	GTTATACCT GTCTACC			
	_____ AC_____			
GAM237 GCLM	ATATGGAGGCAAGATAAGT	3512	_ III	
	ATATGGAGG AGATAGG			

	TATACCTCC TCTATTC			
	GT AII			
GAM237 GFPT2	TATAGGAGGC-ATAGGTGGA	3518	TAT_ AG	II
	GGAGG ATAGGTGG			
	CCTCC TATCCACC			
	ATAT G_ TI			
GAM237 IRAK4	AAAATGGTTGAGATAGGTG	3509	AAT AG	II
	ATGG GAGATAGGT			
	TACC CTCTATCCA			
	TTT AA CI			
GAM237 IRAK4	AAAATGGTTGAGATAGGTG	3509	ATCAAT AG	G
	ATGG GAGATAGGTG			
	TACC CTCTATCCAC			
	_____ AA A			
GAM237 LZTFL1	AATATGGA-GAGACAGGTG	3510	G I	
	AATATGGAG AGATAGGT			
	TTATACCTC TCTGTCCA			
	- C			
GAM237 LZTFL1	AATATGGA-GAGACAGGTG	3510	ATCAAT G	
	ATGGAG AGATAGGTG			
	TACCTC TCTGTCCAC			
	_____ -			
GAM237 NPY2R	TGGAGGAGAAGTTTGGTGG	3521	TA_____ IIIC	
	TGGAGGAGA GGTG			
	ACCTCCTCT CCAC			
	TCAAAA CIII			
GAM237 OAS2	ATATCTGAGGAGATATCTGGTGGG	3511	TATG _____ I	
	GAGGAGATA GGTGG			
	CTCCTCTAT CCACC			
	A_____ AGA I			
GAM237 PACE4	CAATATGGAGAAAGACGAGGTGCGA	3515	A _ _ GGI	
	TATGGAGGA GAT AGGT			
	ATACCTCTT CTG TCCA			
	- T C GII			
GAM237 PACE4	CAATATGGAGAAAGACGAGGTGCGA	3515	ATCA _ _ G I	
	ATATGGAGGA GAT AGGT GA			
	TATACCTCTT CTG TCCA CT			
	_____ T C G T			
GAM237 PTPN1	ATAAATATGGAGTGGAGAGTTG	3513	ATC GA T G GA	
	AATATGGAG GA AG TG			

	TTATACCTC CT TC AC		
	TAT AC C A II		
GAM237 PTPN1	ATAAATATGGAGTGGAGAGTTG 3513 C	___	TAGGI
	AATATGGA GGAGA		
	TTATACCT CCTCT		
	T CA CAIII		
GAM237 RBBP5	CAATATGGA-AATATAGGAGG 3517 _	AG	TGI
	AATATGGAGG ATAGG		
	TTATACCTTT TATCC		
	G A_ TCI		
GAM237 RBBP5	CAATATGGA-AATATAGGAGG 3517 ATCA	AG	T
	ATATGGAGG ATAGG GG		
	II		
	TATACCTTT TATCC CC		
	___ A_ T		
GAM238 ACHE	TGGGAGGCACGGC-CCCCTCCTCC 3542	G	G GCG I
	TGGGAGGCA GGCTCC CT CC		
	II II		
	ACCCTCCGT CCGGGG GA GG		
	G _ GGA I		
GAM238 ALPI	GGGAAGAAGGGCCCCGCTGCGCC 3535 TG	C	I
	GGAGG AGGGCTCCGCTGCGCC		
	CCTTC TCCCGGGGCGACGCGG		
	_ T T		
GAM238 APBA2	GGGAGGCAGGGGTGACGGCTGC 3533 TG	CTCC_	GCC
	GGAGGCAGGG GCTGC		
	CCTCCGTCCC CGACG		
	_ CACTGC GII		
GAM238 CBFA2T2	TGGGAGGCAGAGGTTACCG-TGAGCC 3537	CT_	C C II
	TGGGAGGCAGGG CCG TG GCC		
	II		
	ACCCTCCGTCTC GGC AC CGG		
	CAAT _ T II		
GAM238 CD3Z	GAGGCAGGGAGGCTCCCGCTGC 3525 T_	AGGGC	G
	GGGAGGC TCCGCTGC CC		
	II		
	CCCTCCG GGGCGACG GG		
	CGT A_ _		
GAM238 EPHA8	GGGGGGCAGGGCTGGGCAGCTGGGC 3532 T A	CC_	C CII
	GGG GGCAGGGCT GCTG GC		
	II		
	CCC CCGTCCCGA CGAC CG		
	_ _ CCCGT C AII		
GAM238 FANCF	TGGGAGGCAGAGGTTGCACTGAGC 3538	CTC_	C CI
	TGGGAGGCAGGG CGCTG GC		
	II		

	ACCCTCCGTCTC GTGAC CG		
	CAAC T II		
GAM238 FGFR2	TGGGAGGCATGGTCTCC-CTGC 3536	G _ G GCC	
	TGGGAGGCA GG CTCC CTGC		
	II		
	ACCCTCCGT CC GAGG GACG		
	A A _ III		
GAM238 HMGE	AGGCAGGGCCCTGCTGAGC 3524 TGGGAGGC	C C	
	AGGGCTC GCTG GC		
	II		
	TCCCGGG CGAC CG		
	_____ A T		
GAM238 HMOX1	GGCAGGGCTGACCCCTTCGCC 3529 TGGGA AG	GC G	
	GGC GGCTCC TGC CC		
	II		
	CCG CTGGGG GCG GG		
	_____ A_ AA G		
GAM238 IRAK1	GGAGGCAGGGTTCCACTCTGCC 3528 TGGG	C GC	
	AGGCAGGG TCCGCT GCC		
	TCCGTCCC AGGTGA CGG		
	_____ A GA		
GAM238 LENG4	GGCAGGCAGAGCAGTGTCCGCTGCG 3531 TG G	_____ CCII	
	G AGGCAGGGC TCCGCTGCG		
	I		
	C TCCGTCTCG AGGCGACGC		
	___ G TCAC AIII		
GAM238 MAP4	TGTGGGGCAGGGCTGCTGCTGCCCC 3540 TG_ A	CC _ II	
	GG GGCAGGGCT GCTGC GCC		
	CC CCGTCCCGA CGACG CGG		
	ACA _ _ A GG		
GAM238 PVRL2	TGGGAGGCAGTGTTCCTACT 3541	GGC GCGC	
	TGGGAGGCAG TCCGCT		
	ACCCTCCGTC AGGTGA		
	ACA IIIC		
GAM238 RAB36	TGGGAGGCAGAGGTTGCACTGAGCC 3539	CTC_ C II	
	TGGGAGGCAGGG CGCTG GCC		
	ACCCTCCGTCTC GTGAC CGG		
	CAAC T II		
GAM238 SAS	GGGAGGCAGAGGTTGCGGTGAGCC 3530 TG	CTC_ C C I	
	GGAGGCAGGG CG TG GCC		
	CCTCCGTCTC GC AC CGG		
	_____ CAAC C T C		
GAM238 SREBF2	GGAGGCAGGGGCTTGGCAGC 3526 TGGG	_ CC T GC	
	AGGCAGGG CT GC GC		

	TCCGTCCC GA CG CG		
	_____ C AC T AA		
GAM238 SURF4	GGGAGGCA-GGCTCGGGGCTGGGCC 3534 TG	G C__ C I	
	GGAGGCAGG CTC GCTG GCC		
	CCTCCGTCC GAG CGAC CGG		
	___ _ CCC C C		
GAM238 WASF3	GGAG-CAGGGCTCCTTTGCAGCC 3527 TGGGA	GC _	
	GGCAGGGCTCC TGC GCC		
	TCGTCCCGAGG ACG CGG		
	_____ AA T		
GAM239 ADAM29	TGGGAGGGTGTACCCGAGGT 3561	_____ CAGGTG	
	TGGGAGG TCACCCGAGGT		
	ACCCTCC AGTGGGCTCCA		
	CAC GTG		
GAM239 ADAM29	TGGGAGGGTGTACCCGAGGT 3561	_____	
	TGGGAGG TCACCCGAGG		
	ACCCTCC AGTGGGCTCC		
	CAC A		
GAM239 ALDH1B1	GGGTGGATCACCTGAGGTCAGG 3552 T GA	C TG	
	GG GGTACC GAGGTCAGG		
	CC CTAGTGG CTCCAGTCC		
	_ AC A TI		
GAM239 ALDH1B1	GGGTGGATCACCTGAGGTCAGG 3552 GGA	C I	
	GGTCACC GAGGTCAG		
	CTAGTGG CTCCAGTC		
	CAC A I		
GAM239 CLCN7	GGGAGGTCACCCTCGAGGCCGGG 3554 G	_____ AGI	
	AGGTCACCC GAGGTC		
	TCCAGTGGG CTCCGG		
	_ AG CII		
GAM239 CLCN7	GGGAGGTCACCCTCGAGGCCGGG 3554 TG	_____ A TGI	
	GGAGGTCACCC GAGGTC GG		
	CCTCCAGTGGG CTCCGG CC		
	_____ AG C CII		
GAM239 COX15	TGGGCGGATTACCTGAGGTCAGG 3565 A TC_ C	TGI	
	TGGG GG ACC GAGGTCAGG		
	ACCC CC TGG CTCCAGTCC		
	G TAA A		
GAM239 COX15	TGGGCGGATTACCTGAGGTCAGG 3565 G A TC_ C	I	
	GG GG ACC GAGGTCAG		

		CC CC TGG CTCCAGTC				
		_ G TAA A I				
GAM239 DFFB		GGCAGATCACCTGAGGTCAGG	3555	G	C	I
		G AGGTCACC GAGGTCAG				
		I				
		C TCTAGTGG CTCCAGTC				
		G A I				
GAM239 DFFB		GGCAGATCACCTGAGGTCAGG	3555	TG G	C	TG
		G AGGTCACC GAGGTCAGG				
		I				
		C TCTAGTGG CTCCAGTCC				
		_ G A TI				
GAM239 DFFB		TGGGCGGATCACCTGAGGTCAGG	3563	A _	C	TGI
		TGGG GG TCACC GAGGTCAGG				
		ACCC CC AGTGG CTCCAGTCC				
		G T A III				
GAM239 DFFB		TGGGCGGATCACCTGAGGTCAGG	3563	GA	C	I
		GG GGTACC GAGGTCAG				
		CC CTAGTGG CTCCAGTC				
		GC A I				
GAM239 FCAR		TGGGTGGATCACCTGAGGTCAGG	3568	A _	C	TGI
		TGGG GG TCACC GAGGTCAGG				
		ACCC CC AGTGG CTCCAGTCC				
		A T A III				
GAM239 FCAR		TGGGTGGATCACCTGAGGTCAGG	3568	GA	C	I
		GG GGTACC GAGGTCAG				
		CC CTAGTGG CTCCAGTC				
		AC A I				
GAM239 GNE		GGGCGGATCACCTGAGGTCAGG	3551	T GA	C	TG
		GG GGTACC GAGGTCAGG				
		CC CTAGTGG CTCCAGTCC				
		_ GC A TI				
GAM239 GNE		GGGCGGATCACCTGAGGTCAGG	3551	GGA	C	I
		GGTCACC GAGGTCAG				
		CTAGTGG CTCCAGTC				
		CGC A I				
GAM239 HLCS		GGTGGATCAC--GAGGTCAGG	3547	_ A	CC	I
		G GGTCAC GAGGTCAG				
		I				
		C CTAGTG CTCCAGTC				
		CCA _ _ I				
GAM239 HLCS		GGTGGATCAC--GAGGTCAGG	3547	TGGGA	CC	T
		GGTCAC GAGGTCAGG				

		CTAGTG CTCCAGTCC				
		AC___ T				
GAM239 HYAL4		GGCAGATCACTTGAGGTCAGG	3556	G	CC	I
		G AGGTCAC GAGGTCAG				
		I				
		C TCTAGTG CTCCAGTC				
		G AA I				
GAM239 HYAL4		GGCAGATCACTTGAGGTCAGG	3556	TG G	CC	TG
		G AGGTCAC GAGGTCAGG				
		I				
		C TCTAGTG CTCCAGTCC				
		_ G AA TI				
GAM239 IL11		GGAGGATCACCTGAGGTCAGG	3545	GA	C	I
		GGTCACC GAGGTCAG				
		CTAGTGG CTCCAGTC				
		TC A I				
GAM239 IL11		GGAGGATCACCTGAGGTCAGG	3545	TG A	C	TG
		GG GGTCACC GAGGTCAGG				
		TC CTAGTGG CTCCAGTCC				
		_ _ A TC				
GAM239 KCNJ15		TCACTCCGCAGGTCAGGTG	3558	_ _		III
		TCAC CCG AGGTCAGGT				
		AGTG GGC TCCAGTCCA				
		A G CII				
GAM239 MEFV		TGGGTGCATCACCTGAGGTCAGG	3566	AG_	C	TGI
		TGGG GTCACC GAGGTCAGG				
		ACCC TAGTGG CTCCAGTCC				
		ACG A III				
GAM239 MEFV		TGGGTGCATCACCTGAGGTCAGG	3566	GAG	C	I
		GG GTCACC GAGGTCAG				
		CC TAGTGG CTCCAGTC				
		ACG A I				
GAM239 MEFV		GGGTGGATCACCTGAGGTCAGG	3552	GGA	C	I
		GGTCACC GAGGTCAG				
		CTAGTGG CTCCAGTC				
		CAC A I				
GAM239 MEFV		GGGTGGATCACCTGAGGTCAGG	3552	T GA	C	TG
		GG GGTCACC GAGGTCAGG				
		CC CTAGTGG CTCCAGTCC				
		_ AC A TI				
GAM239 MHC2TA		TGGGTGGATCACCCGAGGTCA	3562	A _		GGTG
		TGGG GG TCACCCGAGGTCA				

	ACCC CC AGTGGGCTCCAGT				
	A T III G				
GAM239 MHC2TA	TGGGTGGATCACCCGAGGTCA	3562	GA		I
	GG GGTACCCGAGGTC				
	II				
	CC CTAGTGGGCTCCAG				
	AC I				
GAM239 MICB	GGCAGATCACCTGAGGTCAGG	3555	G C		I
	G AGGTCACC GAGGTCAG				
	I				
	C TCTAGTGG CTCCAGTC				
	G A I				
GAM239 MICB	GGCAGATCACCTGAGGTCAGG	3555	TG G C		TG
	G AGGTCACC GAGGTCAGG				
	I				
	C TCTAGTGG CTCCAGTCC				
	_ G A TI				
GAM239 MLANA	GGCAGATCACCTGAGGTCAGG	3555	G C		I
	G AGGTCACC GAGGTCAG				
	I				
	C TCTAGTGG CTCCAGTC				
	G A I				
GAM239 MLANA	GGCAGATCACCTGAGGTCAGG	3555	TG G C		TG
	G AGGTCACC GAGGTCAGG				
	I				
	C TCTAGTGG CTCCAGTCC				
	_ G A TI				
GAM239 MPL	TGGGTGGATCACCCGAGGT TAGG	3567	A _		C TGI
	TGGG GG TCACCCGAGGT AGG				
	ACCC CC AGTGGGCTCCA TCC				
	A T A III				
GAM239 MPL	TGGGTGGATCACCCGAGGT TAGG	3567	GA		CAGI
	GG GGTACCCGAGGT				
	II				
	CC CTAGTGGGCTCCA				
	AC ATCI				
GAM239 NCOA6	GGGTGGATCACTTGAGGTCAGG	3553	GGA CC		I
	GGTCAC GAGGTCAG				
	CTAGTG CTCCAGTC				
	CAC AA I				
GAM239 NCOA6	GGGTGGATCACTTGAGGTCAGG	3553	T GA CC		TG
	GG GGTAC GAGGTCAGG				
	II				
	CC CTAGTG CTCCAGTCC				
	_ AC AA TI				
GAM239 NDRG3	GGTGGATCACCTGAGGTCAGG	3548	_ A C		I
	G GGTACACC GAGGTCAG				
	I				

		C CTAGTGG CTCCAGTC			
		A _ A I			
GAM239 NDRG3		GGTGGATCACCTGAGGTCAGG	3548	TGGGA C TG	
		GGTCACC GAGGTCAGG			
		CTAGTGG CTCCAGTCC			
		AC _ A TC			
GAM239 PABPN1		TGGGAA---ACCCGAGGTCA	3569	GTC GG	
		TGGGAG ACCCGAGGTCA			
		ACCCTT TGGGCTCCAGT			
		_ II			
GAM239 PABPN1		TGGGAA---ACCCGAGGTCA	3569 _	GTC	
		GGGAG ACCCGAGGTC			
		CCCTT TGGGCTCCAG			
		A _			
GAM239 PDE6B		GGTGATCACCTGAGGTCAGG	3550	GA C I	
		GGTCACC GAGGTCAG			
		CTAGTGG CTCCAGTC			
		CA A I			
GAM239 PDE6B		GGTGATCACCTGAGGTCAGG	3550	TGGGA C T	
		GGTCACC GAGGTCAGG			
		CTAGTGG CTCCAGTCC			
		A _ A T			
GAM239 PIK3CD		GGGTGGATCACCTGAGGTCAGG	3552	GGA C I	
		GGTCACC GAGGTCAG			
		CTAGTGG CTCCAGTC			
		CAC A I			
GAM239 PIK3CD		GGGTGGATCACCTGAGGTCAGG	3552	T GA C TG	
		GG GGTCACC GAGGTCAGG			
		CC CTAGTGG CTCCAGTCC			
		_ AC A TI			
GAM239 SAS		GGGTGGATCACCTGAGGTCAGG	3552	GGA C I	
		GGTCACC GAGGTCAG			
		CTAGTGG CTCCAGTC			
		CAC A I			
GAM239 SAS		GGGTGGATCACCTGAGGTCAGG	3552	T GA C TG	
		GG GGTCACC GAGGTCAGG			
		CC CTAGTGG CTCCAGTCC			
		_ AC A TI			
GAM239 SCML2		TGGGCGGATCACCTGAGGTCAGG	3563	A _ C TGI	
		TGGG GG TCACC GAGGTCAGG			

	ACCC CC AGTGG CTCCAGTCC			
	G T A III			
GAM239 SCML2	TGGGCGGATCACCTGAGGTCAGG 3563	GA	C	I
	GG GGTCACC GAGGTCAG			
	II IIIII IIIIIII			
	CC CTAGTGG CTCCAGTC			
	GC A I			
GAM239 SH3BP2	TGGGCGGATCAGTTGAGGTCAGG 3564	A _	CCC	TGI
	TGGG GG TCA GAGGTCAGG			
	IIII II III IIIIIII			
	ACCC CC AGT CTCCAGTCC			
	G T CAA III			
GAM239 SH3BP2	TGGGCGGATCAGTTGAGGTCAGG 3564	GA	CCC	I
	GG GGTC A GAGGTCAG			
	II IIIII IIIIIII			
	CC CTAGT CTCCAGTC			
	GC CAA I			
GAM239 SH3BP2	TGGGCAGATCACCTGAGGTCAGG 3559	_	C	TGI
	TGGG AGGTCACC GAGGTCAGG			
	IIII IIIIIII IIIIIII			
	ACCC TCTAGTGG CTCCAGTCC			
	G A III			
GAM239 SH3BP2	TGGGCAGATCACCTGAGGTCAGG 3559	G	C	I
	GG AGGTCACC GAGGTCAG			
	II IIIIIII IIIIIII			
	CC TCTAGTGG CTCCAGTC			
	G A I			
GAM239 SH3GL3	GGCGGATCAC--GAGGTCAGG 3546	_ A	CC	I
	G GGTCAC GAGGTCAG			
	I IIIII IIIIIII			
	C CTAGTG CTCCAGTC			
	CCG _ _ I			
GAM239 SH3GL3	GGCGGATCAC--GAGGTCAGG 3546	TGGGA	CC	T
	GGTCAC GAGGTCAGG			
	IIII IIIIIII			
	CTAGTG CTCCAGTCC			
	GC _ _ T			
GAM239 SHOX	GGCAGATCACCTGAGGTCAGG 3555	G	C	I
	G AGGTCACC GAGGTCAG			
	I IIIIIII IIIIIII			
	C TCTAGTGG CTCCAGTC			
	G A I			
GAM239 SHOX	GGCAGATCACCTGAGGTCAGG 3555	TG G	C	TG
	G AGGTCACC GAGGTCAGG			
	I IIIIIII IIIIIII			
	C TCTAGTGG CTCCAGTCC			
	_ G A TI			
GAM239 SHOX	GGGTGGATCACCTGAGGTCAGG 3552	GGA	C	I
	GGTCACC GAGGTCAG			
	IIIIII IIIIIII			

		CTAGTGG CTCCAGTC				
		CAC A I				
GAM239 SHOX		GGGTGGATCACCTGAGGTCAGG	3552	T GA	C	TG
		GG GGTCAACC GAGGTCAGG				
		CC CTAGTGG CTCCAGTCC				
		_ AC A TI				
GAM239 SLA2		TGGGTGGATCACCTGAGGTCAGG	3568	A _	C	TGI
		TGGG GG TCACC GAGGTCAGG				
		ACCC CC AGTGG CTCCAGTCC				
		A T A III				
GAM239 SLA2		TGGGTGGATCACCTGAGGTCAGG	3568	GA	C	I
		GG GGTCAACC GAGGTCAG				
		CC CTAGTGG CTCCAGTC				
		AC A I				
GAM239 SMAC		GGGTGGATCACTTGAGGTCAGG	3553	GGA	CC	I
		GGTCAC GAGGTCAG				
		CTAGTG CTCCAGTC				
		CAC AA I				
GAM239 SMAC		GGGTGGATCACTTGAGGTCAGG	3553	T GA	CC	TG
		GG GGTCAAC GAGGTCAGG				
		CC CTAGTG CTCCAGTCC				
		_ AC AA TI				
GAM239 SPN		GGTAGATCACCTGAGGTCAGG	3557	GG	C	I
		AGGTCACC GAGGTCAG				
		TCTAGTGG CTCCAGTC				
		CA A I				
GAM239 SPN		GGTAGATCACCTGAGGTCAGG	3557	TGGG	C	TG
		AGGTCACC GAGGTCAGG				
		TCTAGTGG CTCCAGTCC				
		CA_ A TI				
GAM239 SULT2B1		TGGGTGGATCACCTGAGGTCAGG	3568	A _	C	TGI
		TGGG GG TCACC GAGGTCAGG				
		ACCC CC AGTGG CTCCAGTCC				
		A T A III				
GAM239 SULT2B1		TGGGTGGATCACCTGAGGTCAGG	3568	GA	C	I
		GG GGTCAACC GAGGTCAG				
		CC CTAGTGG CTCCAGTC				
		AC A I				
GAM239 TAPBP		TGGGCAGATCACCTGAGGTCAGG	3559	_	C	TGI
		TGGG AGGTCACC GAGGTCAGG				

	ACCC TCTAGTGG CTCCAGTCC			
	G A III			
GAM239 TAPBP	TGGGCAGATCACCTGAGGTCAGG	3559	G C I	
	GG AGGTCACC GAGGTCAG			
	II IIIIIII IIIIIII			
	CC TCTAGTGG CTCCAGTC			
	G A I			
GAM239 TGFB1	GGGGGTGCGCCCGAGGTCTGG	3549	GA CA_ AGI	
	GGT CCCGAGGTC			
	III IIIIIII			
	CCA GGGCTCCAG			
	C_ CGC ACI			
GAM239 TGFB1	GGGGGTGCGCCCGAGGTCTGG	3549	T AG CA A TG	
	GGG GT CCCGAGGTC GG			
	III II IIIIIII II			
	CCC CG GGGCTCCAG CC			
	_ A_ C_ A CC			
GAM239 TNFRSF10B	GGTGGATCACCTGAGGTCAGG	3548	_ A C I	
	G GGTCAACC GAGGTCAG			
	I IIIIIII IIIIIII			
	C CTAGTGG CTCCAGTC			
	A_ A I			
GAM239 TNFRSF10B	GGTGGATCACCTGAGGTCAGG	3548	TGGGA C TG	
	GGTCAACC GAGGTCAGG			
	IIIIII IIIIIII			
	CTAGTGG CTCCAGTCC			
	AC___ A TC			
GAM239 TPMT	TGGGTAGATCACCTGAGGTCAGG	3560	_ C TGI	
	TGGG AGGTCACC GAGGTCAGG			
	III IIIIIII IIIIIII			
	ACCC TCTAGTGG CTCCAGTCC			
	A A III			
GAM239 TPMT	TGGGTAGATCACCTGAGGTCAGG	3560	G C I	
	GG AGGTCACC GAGGTCAG			
	II IIIIIII IIIIIII			
	CC TCTAGTGG CTCCAGTC			
	A A I			
GAM239 TRPV1	TGGGCGGATCACCTGAGGTCAGG	3563	A _ C TGI	
	TGGG GG TCACC GAGGTCAGG			
	III II IIIIIII IIIIIII			
	ACCC CC AGTGG CTCCAGTCC			
	G T A III			
GAM239 TRPV1	TGGGCGGATCACCTGAGGTCAGG	3563	GA C I	
	GG GGTCACC GAGGTCAG			
	II IIIIIII IIIIIII			
	CC CTAGTGG CTCCAGTC			
	GC A I			
GAM239 TUFT1	TGGGTGGATCACCTGAGGTCAGG	3568	A _ C TGI	
	TGGG GG TCACC GAGGTCAGG			
	III II IIIIIII IIIIIII			

	ACCC CC AGTGG CTCCAGTCC			
	A T A III			
GAM239 TUFT1	TGGGTGGATCACCTGAGGTCAGG 3568	GA	C	I
	GG GGTCACC GAGGTCAG			
	II IIIII IIIIIII			
	CC CTAGTGG CTCCAGTC			
	AC A I			
GAM239 VHL	TGGGCGGATCACCTGAGGTCAGG 3563	A _	C	TGI
	TGGG GG TCACC GAGGTCAGG			
	IIII II IIIII IIIIIII			
	ACCC CC AGTGG CTCCAGTCC			
	G T A III			
GAM239 VHL	TGGGCGGATCACCTGAGGTCAGG 3563	GA	C	I
	GG GGTCACC GAGGTCAG			
	II IIIII IIIIIII			
	CC CTAGTGG CTCCAGTC			
	GC A I			
GAM240 ABCC1	AAAACTCCTCCGTGGGAAGCACC 3572	TAAC _	C_	TTI
	AC CCTCCGTGGGA CACC			
	II IIIIIIIII IIII			
	TG GGAGGCACCCT GTGG			
	TT_ A TC TII			
GAM240 FCN2	CACCCTCCGCTGGAAACCT 3576	TAACAC	G	CC
	CCTCCGT GGA ACCT			
	IIIIII III IIII			
	GGAGGCG CCT TGGA			
	_____ A TT			
GAM240 HOXB3	AACACCCTCCTCTGAGCCCA 3574	TA	G_	A CCT
	ACACCCTCC TGGG CCA			
	IIIIIIII III III			
	TGTGGGAGG ACTC GGT			
	_____ AG G CII			
GAM240 NYX	CACCCAGCCGTGGGACC-CCT 3575	TAACA CT		A
	CC CCGTGGGACC CCT			
	II IIIIIIIII III			
	GG GGCACCCTGG GGA			
	_____ TC _			
GAM240 SFRP5	AACACCCTCCAGTAGGGCC 3573	TA	_	A ACCT
	ACACCCTCC GTGGG CC			
	IIIIIIII IIII II			
	TGTGGGAGG CATCC GG			
	_____ T C CIII			
GAM240 SOST	CCCTGCCCGTGGGACC-CCT 3577	TAACACC		A
	CTCCGTGGGACC CCT			
	IIIIIIIIII III			
	GGGGCACCCTGG GGA			
	_____ _			
GAM241 KIF1B	TAACTGTTGCAGTTCTATGCTCAC 3582	C_ _	_	CGGTGI
	TAACTGTTGT CTA CTCAC			
	IIIIIIII III IIII			

	ATTGACAACG GAT GAGTG		
	TCAA AC IIIGTG		
GAM241 KIF1B	TAACTGTTGCAGTTCTATGCTCAC 3582	C___ _	IIIG
	TAACTGTTGT CTA CTCA		
	III		
	ATTGACAACG GAT GAGT		
	TCAA AC GIII		
GAM241 PDE4D	TACCTGTT-TCTTT-TCACCGGTG 3583 AA_	G CTAC	I
	CTGTT TC TCACCGGT		
	GACAA AG AGTGGCCA		
	ATG _ AAA_ I		
GAM241 PDE4D	TACCTGTT-TCTTT-TCACCGGTG 3583 TAA	G CTAC	
	CTGTT TC TCACCGGTG		
	GACAA AG AGTGGCCAC		
	ATG _ AAA_		
GAM241 PPT2	CTGTTGTC---CTCACAGG 3580	TAC CG	
	CTGTTGTCC TCAC		
	GACAACAGG AGTG		
	___ TC		
GAM241 PPT2	CTGTTGTC---CTCACAGG 3580 TAACTG	TAC C	
	TTGTCC TCAC G		
	I		
	AACAGG AGTG C		
	___ T		
GAM241 TCF7	CTGTTGTCC-ACT-ACTGG 3581	T C CGI	
	CTGTTGTCC ACT AC		
	GACAACAGG TGA TG		
	_ _ ACC		
GAM241 TCF7	CTGTTGTCC-ACT-ACTGG 3581 TAACTG	T C C	
	TTGTCC ACT AC GG		
	AACAGG TGA TG CC		
	___ A		
GAM242 CCNK	GGCACTGATGAGGCTACTC 3592 A	_ II	
	GG ACTGATGAGGTT CT		
	CC TGA TACTCCGA GA		
	G T GI		
GAM242 CCNK	GGCACTGATGAGGCTACTC 3592 CAGGA	_ I	
	ACTGATGAGGTT CTC		
	TGA TACTCCGA GAG		
	G___ T A		
GAM242 HPS3	CAGTGA ACTGATGTTGTTC 3588	_ AG TCI	
	CAG GA ACTGATG GTTC		

	GTC CTTGACTAC CAAG		
	A AA III		
GAM242 HPS3	CAGTGAAGTATGTTGTTCTC 3588	AG II	
	CAG GAACTGATG GTT		
	III IIIIIII III		
	GTC CTTGACTAC CAA		
	A AA GI		
GAM242 IGHMBP2	CAGGTACATCATCTGAGGTTCTC 3590	A TGA___	III
	CAGG AC TGAGGTTCTC		
	III II IIIIIIIII		
	GTCC TG ACTCCAAGAG		
	A TAGTAG III		
GAM242 IGHMBP2	CAGGTACATCATCTGAGGTTCTC 3590	AGGAACTGA	I
	TGAGGTTCT		
	IIIIIIII		
	ACTCCAAGA		
	ATGTAGTAG I		
GAM242 PPP1R12B	GGAAGTAAAGATTGAGGTTCT 3591	___	IIIA
	GGAAGTGA TGAGGTTCT		
	IIIIII IIIIIII		
	CCTTGATT ACTCCAAG		
	TCTA AIII		
GAM242 PPP1R12B	GGAAGTAAAGATTGAGGTTCT 3591	CAGG ___	CII
	AACTGA TGAGGTTCT		
	IIII IIIIIII		
	TTGATT ACTCCAAGA		
	___ TCTA ACI		
GAM242 PRDM2	CAGGTGCACCTGATCTGAGGTTCTC 3589	AGGAA ___	I
	CTGA TGAGGTTCT		
	III IIIIIII		
	GACT ACTCCAAGA		
	GTG___ AG I		
GAM242 PRDM2	CAGGTGCACCTGATCTGAGGTTCTC 3589	AA___	III
	CAGG CTGA TGAGGTTCTC G		
	III III IIIIIII I		
	GTCC GACT ACTCCAAGAG C		
	ACGTG AG III		
GAM242 RASA1	AGGCAGCTGATGAGGTTGTC 3586	AA_ CTII	
	AGG CTGATGAGGTT		
	III IIIIIIIII		
	TCC GACTACTCCAA		
	GTC CAGI		
GAM242 RASA1	AGGCAGCTGATGAGGTTGTC 3586	CA AA_ C I	
	GG CTGATGAGGTT TC		
	II IIIIIIIII II		
	CC GACTACTCCAA AG		
	___ GTC C A		
GAM242 ZNF18	AGGGGCTGATCTGAGGTTCT 3587	AA ___	III
	AGG CTGA TGAGGTTCT		
	III III IIIIIII		

	TCC GACT ACTCCAAG			
	CC AG AII			
GAM242 ZNF18	AGGGGCTGATCTGAGGTTCT	3587	CA AA	CI
	GG CTGA TGAGGTTCT			
	II IIII IIIIIII			
	CC GACT ACTCCAAGA			
	__ CC AG AI			
GAM243 AIM2	CAGCCTCCTGATC-CCTG-GGGC	3602	GC	CTC GA
	AGCCTCCTG TCCC GGGC			
	IIIIII III III			
	TCGGAGGAC AGGG CCCG			
	__ T__ AC			
GAM243 BMP8	CAGCCACTCCTGCTCTGCCG	3596	_ AGC	C AGGG
	GC CTCCTGCTCT CCG			
	II IIIIIII III			
	CG GAGGACGAGA GGC			
	T GT_ C CIII			
GAM243 CDH23	GCAGCCCGCGTCCCTCTCTCCCGAG	3606	___ G	GGCII
	GCAGCC TCCT CTCTCCCGAG			
	IIII III IIIIIII			
	CGTCGG AGGG GAGAGGGCTC			
	GCGC A IIICG			
GAM243 COL1A1	GCCTCCTGCTCCGACCCCGAGG	3615	GCAGCC	___ C
	TCCTGCTCT CCCGAGGG			
	IIIIII IIIIIII			
	AGGACGAGG GGGCTCCT			
	___ CTG C			
GAM243 CRAT	CAGTCTCCTGCTCT--GGAGGGC	3603	GC C	CCC
	AG CTCCTGCTCT GAGGGC			
	II IIIIIII IIIII			
	TC GAGGACGAGA CTCCCG			
	__ A C__			
GAM243 DPEP1	GCCTCCTGC-CTCCC-AGG	3617	GCAGCC	T G
	TCCTGC CTCCC AGG			
	IIII IIII III			
	AGGACG GAGGG TCC			
	___ - -			
GAM243 FOXO1A	GCCGCTTGCTCTCCCCAGCGGC	3616	GCAGCCTCC	G _
	TGCTCTCCC AG GGC			
	IIIIII II III			
	ACGAGAGGG TC CCG			
	CGA___ G G			
GAM243 HMX1	GCCGCGGCCTGCGCTCCCGAGG	3614	A CT	T GC
	GC GC CCTGC CTCCCGAGG			
	II II IIII IIIIIII			
	CG CG GGACG GAGGGCTCC			
	G CC C II			
GAM243 KCNMB4	AGCCTCCTGCACCCTCGGGCGC	3595	GCAG	TCT GA
	CCTCCTGC CCC GGGC			
	IIIIII III III			

		GGAGGACG GGG CCG		
		_____ T_ AG		
GAM243 KRT18		GCCTCCTGCTCCCCAAAGGG 3620 GCAGCC C		
		TCCTGCTCTCC GAGGG		
		AGGACGAGGGG TTCCC		
		_____ T		
GAM243 MAP3K7IP1		CAGGC-CCTGCTCTCCCGCAGG 3599 GCA TC _ C		
		GCC CTGCTCTCCG AGGG		
		CGG GACGAGAGGGC TCCT		
		TC_ _ G I		
GAM243 MBTPS1		CAGCCTTTCCAGTTCTCCCGAG 3597 GC _ TGC GGC		
		AGCC TCC TCTCCGAG		
		TCGG AGG AGAGGGCTC		
		_ AA TCA AII		
GAM243 MTMR1		GCCTCCTGC-CGCCCCGCCGGC 3621 GCAGCC TT AG		
		TCCTGC C CCG GG		
		AGGACG G GGGC CC		
		_____ _C GG		
GAM243 NCKAP1		GCAGCCTCCTGC-CTTCCG 3612 TC CGAGG		
		GCAGCCTCCTGC TCC		
		CGTCGGAGGACG AGG		
		GA CIIIC		
GAM243 PAX5		GCAGCTCCTCACTGCTCTCC 3605 _ _ CGAGGG		
		GCAGC CTC CTGCTCTCC		
		CGTCG GAG GACGAGAGG		
		AG T IIICGG		
GAM243 PKIA		GCAGCCTCC-GCTCCCGCCGCGG 3609 T _ A GC		
		GCAGCCTCC GCTCTC CCG GG		
		CGTCGGAGG CGAGGG GGC CC		
		_ C G II		
GAM243 PLA2G4C		CAGC-TCCAGGATCTCCCGAGGG 3598 GC C TGC_ C		
		AGC TCC TCTCCCGAGGG		
		TCG AGG AGAGGGCTCCC		
		_ _ TCCT T		
GAM243 PLCG1		GCA-CCTGCTGCTCTCCAACGAGG 3610 G C _ GCI		
		GCA CCT CTGCTCTCC CGAGG		
		CGT GGA GACGAGAGG GCTCC		
		_ C TT		
GAM243 PRKY		GCAGCCTCC-GC-CTCCTGAG 3613 T T C GG		
		GCAGCCTCC GC CTCC GAG		

	CGTCGGAGG CG GAGG CTC		
	— — A II		
GAM243 PTEN	GCAGGCCGGCCGGCTC-CCCGAGGGC 3604	_ T_ T T	II
	GCAG CC CC GCTC CCCGAGGGC		
	CGTC GG GG CGAG GGGCTCCCG		
	C CC C _ II		
GAM243 PTPRJ	GCCGCCTCCTGCCGTCTCC 3607 A	___ CGAGGG	
	GC GCCTCCTGC TCTCC		
	CG CGGAGGACG AGAGG		
	G GC IIICGG		
GAM243 RASGRP2	CAGCCTCCTGC---CCCGA 3600 GC	TCT G	
	AGCCTCCTGC CCCGA		
	TCGGAGGACG GGGCT		
	— — G		
GAM243 RPL18	GCCTCCTGCTCGGCC-AGG 3619 GCAGCC	TC G	
	TCCTGCTC CC AGG		
	AGGACGAG GG TCC		
	— — CC _		
GAM243 SCN2B	GCCTCCTGC-CTCCCCAGG 3618 GCAGCC	T G	
	TCCTGC CTCCC AGG		
	AGGACG GAGGG TCC		
	— — G		
GAM243 SNRPA1	GCAGCCTCCCGTTCCCCCG 3611	C AGGG	
	GCAGCCTCCTG TCTCCG		
	CGTCGGAGGGC AGGGGGC		
	A IIIC		
GAM243 ST5	CAGCATC-TGCTCTCC--AGGGC 3601 GC CTC	CG	
	AGC CTGCTCTCC AGGG		
	TCG GACGAGAGG TCCC		
	— TA_ —		
GAM243 TCF8	GCAGCCTCCTGCACTGGGCCCG 3608	T ___ AGGGC	
	GCAGCCTCCTGC CT CCCG		
	CGTCGGAGGACG GA GGGC		
	T CCC IIICG		
GAM244 ASTN	TAAG-ACCTGTTT--GGCAGC 3640 TA	_ AI	
	AGGACCTGTTTGG GGC		
	TTCTGGACAAACC TCG		
	A_ G II		
GAM244 ASTN	TAAG-ACCTGTTT--GGCAGC 3640 TA	GG A	
	AGGACCTGTTT GGCAGC		

	TTCTGGACAAA CCGTCG	
	A_ _ I	
GAM244 CA7	AGGGCCTGCCCCGTGGCAGCAGG 3626 _ A G I	
	GG CCTGTTTG GGCAGCAG	
	CC GGACGGGC CCGTCGTC	
	C _ A I	
GAM244 CA7	AGGGCCTGCCCCGTGGCAGCAGG 3626 TAA A G	
	GG CCTGTTTG GGCAGCAGG	
	CC GGACGGGC CCGTCGTCC	
	_ _ A	
GAM244 CDK10	CCTTTTTCTGGGGGCAGCAG 3627 C_ TTT III	
	CTG GGGGCAGCA	
	GAC CCCCCTCGT	
	GGAAAA _ CII	
GAM244 CDK10	CCTTTTTCTGGGGGCAGCAG 3627 TAAGGAC TTT	
	CTG GGGGCAGCAG	
	GAC CCCCCTCGTC	
	A_ _	
GAM244 FGFR2	CCTGTTTGGGGACAGGCAG 3628 _ _ III	
	CCTGTTTGGGG CAG CA	
	GGACAAACCCC GTC GT	
	T C CII	
GAM244 GRLF1	TAATGGACTGTGTTCTGGGGCAGC 3637 AA C_ _ I	
	GGAC TGT TTGGGGCAG	
	CCTG ACA GACCCCGTC	
	_ AC A I	
GAM244 GRLF1	TAATGGACTGTGTTCTGGGGCAGC 3637 TAA_ C_ _ AGGI	
	GGAC TGT TTGGGGCAGC	
	CCTG ACA GACCCCGTCG	
	ATTA AC A IIIG	
GAM244 HAMP	GACCTATGTTCTGGGGCAGCAGG 3634 ACC _ I	
	TGT TTGGGGCAGCAG	
	ACA GACCCCGTCGTC	
	AT_ A I	
GAM244 HAMP	GACCTATGTTCTGGGGCAGCAGG 3634 TAAGGACC _ I	
	TGT TTGGGGCAGCAGG	
	ACA GACCCCGTCGTCC	
	AT_ A T	
GAM244 INHBC	TAAGCCTCTATTTTGGGCAGCAG 3641 GAC G GI	
	TAAG CTGTTT GGCAGCAG	

	ATTC GATAAA CCCGTCGTC	
	GGA A II	
GAM244 INHBC	TAAGCCTCTATTTTGGGCAGCAG	3641 AAGGAC G I
	CTGTTT GGGCAGCA	
	GATAAA CCCGTCGT	
	TTCGGA A I	
GAM244 MAGEA12	GACTCTGGTCAGGGCAGCAGG	3633 AC T TG I
	CTG T GGGCAGCAG	
	GAC A CCCGTCGTC	
	GA C GT I	
GAM244 MAGEA12	GACTCTGGTCAGGGCAGCAGG	3633 TAAGGAC T TG
	CTG T GGGCAGCAGG	
	GAC A CCCGTCGTCC	
	_____ C GT	
GAM244 MAGEA2	GACTCTGGTCAGGGCAGCAGG	3633 AC T TG I
	CTG T GGGCAGCAG	
	GAC A CCCGTCGTC	
	GA C GT I	
GAM244 MAGEA2	GACTCTGGTCAGGGCAGCAGG	3633 TAAGGAC T TG
	CTG T GGGCAGCAGG	
	GAC A CCCGTCGTCC	
	_____ C GT	
GAM244 MAGEA4	GACTCTGCTCAGGGCAGCAGG	3632 AC TG I
	CTGTT GGGCAGCAG	
	GACGA CCCGTCGTC	
	GA GT I	
GAM244 MAGEA4	GACTCTGCTCAGGGCAGCAGG	3632 TAAGGAC TG
	CTGTT GGGCAGCAGG	
	GACGA CCCGTCGTCC	
	_____ GT	
GAM244 MAGEA9	GACTCTGGTCAGGGCAGCAG	3630 _ T TG II
	GAC CTG T GGGCAGCA	
	CTG GAC A CCCGTCGT	
	A C GT CI	
GAM244 MAGEA9	GACTCTGGTCAGGGCAGCAG	3630 TAAGGAC T TG
	CTG T GGGCAGCAG	
	GAC A CCCGTCGTC	
	_____ C GT	
GAM244 MSI1	GACGCTGTTGGGGGCAGCAGG	3631 AC T I
	CTGTT GGGGCAGCAG	

	GACAA CCCC	CGTCGTC	
	GC	C	I
GAM244 MSI1	GACGCTGTTGGGGG	CAGCAGG	3631 TAAGGAC T
	CTGTT	GGGGCAGCAGG	
	GACAA CCCC	CGTCGTCC	
	_____	C	
GAM244 MYL4	TAAGGTCCT---	TGGGGCAG	3639 A GTT CA
	TAAGG	CCT TGGGGCAG	
	ATTCC	GGA ACCCCGTC	
	A	_____	II
GAM244 MYL4	TAAGGTCCT---	TGGGGCAG	3639 _ A GTT
	AAGG	CCT TGGGGCA	
	TTCC	GGA ACCCCGT	
	A	A	_____
GAM244 NUP98	AGGATGCTGCTTCTGGC	CAGCAGG	3625 GGAC GG I
	CTGTTT	GGCAGCAG	
	GACGAA	CCGTCGTC	
	CTAC	GA I	
GAM244 NUP98	AGGATGCTGCTTCTGGC	CAGCAGG	3625 TAAGGAC GG I
	CTGTTT	GGCAGCAGG	
	GACGAA	CCGTCGTCC	
	CTAC	_____	GA C
GAM244 PCTK1	TGTTTGGGCAGGCAGCAGG		3642 _____ III
	TGTTTGGG	GCAGCAG	
	ACAAACCC	CGTCGTC	
	GTC	CII	
GAM244 RAB6A	AGGAGCCCGGCTGGAGGGCAGCAGG		3624 GGA T _____ I
	CCTG	TTGG GGCAGCAG	
	GGGC	GACC CCGTCGTC	
	C	_____	C TC I
GAM244 RAB6A	AGGAGCCCGGCTGGAGGGCAGCAGG		3624 TAA GA T _____ II
	G	CCTG TTGG GGCAGCAGG	
	I		
	C	GGGC GACC CCGTCGTCC	
	_____	TC C TC TG	
GAM244 SCEL	TAAGGACCTCTATTGAGCAG		3638 GTTTG CAG
	TAAGGACCT	GGGCAG	
	ATTCCTGGA	CTCGTC	
	GATAA	III	
GAM244 SCEL	TAAGGACCTCTATTGAGCAG		3638 GTTTG I
	AAGGACCT	GGGCA	

	TTCCTGGA	CTCGT			
	GATAA	I			
GAM244 SLA2	CTGTTTATGGAGGCAGCAGG	3629	—	—	III
	CTGTT TGG GGCAGCAG				
	III				
	GACAA ACC CCGTCGTC				
	AT T CII				
GAM244 SLC22A1	GACCTGTTTTGGGGTGCAG	3635	—	CA	II
	GACCTGTTT GGGG GCA				
	III				
	CTGGACAAA CCCC CGT				
	A A_ CI				
GAM244 SLC22A1	GACCTGTTTTGGGGTGCAG	3635	TAAGGACCTG	CA	
	TTTGGGG GCAG				
	AAACCCC CGTC				
	ACA_____ A_				
GAM244 XPC	GGGCCTGTAGTGGGGCAGCAG	3636	GA	T_	I
	CCTGT TGGGGCAGCA				
	GGACA ACCCCGTCGT				
	C_ TC I				
GAM244 XPC	GGGCCTGTAGTGGGGCAGCAG	3636	TAAGGA	T_	G
	CCTGT TGGGGCAGCAG				
	GGACA ACCCCGTCGTC				
	_____ TC G				
GAM245 ASTN	TAAG-ACCTGTTT--GGCAGC	3640	TA	GG	A
	AGGACCTGTTT GGCAGC				
	TTCTGGACAAA CCGTCG				
	A_ _ I				
GAM245 CA7	AGGGCCTGCCCCGTGGCAGCAGG	3626	TAA A	G	
	GG CCTGTTTG GGCAGCAGG				
	CC GGACGGGC CCGTCGTCC				
	_____ A				
GAM245 CDK10	CCTTTTCTGGGGGCAGCAG	3627	TAAGGAC	TTT	
	CTG GGGGCAGCAG				
	GAC CCCCCGTCGTC				
	A_____				
GAM245 GRLF1	TAATGGACTGTGTTCTGGGGCAGC	3637	TAA_	C_	AGGI
	GGAC TGT TTGGGGCAGC				
	CCTG ACA GACCCCGTCG				
	ATTA AC A G				
GAM245 HAMP	GACCTATGTTCTGGGGCAGCAGG	3634	TAAGGACC	_	I
	TGT TTGGGGCAGCAGG				

	ACA GACCCCGTCGTCC	
	AT_____ A T	
GAM245 INHBC	TAAGCCTCTATTTTGGGCAGCAG 3641	GAC G GI
	TAAG CTGTTT GGGCAGCAG	
	ATTC GATAAA CCCGTCGTC	
	GGA A II	
GAM245 MAGEA12	GACTCTGGTCAGGGCAGCAGG 3633	TAAGGAC T TG
	CTG T GGGCAGCAGG	
	GAC A CCCGTCGTCC	
	_____ C GT	
GAM245 MAGEA2	GACTCTGGTCAGGGCAGCAGG 3633	TAAGGAC T TG
	CTG T GGGCAGCAGG	
	GAC A CCCGTCGTCC	
	_____ C GT	
GAM245 MAGEA4	GACTCTGCTCAGGGCAGCAGG 3632	TAAGGAC TG
	CTGTT GGGCAGCAGG	
	GACGA CCCGTCGTCC	
	_____ GT	
GAM245 MAGEA9	GACTCTGGTCAGGGCAGCAG 3630	TAAGGAC T TG
	CTG T GGGCAGCAG	
	GAC A CCCGTCGTC	
	_____ C GT	
GAM245 MSI1	GACGCTGTTGGGGCAGCAGG 3631	TAAGGAC T
	CTGTT GGGGCAGCAGG	
	GACAA CCCCGTCGTCC	
	_____ C	
GAM245 MYL4	TAAGGTCCT---TGGGGCAG 3639	A GTT CA
	TAAGG CCT TGGGGCAG	
	ATTCC GGA ACCCGTC	
	A _____ II	
GAM245 NUP98	AGGATGCTGCTTCTGGCAGCAGG 3625	TAAGGAC GG I
	CTGTTT GGCAGCAGG	
	GACGAA CCGTCGTCC	
	CTAC_____ GA C	
GAM245 RAB6A	AGGAGCCCGGCTGGAGGGCAGCAGG 3624	TAA GA T _____ II
	G CCTG TTGG GGCAGCAGG	
	C GGGC GACC CCGTCGTCC	
	_____ TC C TC TG	
GAM245 SCEL	TAAGGACCTCTATTGAGCAG 3638	GTTTG CAG
	TAAGGACCT GGGCAG	

	ATTCCTGGA CTCGTC	
	GATAA III	
GAM245 SLC22A1	GACCTGTTTTGGGGTGCA	3635 TAAGGACCTG CA
	TTTGGGG GCAG	
	AAACCCC CGTC	
	ACA_____ A_	
GAM245 XPC	GGGCCTGTAGTGGGGCAGCAG	3636 TAAGGA T_ G
	CCTGT TGGGGCAGCAG	
	GGACA ACCCCGTCGTC	
	_____ TC G	
GAM246 ABCC3	AAGGAGCCGTTGCGCTGCAGCAGG	3663 A C _ G I
	GGA CTGTT TG TGCAGCAG	
	CCT GGCAA GC ACGTCGTC	
	_ C C G I	
GAM246 ABCC3	AAGGAGCCGTTGCGCTGCAGCAGG	3663 TA C _ G I
	AGGA CTGTT TG TGCAGCAGG	
	TCCT GGCAA GC ACGTCGTCC	
	_ C C G C	
GAM246 ASTN	TAAG-ACCTGTTTG--GCAGC	3674 TA _ AI
	AGGACCTGTTTGGT GC	
	TTCTGGACAAACCG CG	
	A_ T II	
GAM246 ASTN	TAAG-ACCTGTTTG--GCAGC	3674 TA GT A
	AGGACCTGTTTG GCAGC	
	TTCTGGACAAAC CGTCG	
	A_ _ I	
GAM246 CD5	GAGCTGTT--GTGCAGCAG	3669 C TG I
	GA CTGTT GTGCAGCA	
	CT GACAA CACGTCGT	
	C _ C	
GAM246 COL15A1	TATGAACCTGTTTGTTCAG	3673 AA GTG I
	GGACCTGTTTG CA	
	CTTGGACAAAC GT	
	TA AAA I	
GAM246 COL15A1	TATGAACCTGTTTGTTCAG	3673 TAA GTG CAG
	GGACCTGTTTG CAG	
	CTTGGACAAAC GTC	
	ATA AAA III	
GAM246 DDX11	TAAGGACCTGTAGCTGTGCAG	3670 TTG_ CAGG
	TAAGGACCTGT GTGCAG	

	ATTCCTGGACA CACGTC			
	TCGA III G			
GAM246 DDX11	TAAGGACCTGTAGCTGTGCAG 3670 A	TTG_ I		
	AGGACCTGT GTGCA			
	TCCTGGACA CACGT			
	_ TCGA I			
GAM246 DRD1	AGCACCTGTTTGTATACAGCA 3667 GG	_ I		
	ACCTGTTTG GTGCAGC			
	TGGACAAAC TATGTCG			
	G_ A I			
GAM246 DRD1	AGCACCTGTTTGTATACAGCA 3667 TAAGG	_		
	ACCTGTTTG GTGCAGCAGG			
	TGGACAAAC TATGTCGTTT			
	G_ A			
GAM246 GAS7	TAAGG---GTTTGGTGCAG 3672 ACCT	C		
	TAAGG GTTTGGTGCAG			
	ATTCC CAAACCACGTC			
	_ I			
GAM246 GAS7	TAAGG---GTTTGGTGCAG 3672 _ ACCT			
	AAGG GTTTGGTGCA			
	TTCC CAAACCACGT			
	A _			
GAM246 IL18	CTGTGTAGACTGCAGCAGG 3668 T _ III			
	CTGT TGG TGCAGCAG			
	GACA ATC ACGTCGTC			
	C TG CII			
GAM246 RNTRE	TAATGGCCTGATGAGGTGCAGCA 3671 AA A TTT_ I			
	GG CCTG GGTGCAGC			
	CC GGAC CCACGTCG			
	TA _ TACT I			
GAM246 RNTRE	TAATGGCCTGATGAGGTGCAGCA 3671 TAA_ A TTT_ GGI			
	GG CCTG GGTGCAGCA			
	CC GGAC CCACGTCGT			
	ATTA _ TACT III			
GAM246 RPL29	AAGGGGCTGC--GGTGCAGCA 3665 _ AC TT I			
	AGG CTGT GGTGCAGC			
	TCC GACG CCACGTCG			
	T CC _ I			
GAM246 RPL29	AAGGGGCTGC--GGTGCAGCA 3665 TA AC TT G			
	AGG CTGT GGTGCAGCA			

	TCC GACG CCACGTCGT		
	__ CC __ G		
GAM246 SCEL	TAAGGACCTCTATTGAGCAG 3638	G TGG C	
	TAAGGACCT TT TG AGCAG		
	ATTCCTGGA GA AC TCGTC		
	__ TA__		
GAM246 SCEL	TAAGGACCTCTATTGAGCAG 3638	GT_ T I	
	AAGGACCT TTGG GCA		
	TTCCTGGA AACT CGT		
	GAT _ I		
GAM246 SCN3A	AAGG---TGTTTGGTGTAG 3664	ACC CA	
	AAGG TGTTTGGTG		
	TTCC ACAAACCAC		
	__ AT		
GAM246 SCN3A	AAGG---TGTTTGGTGTAG 3664	TA ACC C C	
	AGG TGTTTGGTG AG		
	TCC ACAAACCAC TC		
	__ __ A A		
GAM246 SLC22A1	GACCTGTTTTGGGGTGCAG 3635	__	
	GACCTGTTT GGTGCA		
	CTGGACAAA CCACGT		
	ACC CII		
GAM246 SLC7A8	AAGGATCCTAAGTCCTTAGTGCAGCAGG3662	TA _ ____	
	AGGA CCTG TTTGGTGCAGCAGG		
	TCCT GGAT GAATCACGTCGTCC		
	__ A TCAG TII		
GAM246 SLC7A8	AAGGATCCTAAGTCCTTAGTGCAGCAGG3662	AGGA ____ I	
	CCTG TTTGGTGCAGCAG		
	GGAT GAATCACGTCGTC		
	__ TCAG I		
GAM246 TEM6	AGGCACTTGGTTTGGTGCATCA 3666	AGGACCT GI	
	GTTTGGTGCA		
	CAAACCACGT		
	TGAAC__ AG		
GAM246 TEM6	AGGCACTTGGTTTGGTGCATCA 3666	TAA G CT_ G G	
	G AC GTTTGGTGCA CAG		
	C TG CAAACCACGT GTT		
	__ G AAC A A		
GAM247 ATP6V0E	CAAAACAGGCAAGTCAAGAAAAGTGG 3688	TACA AAC____ II	
	AGACAGGCAAG AAGTGG		

	TTTGTCCGTTC	TTCACC	
	_____	AGTTCTT	AG
GAM247 ATRN	TAAAAGACCATGTTCAAGAACA	ACTG 3693	TAC AGG_____ G GII
	AAGAC	CAAGAACAA	TG
	TTCTG	GTTCTTGTT	AC
	ATT	GTACAA	G
GAM247 BLNK	CAGGTCAGGCAATAGAACAAGT	3687	TACAAGA _____ GG
	CAGGCA	AGAACAAGT	
	GTCCGT	TCTTGTTCA	
	CCA_____	TA	GG
GAM247 BLTR2	TACAAGACAAGAAAGGA-AAG	3694	C AACAAGTG
	TACAAGACAGG	AAG	
	ATGTTCTGTTC	TTC	
	T	CTTTC	
GAM247 CYP17	CAGGCAAGATAGACAGCAGTGG	3690	TACA G AGAACAA
	AGACAG	CA	GTGG
	TCTGTC	GT	CACC
	CTA_	_____	
GAM247 DPYSL3	AGACAGTCGTGAAGAACAAG	3683	TACAAGACAGGC TG
	AAGAACAAG		
	TTCTTGTTTC		
	TCAGCAC_____	CG	
GAM247 EIF4EBP2	ACAGGAAAGGCAAGAA-AACTGG	3682	TA A C C G
	CA	GA AGGCAAGAA	AA TGG
	GT	CT TCCGTTCTT	TT ACC
	___	C T	___
GAM247 FLRT2	ACAAGAC---CAAGAACAAG	3679	TA AGG T
	CAAGAC	CAAGAACAAG	
	GTTCTG	GTTCTTGTTTC	
	___	___	T
GAM247 FOXO1A	TACAAGACA---AAG--CAAGTG	3695	___ AACAAAGT
	TACAAGACAG	GCAAG	
	ATGTTCTGTT	CGTTC	
	T	AC GG	
GAM247 KCNJ1	TACAAGACAAAAGTAAGATCA	3692	___ C A AGTGG
	TACAAGACA	GG AAGA	CA
	ATGTTCTGT	TC TTCT	GT
	TT	A A GG	
GAM247 LARGE	AAG-CAGGCAAGAACCAGAGG	3677	TACAAGA A T
	CAGGCAAGAAC	AG G	

	GTCCGTTCTTG TC C		
	_____ G T		
GAM247 MTMR2	ACAAGACAGAC-TGAACCAAAGTGG 3678 TA	AA	___ I
	CAAGACAGGC GAAC AAGTGG		
	GTTCTGTCTG CTTG TTCACC		
	_____ A_ GT C		
GAM247 PCSK1	ACAAGACAGG---GAACAAG 3680 TA	CAA	
	CAAGACAGG GAACAAGT		
	GTTCTGTCC CTTGTTCC		

GAM247 PIK4CB	CAAGACAGGCAGGGA AAAAAG 3686 TACA	A_ C	
	AGACAGGCA GAA AAGTG		
	TCTGTCCGT CTT TTCGT		
	_____ CC T		
GAM247 PRKAB1	CAAGCCGCGGCAAGAACGCAAGGGG 3684 TACAAGACA	___ T II	
	GGCAAGAAC AAG GG		
	CCGTTCTTG TTC CC		
	TCGGCG_____ CG _ CG		
GAM247 RP42	CAAGACAGGAAACAAAACAGT 3689 TACA	CA___ A G	
	AGACAGG AGAACA GTG		
	TCTGTCC TTTTGT CAT		
	_____ TTTG _ G		
GAM247 TEK	TACAAGTTAGAGGCAAGAA 3691	AC___ CAAGTG	
	TACAAG AGGCAAGAA		
	ATGTTC TCCGTTCTT		
	AATC IIIGGT		
GAM247 TPI1	ACATGATCCGCAAGAACAAGT 3681 TACAAGACAG	G	
	GCAAGAACAAGTG		
	CGTTCTTGTTTCAT		
	GTACTAGG_____ I		
GAM247 WNT10B	CAA-ACAGGAACCAAGAACAAGT 3685 TACAA	___ GG	
	GACAGG CAAGAACAAGT		
	TTGTCC GTTCTTGTTCA		
	_____ TTG GA		
GAM248 ADRBK1	CCAGCCTCCTTGCTGTGCTGCC 3704 TACC	CA_ G	
	AGCCTCC CTGTG TGCCT		
	TCGGAGG GACAC ACGGG		
	_____ AAC G		
GAM248 CORO2B	CCAGCACTTACACTGTGGTACCT 3702 TACC	_ CC I	
	AGC CT CACTGTGGTGCCT		

	TCG GA GTGACACCATGGA		
	____ T AT A		
GAM248 DRG2	TACCAGCCTGGCACTGAGCATGCC 3708	CC	TG_ TI
	TACCAGCCT CACTG GTGCC		
	ATGGTCGGA GTGAC TACGG		
	CC TCG II		
GAM248 HDAC5	ACCAGCCTCCCATCAGTGCTG 3699 TA	CTG	CT
	CCAGCCTCCCA TGGTGC		
	GGTCGGAGGGT GTCACG		
	____ A__ AC		
GAM248 IRAK1	CCAGCCTCCTCACTGGATGATGCC 3703 TACC	_ _	TI
	AGCCTCC CACTG TGGTGCC		
	TCGGAGG GTGAC ACTACGG		
	____ A CT TC		
GAM248 JPH3	ACCAGGC--CCACTGTGGTG 3701 TA CCT	C	
	CCAG CCCACTGTGGTG		
	GGTC GGGTGACACCAC		
	_ C__ A		
GAM248 PAX4	ACCACCTCTCCCACTGCCCTGCC 3698_ AGC	GG	I
	TACC CTCCCACTGT TGCCT		
	GTGG GAGGGTGACG ACGGG		
	G A__ GG I		
GAM248 PPARA	CCAGCCTCCAGAACTGTGGTG 3705 TACC	C__	CCT
	AGCCTCC ACTGTGGTG		
	TCGGAGG TGACACCAC		
	____ TCT TGI		
GAM248 SH3BP2	CCAGCCTCGG-CTGTGGTGC 3706 TACC	CCA	C
	AGCCTC CTGTGGTGC		
	TCGGAG GACACCACG		
	____ CC_ T		
GAM248 SLC39A1	CCAGCCTCCCA-TGT-GAGCCT 3707 TACC	C	T
	AGCCTCCCA TGTGG GCC		
	TCGGAGGGT AACT CGG		
	____ _ _		
GAM248 SREBF2	ACCAGCCTCCCAGGGCTGG-GCC 3700 TA	CT_	T
	CCAGCCTCCCA G TGG GCCT		
	GGTCGGAGGGT C ACC CGGG		
	____ CC G _		
GAM249 ARL4	GAGTCT-GGGTCCAAATGAGAA 3716 TAGAA	A	AAG
	TCT GGG AAATGAGAA		

	AGA CCC TTTACTCTT	
	C_____ AGG	
GAM249 CDC25C	AATCTAGGG--GAAAGGAG 3712 TAGAAT AA T	
	CTAGGG GAAA GAG	
	GATCCC CTTT CTC	
	_____ C	
GAM249 GPR81	AGAAACTTCAGCCAGGAAATGAGA 3713 TAGAAT_____ AGAA AI	
	CTAGGGA ATGAGA	
	GGTCCTT TACTCT	
	CTTTGAAGTC _____ CI	
GAM249 PDE4B	ATCTCAAGGA-GAAATGAG 3715 TAGAATC A	
	TAGGGA GAAATGAG	
	G TTCCT CTTTACTC	
	_____ -	
GAM249 TDGF1	AATTTAAG-AAGAAATGAGAA 3711 TAGAATC AG	
	TAGGGA AAATGAGAA	
	ATTCTT TTTACTCTT	
	A_____ CT	
GAM249 TGFBR2	AGAA-CTAG--AAGAAATG 3714 TAGAATCTAG A	
	GGAAGAAATG	
	TCTTCTTTAC	
	CTTGA_____ A	
GAM250 BACE	ATGATCTTGGGATGCTGGAT 3721 CA CGCC C CT	
	TGATCTTG GCT GAT	
	ACTAGAAC CGA CTA	
	_____ CCTA C AI	
GAM250 BIN1	GATCTTGCGCGCCGCGCTC 3729 CATGAT C _ A	
	CTTGCGC GCT CG TCT	
	GAACGCG CGG GC AGG	
	_____ C G	
GAM250 CD83	TGCGCCGCTGCCACGAGCTG 3734 _____ T T CC CGATCT	
	CATGA CT GCG GCT	
	GTGCT GA CGT CGA	
	ACG C _ CT CIIIGT	
GAM250 DDX10	ATCATCCACC-CTCGATCTG 3720 CATGATCTTG G	
	CGCC CTCGATCT	
	GTGG GAGCTAGA	
	AG_____ -	
GAM250 EGLN1	TCTTGCGCCCCGTTTCGACCT 3731 CATGATCTT G C_	
	GC CCG TCGATCTG	

	CG GGC AGCTGGAT			
	G_____ G AA			
GAM250 MAP3K8	TGGAGGCACATTCATGGGTC	3732	A _	GCTTG
	TG AGGC GTTCATGGGTC			
	AC TCCG TAAGTACCCAG			
	C TG IIIAG			
GAM250 MAP3K8	TGGAGGCACATTCATGGGTC	3732	A _	III
	TG AGGC GTTCATGGGT			
	AC TCCG TAAGTACCCA			
	C TG GII			
GAM250 MSL3L1	CATGATCTTCTGCTGC-CCATCT	3724		GC C G G
	CATGATCTT GC GCTC ATCT			
	GTACTAGAA CG CGGG TAGA			
	GA A _ I			
GAM250 NCOA6IP	CATGATCTTTTGTC-CTCGCACTG	3726		GCGCCG AT I
	CATGATCTT CTCG CTG			
	GTACTAGAA GAGC GAC			
	AACAG_ GT I			
GAM250 NR1I2	GATGGCCTATCCTTGGTGCTTG	3728	AA GT_ ATG	I
	GGC TC GGTCGCTT			
	CCG AG CCAGCGAA			
	A_ GAT GAA I			
GAM250 NR1I2	GATGGCCTATCCTTGGTGCTTG	3728	TGAA GT_ ATG	AI
	GGC TC GGTCGCTTG			
	CCG AG CCAGCGAAC			
	TA_ GAT GAA CI			
GAM250 PDXK	CACGGTCTC-CGCCGCTCGCTC	3723	A G	A TG
	CATG TCTT CGCCGCTCG TC			
	GTGC AGAG GCGGCGAGC AG			
	C _ G II			
GAM250 SLC17A4	GAAGGCAGATATCATGGGTCACT	3727	A_ CGT	I
	AGG TCATGGGTCTGC			
	TCT AGTACCCAGTG			
	CG AT_ I			
GAM250 SLC17A4	GAAGGCAGATATCATGGGTCACT	3727	TG T_	TGAI
	AAGGCG TCATGGGTCTGCT			
	TTCCGT AGTACCCAGTGA			
	_ CTAT CII			
GAM250 TGFBR2	AATGCTGTATGGGTCCCTT	3719	AG GT	G I
	GC TCATGGGTCT CT			

	CG AGTACCCAG GA		
	TA AC G I		
GAM250 TGFBR2	AATGCTGTCATGGGTCCCTT 3719 TGAAG GT G G		
	GC TCATGGGTC CTT		
	II IIIIIII III		
	CG AGTACCCAG GAA		
	A___ AC G G		
GAM250 UBQLN1	TGTTTCAGGCGCCGCTCGCTC 3733 CATGA TT A T		
	TC GCGCCGCTCG TC		
	II IIIIIII II		
	AG CGCGGCGAGC AG		
	A___ TC G T		
GAM250 USP6	GTTTCATGGGAATTCCCTTG 3730 ___ G III		
	GTTTCATGGG TC CTT		
	IIIIII II III		
	CAAGTACCC AG GAA		
	TTA G CII		
GAM250 USP6	GTTTCATGGGAATTCCCTTG 3730 TGAA C ATGG _ G		
	GG GTTC GT CGCTT		
	II III II IIII		
	CC TAAG CA GTGAG		
	___ T GGAA T I		
GAM250 USP6	CATGATCTTGC-TTTCTCCATCT 3725 GCCG G G		
	CATGATCTTGC CTC ATCT		
	IIIIIIII III III		
	GTACTAGAACG GAG TAGA		
	AAA_ G I		
GAM250 WHSC1	ATGATCTTG-GTCTCTGGGTACTG 3722 CA CGCCG GAT___ I		
	TGATCTTG CTC CTG		
	IIIIII III III		
	ACTAGAAC GAG GAC		
	___ CA___ ACCCAT C		
GAM251 CD59	GAA-AGCGT--TCCATGTGAGA 3743 T CT C		
	GAA AGCGT TCCATGTGGGA		
	III IIII IIIIIIIII		
	CTT TCGCA AGGTACACTCT		
	___ I		
GAM251 CTSH	GAATATTCGTGGTCCATGTGG 3740 G_ CT GACA		
	GAATA CGT TCCATGTGG		
	IIII III IIIIIII		
	CTTAT GCA AGGTACACC		
	AA CC IIIA		
GAM251 HAP1	GAAAAGCCTCCAACATGTGGGA 3744 T G TC CA		
	GAA AGC TCT CATGTGGGA		
	III III IIIIIII		
	CTT TCG AGG GTACACCCT		
	T G TT II		
GAM251 IDH3B	GAATCATCATCATCCATGTGG 3738 AG_ T GACA		
	GAAT CGTC TCCATGTGG		
	IIII IIII IIIIIII		

	CTTA GTAG AGGTACACC		
	GTA T IIIA		
GAM251 PRDM2	GAAGGGGGTTTTCCATGTG	3741	GAATAGC C GGAC
	GT TTCCATGTG		
	II IIIIIII		
	CA AAGGTACAC		
	CTTCCCC A IIIA		
GAM251 SLA	GAATTTGAGTCT-CCATGTGG	3739	GAATAGC_ T GAC
	GTCT CCATGTGG		
	IIII IIIIIII		
	CAGA GGTACACC		
	CTTAAACT _ III		
GAM251 STK9	AATTGGTTCTTCCATGAGAGA	3737	GAATAGCG T CA
	TCTTCCATG GGGA		
	IIIIIIII IIII		
	AGAAGGTAC CTCT		
	TAACCA_ T CI		
GAM251 VANGL2	GAA-AG-GTCCTCCATGTGG	3742	T C GA
	GAA AG GTCTTCCATGTGG		
	III II IIIIIIIIIII		
	CTT TC CAGGAGGTACACC		
	_ _ II		
GAM252 ANK2	ATCTTTGG-TCACAAATTA	3753	T CTI
	ATCTTTGGT CACAGA		
	IIIIIIII IIIII		
	TAGAAACCA GTGTTT		
	_ AAT		
GAM252 ANK2	ATCTTTGG-TCACAAATTA	3753	TGAAATCT T CT
	TTGGT CACAGA		
	IIII IIIII		
	AACCA GTGTTT		
	_ _ AA		
GAM252 CA5B	TGAAATCTTGATCAGTTCCAG	3756	_ TG A ACTAT
	TGAAATCT T GTTC CAG		
	IIIIII I IIII III		
	ACTTTAGA A CAAG GTC		
	ACT GT G IIIA		
GAM252 CA5B	TGAAATCTTGATCAGTTCCAG	3756	_ TG ACAIII
	TGAAATCT T GTTC		
	IIIIII I IIII		
	ACTTTAGA A CAAG		
	ACT GT GGTCII		
GAM252 CPSF6	AAATCTTTGATTAAGTAACTAT	3751	CACA I
	AATCTTTGGTT GACTA		
	IIIIIIII IIII		
	TTAGAAACTAA TTGAT		
	TTCA I		
GAM252 CPSF6	AAATCTTTGATTAAGTAACTAT	3751	TGAA CACA
	ATCTTTGGTT GACTAT		
	IIIIIIII IIIII		

		TAGAACTAA	TTGATA						
		_____	TTCA						
GAM252	NAB1	ATCTTCCTGGTTTTCCACAGACTA	3752	__	__			IIIT	
		ATCTT TGGT TCACAGACT							
		TAGAA ACCA GGTGTCTGA							
		GG AA TIII							
GAM252	NAB1	ATCTTCCTGGTTTTCCACAGACTA	3752	TGAAATC	__			I	
		TTTGGT TCACAGACTAT							
		GGACCA GGTGTCTGATG							
		A_____ AA G							
GAM252	PABPC4	AAATCTTTGTGGGCGCCGACT	3747	TGAA		G TTCACA_		AT	
		ATCTTTG GACT							
		TAGAAAC CTGA							
		_____ ACCGCGG GC							
GAM252	PCDHB16	TGAAAAGTT-GGTTCACAGA	3759	TCT				CTA	
		TGAAA TTGGTTCACAGA							
		ACTTT AACCAAGTGTCT							
		TC_ III							
GAM252	PCDHB16	TGAAAAGTT-GGTTCACAGA	3759	_ TCT				I	
		GAAA TTGGTTCACAG							
		CTTT AACCAAGTGTC							
		A TC_ I							
GAM252	PRKWNK3	GAATTCTATTTAGGTTTCACAGACT	3754	AAATCTTT	_			I	
		GGTT CACAGAC							
		CCAA GTGTCTG							
		GATAAAT_ A I							
GAM252	PRKWNK3	GAATTCTATTTAGGTTTCACAGACT	3754	TGAAA	TT____	_		ATI	
		TCT GGTT CACAGACT							
		AGA CCAA GTGTCTGA							
		TTA_ TAAAT A CIII							
GAM252	ROCK2	AAATATTTTGTAGTCACAGACTA	3748	AATC	GT_			I	
		TTTG TCACAGACT							
		AAAC AGTGTCTGA							
		ATA_ ATC I							
GAM252	ROCK2	AAATATTTTGTAGTCACAGACTA	3748	TGAAATC	GT_			TI	
		TTTG TCACAGACTA							
		AAAC AGTGTCTGAT							
		TATA_ ATC TA							
GAM252	RPH3AL	TGAAGTCA--GGTTCACAG	3758	A TTT				ACT	
		TGAA TC GGTTCACAG							

	ACTT AG CCAAGTGTC			
	C T__ III			
GAM252 RPH3AL	TGAAGTCA--GGTTCACAG	3758	A TTT	I
	TGAA TC GGTTCACA			
	ACTT AG CCAAGTGT			
	C T__ C			
GAM252 SCN1A	TGAGAGCTTC--TTCACAGACT	3760	AAT GG	A
	TGA CTTT TTCACAGACT			
	ACT GAAG AAGTGTCTGA			
	CTC _ I			
GAM252 SCN1A	TGAGAGCTTC--TTCACAGACT	3760	_ AAT GG	I
	GA CTTT TTCACAGAC			
	CT GAAG AAGTGTCTG			
	A CTC _ I			
GAM252 SEDL	GACATCTTTGGTTGTCACACT	3755	AA _	GAI
	ATCTTTGGT TCACA			
	TAGAAACCA AGTGT			
	G_ AC GII			
GAM252 SEDL	GACATCTTTGGTTGTCACACT	3755	TGAA	CA G AT
	ATCTTTGGTT CA ACT			
	TAGAAACCAA GT TGA			
	TG_ CA G AI			
GAM252 SLC21A9	AACTCTTTGGTT--CAGACTA	3750	AA_	CA I
	TCTTTGGTTCA GACT			
	AGAAACCAAGT CTGA			
	TTG _ I			
GAM252 SLC21A9	AACTCTTTGGTT--CAGACTA	3750	TGAAA	CA
	TCTTTGGTTCA GACTA			
	AGAAACCAAGT CTGAT			
	G_ _			
GAM252 SRD5A2	TGAAATCTTCTGGAAAACAGA	3757	_ TTC	CTAT
	TGAAATCT TTGG ACAGA			
	ACTTTAGA GACC TGTCT			
	A TTT IIIT			
GAM252 SRD5A2	TGAAATCTTCTGGAAAACAGA	3757	G _ TTC	I
	AAATCT TTGG ACAG			
	TTTAGA GACC TGTC			
	_ A TTT I			
GAM252 SSRP1	AAATCATT--TTCACAGAC	3749	TTTGG	I
	AAATC TTCACAGA			

	TTTAG AAGTGTCT			
	TAA__ G			
GAM252 SSRP1	AAATCATT--TTCACAGAC	3749	TGAA TTTGG	
	ATC TTCACAGACT			
	TAG AAGTGTCTGG			
	__ TAA__			
GAM253 BSG	TGAAACACTTCAGAAGGAA	3777	G TGGT	
	TGGAATA TTCAGAAGGAA			
	ACTTTGT AAGTCTTCCTT			
	G IIIA			
GAM253 BSG	TGAAACACTTCAGAAGGAA	3777	G II	
	TGGAATA TTCAGAAGGA			
	ACTTTGT AAGTCTTCCT			
	G TI			
GAM253 CHD4	TGGAAGATGGGCAGAAGGAA-GGT	3775	TAGTT_ T AI	
	TGGAA CAGAAGGAA GGT			
	ACCTT GTCTTCCTT CCA			
	CTACCC _ II			
GAM253 CHD4	TGGAAGATGGGCAGAAGGAA-GGT	3775	TAGTT_ T I	
	GGAA CAGAAGGAA GG			
	CCTT GTCTTCCTT CC			
	CTACCC _ I			
GAM253 DNAJB9	AATAGTTCACAGAAAATTGT	3764	GA TGGI	
	ATAGTTCA AGGAA			
	TATCAAGT TCTTT			
	G_ TAAC			
GAM253 DNAJB9	AATAGTTCACAGAAAATTGT	3764	TGGAAT GA TG_	
	AGTTCA AGGAA GT			
	TCAAGT TCTTT CA			
	__ G_ TAA			
GAM253 DRD2	GGAA-AGGCCAGAAGGAAT	3771	T TT I	
	GGAA AG CAGAAGGAA			
	CCTT TC GTCTTCCTT			
	_ CG A			
GAM253 DRD2	GGAA-AGGCCAGAAGGAAT	3771	TG T TT G	
	GAA AG CAGAAGGAATG			
	CTT TC GTCTTCCTTAT			
	_ _ CG I			
GAM253 DTR	TGTAACAGTTCAGA---AATGG	3778	G GAAI	
	TG AATAGTTCAGAAG			

	AC TTGTCAAGTCTTT		
	A ACCI		
GAM253 DTR	TGTAACAGTTCAGA--AATGG 3778 G	GGA T	
	TG AATAGTTCAGAA ATGG		
	AC TTGTCAAGTCTT TACC		
	A _ I		
GAM253 GTF2F1	GAAGATTCCAGAAGGAAGGG 3767 GAATAG	TI	
	TTCAGAAGGAA		
	AGGTCTTCCTT		
	TCTA_ CC		
GAM253 GTF2F1	GAAGATTCCAGAAGGAAGGG 3767 TGAATAG	T	
	TTCAGAAGGAA GGT		
	AGGTCTTCCTT CCG		
	TCTA_ C		
GAM253 IHPK1	GGAA-AG--CATGAAGGAATGAGTA 3770_ T TCA	TI	
	GAA AGT GAAGGAATGG		
	CTT TCG CTCCTTACT		
	C _ TA_ CA		
GAM253 IHPK1	GGAA-AG--CATGAAGGAATGAGTA 3770 TG T TCA	_	
	GAA AGT GAAGGAATG GTA		
	CTT TCG CTCCTTAC CAT		
	_ _ TA_ T		
GAM253 KIF5C	GGAAAAGTGTTCCAGAAGGAA 3769 TA_		
	GGAA GTTCAGAAGGA		
	CCTT CAAGTCTTCCT		
	TTCA TII		
GAM253 KIF5C	GGAAAAGTGTTCCAGAAGGAA 3769 TGGAATA	TGGT	
	GTTCAGAAGGAA		
	CAAGTCTTCCTT		
	CTTTTCA TIII		
GAM253 MAFG	GGGAGAGATTAGAAGGAAT 3772_ AT TTC	II	
	GGA AG AGAAGGAA		
	CCT TC TCTTCCTT		
	C C_ TAA AI		
GAM253 MAFG	GGGAGAGATTAGAAGGAAT 3772 T AT TTC	GT	
	GGA AG AGAAGGAATG		
	CCT TC TCTTCCTTAT		
	_ C_ TAA II		
GAM253 MMP25	GAATAGTTCAGAGGCAAT 3766	_ A AAI	
	GAATAGTTC AGA GG		

	CTTATCAAG TCT CC		
	G _ GTTA		
GAM253 MMP25	GAATAGTTCCAGAGGCAAT	3766 TGGA	_ A _ GGT
	ATAGTTC AGA GG AAT		
	TATCAAG TCT CC TTA		
	_____ G _ G GTI		
GAM253 PACSIN1	GAAGAGGACAGA-GGAATGGT	3768 AAT_ TT	A I
	AG CAGA GGAATGG		
	TC GTCT CCTTACC		
	CTTC CT _ I		
GAM253 PACSIN1	GAAGAGGACAGA-GGAATGGT	3768 TGG AAT TT	A
	AG CAGA GGAATGGT		
	TC GTCT CCTTACCA		
	TC_____ CT _		
GAM253 PIK3CD	TGGAATAGTCCAAGAAAGA	3776	_ ATGGT
	TGGAATAGTTCA GAAGGA		
	ACCTTATCAGGT CTTTCT		
	T IIIAT		
GAM253 PIK3CD	TGGAATAGTCCAAGAAAGA	3776	_ II
	TGGAATAGTTCA GAAGG		
	ACCTTATCAGGT CTTTC		
	T TI		
GAM253 PMP22	GATTAGTGATAATAAGGAATGGTA	3765 AA TCAG_	I
	TAGT AAGGAATGGT		
	ATCA TTCCTTACCA		
	_ CTATTA I		
GAM253 PMP22	GATTAGTGATAATAAGGAATGGTA	3765 TGGAA TCAG_	I
	TAGT AAGGAATGGTA		
	ATCA TTCCTTACCAT		
	A_____ CTATTA T		
GAM253 RAD52	AATAGTTCAGTAATAAATAGT	3763 A _ G	I
	TAGTTCAG AA GAATGG		
	ATCAAGTC TT TTTATC		
	_ A A I		
GAM253 RAD52	AATAGTTCAGTAATAAATAGT	3763 TGG AAT _ G	A
	AGTTCAG AA GAATGGT		
	TCAAGTC TT TTTATCA		
	_____ A A C		
GAM253 SLC19A1	TGGACACACTTCAGAAGGA	3774 _ G	ATGGT
	TGGA ATA TTCAGAAGGA		

	ACCT TGT AAGTCTTCCT			
	G G IIIAT			
GAM253 SLC19A1	TGGACACACTTCAGAAGGA	3774	_ G	II
	TGGA ATA TTCAGAAGG			
	ACCT TGT AAGTCTTCC			
	G G TI			
GAM253 UPF3A	TAGTTTATAACAGGAATGGTA	3773	CAGA__	III
	TAGTT AGGAATGGT			
	ATCAA TCCTTACCA			
	ATATTG TII			
GAM253 UPF3A	TAGTTTATAACAGGAATGGTA	3773	TGGAATAGTTCAGA	
	AGGAATGGTA			
	TCCTTACCAT			
	ATATTG_____			
GAM254 BACH1	ATTCACAAACCTGCAGAGTT	3782	CA TT_	CAT
	TTTC AGCCTGCAGAGTT			
	AAAG TTGGACGTCTCAA			
	_ TGT CII			
GAM254 BACH1	ATTCACAAACCTGCAGAGTT	3782	T TT_	I
	TTC AGCCTGCAGAGT			
	AAG TTGGACGTCTCA			
	_ TGT I			
GAM254 C18orf1	TCTTAGCCTGTCCAAGTCCAT	3796	C CA_	I
	TTAGCCTG GAGTTCA			
	AATCGGAC TTCAGGT			
	_ AGG I			
GAM254 C18orf1	TCTTAGCCTGTCCAAGTCCAT	3796	CATTCTT CA_	
	AGCCTG GAGTTCAT			
	TCGGAC TTCAGGTA			
	_____ AGG			
GAM254 C18orf1	TCTTAGCCTGTCCAAGTCCATC	3797	TTTC CA_	I
	TTAGCCTG GAGTTCATC			
	AATCGGAC TTCAGGTAG			
	_____ AGG C			
GAM254 COX6C	ATTTCTTAGCCCACATA-TTCAT	3784	_ TG GA	I
	TTTCTTAGCC CA GTTCA			
	AAAGAATCGG GT TAAGT			
	T GT A_ I			
GAM254 COX6C	ATTTCTTAGCCCACATA-TTCAT	3784	CA TG GA	
	TTTCTTAGCC CA GTTCAT			

	AAAGAATCGG GT TAAGTA	
	___ GT A_	
GAM254 COX6C	TTTCTTAGCCACATA-TTCAT 3814	TG GA C
	TTTCTTAGCC CA GTTCAT	
	AAAGAATCGG GT TAAGTA	
	GT A_ I	
GAM254 CTSK	CATCTCTTAGCCT-AAGAGTACA 3789	C T T
	CATTTCTTAGCCTG AGAGT CA	
	GTAGAGAATCGGAT TCTCA GT	
	_ T I	
GAM254 CTSK	CATCTCTTAGCCT-AAGAGTACA 3789_	C TCI
	ATTTCTTAGCCTG AGAGT	
	TAGAGAATCGGAT TCTCA	
	G _ TGI	
GAM254 CTSK	TCTTAGCCT-AAGAGTACA 3798 TTTC	C T
	TTAGCCTG AGAGT CAT	
	AATCGGAT TCTCA GTG	
	___ _ T	
GAM254 CYP4A11	CTTGGACCT-CAGAGTTCA 3792 TTTCTTA	G T
	GCCT CAGAGTTCA	
	TGGA GTCTCAAGT	
	CC___ _ C	
GAM254 CYP4A11	CTTGGACCT-CAGAGTTCA 3792 CTTA_	G II
	GCCT CAGAGTTC	
	TGGA GTCTCAAG	
	GAACC _ TI	
GAM254 ELAVL2	ATTTCTTAGGATGCTAAGTAGTCAT 3783	CC A TCAI
	TCTTAG TGC GAGT	
	AGAATC ACG TTCA	
	CT A TCAI	
GAM254 ELAVL2	ATTTCTTAGGATGCTAAGTAGTCAT 3783 CA	CC A _ II
	TTTCTTAG TGC GAGT TCAT	
	AAAGAATC ACG TTCA AGTA	
	_ CT A TC AI	
GAM254 EPHA3	CATTTCTTATACT-CA-AGATCAT 3790	GC G G T
	CATTTCTTA CT CA AG TCAT	
	GTAAAGAAT GA GT TC AGTA	
	AT _ _ T	
GAM254 EPHA3	CATTTCTTATACT-CA-AGATCAT 3790	GC G GA CI
	CATTTCTTA CT CA GTT	

	GTAAAGAAT GA GT TAG	
	AT _ TC TA	
GAM254 EYA1	TTTTCAGTCTGCAGAGTACA 3810 TTTC C T TC	
	TTAG CTGCAGAGT CA	
	AGTC GACGTCTCA GT	
	AA__ A T TI	
GAM254 GNAL	CATCTCTCGTCAGCCTGCAG-CTTCAT3785 ____ AG II	
	CATTTCTT AGCCTGCAG TTCAT	
	GTAGAGAG TCGGACGTC AAGTA	
	CAG G_ II	
GAM254 GNAL	CATCTCTCGTCAGCCTGCAG-CTTCAT3785 A _ AG I	
	TTTC TTAGCCTGCAG TTCA	
	AGAG AGTCGGACGTC AAGT	
	G C G_ I	
GAM254 GOLGA4	ACTCTTTC-TTCAACTGTGT 3781 _ TTAA I	
	CTCTTTCTTT TGTG	
	GAGAAAGAAG ACAC	
	T TTG_ I	
GAM254 GOLGA4	ACTCTTTC-TTCAACTGTGT 3781 TGGACT TTAA	
	CTTTCTTT TGTGT	
	GAAAGAAG ACACA	
	____ TTG_	
GAM254 GPT	TTTATTAGGGACCTGCAGAG 3813 CATTTCTTA TTCA	
	GCCTGCAGAG	
	TGGACGTCTC	
	ATAATCCC_ TCII	
GAM254 GPT	TTTATTAGGGACCTGCAGAG 3813 TTTCTTA__ TTCATC	
	GCCTGCAGAG	
	TGGACGTCTC	
	AAATAATCCC IICTA	
GAM254 GPT	TTTATTAGGGACCTGCAGAG 3813 TTTCTTA__ III	
	GCCTGCAGA	
	TGGACGTCT	
	AAATAATCCC CII	
GAM254 GRLF1	TGGTTTCTTCCTTTTAAAT 3807 AC GTGT	
	TGG TCTTTCTTTTAAAT	
	ACC AGAAGGAAAAATTA	
	AA IIIC	
GAM254 GRLF1	TGGTTTCTTCCTTTTAAAT 3807 AC II	
	TGG TCTTTCTTTTAA	

	ACC AGAAGGAAAAATT			
	AA AI			
GAM254 GSTM3	GGGCTCTATTATTTTAAATGAGT	3794	T A	TTC_ T CI
	GG CTCT TTTTAAATG GT			
	CC GAGA AAAAATTAC CA			
	_ _ TAAT T TI			
GAM254 HSPA5	TGAAGTCTATCTTTTAAAT	3805	C T	GTGT
	TGGA TCT TCTTTTAAAT			
	ACTT AGA AGAAAAATTA			
	C T IIIC			
GAM254 HSPA5	TGAAGTCTATCTTTTAAAT	3805	C T	II
	TGGA TCT TCTTTTAA			
	ACTT AGA AGAAAAATT			
	C T AI			
GAM254 LCP1	CATTTCTTATCCAGCATAGATTCAT	3787	G T G _	II
	CATTTCTTA CC GCA AG TTCAT			
	GTAAAGAAT GG CGT TC AAGTA			
	A T A T II			
GAM254 LCP1	CATTTCTTATCCAGCATAGATTCAT	3787	A G T G _	I
	TTTCTTA CC GCA AG TTCA			
	AAAGAAT GG CGT TC AAGT			
	_ A T A T I			
GAM254 MAP2	TGGCTTCTTTC-TTTTAAAT	3806	AC	TAAI
	TGG TCTTCTTTT			
	ACC AGAAAGAAAA			
	GA TTAI			
GAM254 MAP2	TGGCTTCTTTC-TTTTAAAT	3806	AC	TAATGTG
	TGG TCTTCTTTT			
	ACC AGAAAGAAAA			
	GA TTAIIIC			
GAM254 MEF2C	TGGTCTCTGATCCTTTTAAATGAGT	3804	A _	T CII
	TGG CTCT TTCTTTTAAATG GT			
	ACC GAGA AGGAAAAATTAC CA			
	A CT T III			
GAM254 MEF2C	TGGTCTCTGATCCTTTTAAATGAGT	3804	GA _	TGI
	CTCT TTCTTTTAAATG			
	GAGA AGGAAAAATTAC			
	A_ CT TII			
GAM254 NCALD	TTTTTTCGAGTCTGCAGAGT	3811	_ TT C	TCATC
	TTTC AG CTGCAGAGT			

	AAAG TC GACGTCTCA		
	AAA C_ A IIICT		
GAM254 NT5C2	GACTCTTTCCTTTTCCTCGTGT 3793 A	AA_ I	
	CTCTTTCTTTTT TGTG		
	GAGAAAGGAAAA GCAC		
	_ GGA I		
GAM254 NT5C2	GACTCTTTCCTTTTCCTCGTGT 3793 TGGA	AA_ C	
	CTCTTTCTTTTT TGTGT		
	GAGAAAGGAAAA GCACA		
	____ GGA T		
GAM254 OXCT	CATTTCTTAACATGTATAG 3786	C CAGAGTTCA	
	CATTTCTTAGC TG		
	GTAAAGAATTG AC		
	T ATATCIIT		
GAM254 OXCT	CATTTCTTAACATGTATAG 3786	C CAGAI	
	CATTTCTTAGC TG		
	GTAAAGAATTG AC		
	T ATATCI		
GAM254 PDGFRA	TCTTTCTTTTATTATTTT 3803	A GTII	
	TCTTTCTTTTTA TGT		
	AGAAAGAAAAAT ATA		
	A AAGI		
GAM254 SLC6A3	GGACACTTGGCTTTTAAATATG 3795 TG T T_ TC		
	GAC CTT CTTTTTAATGTG		
	CTG GAA GAAAAATTATAC		
	_ T CC CI		
GAM254 TAL1	TTGCTTGAGCC--CAGAGTTCA 3812 TTT _ TG TC		
	CTT AGCC CAGAGTTCA		
	GAA TCGG GTCTCAAGT		
	AAC C _ II		
GAM254 THBD	TCTTCTTTTCATACATGT 3800	ATGIII	
	TCTTCTTTTTA		
	AGAAAGAAAAGT		
	ATGTAC		
GAM254 TOX	CTTTTCTTTTTTAAATGTG 3791 TGGAC CT T		
	TCTTT TTTAATGTG		
	AGAAA AAAATTACAC		
	A____ _ T		
GAM254 TRIM9	TCTTCTTTATTACTTTCTC 3799 TGGACT_ AATGTGT		
	CTTCTTTTT		

	GAAAGAGAAG			
	GAAATAAT AAIICT			
GAM254 TRIM9	TCTTCTTTCTTTTGTTTC	3802	AA	GTII
	TCTTCTTTTT TGT			
	AGAAAGAAAGA ACA			
	AA AAGI			
GAM254 TRPS1	TTCTGTTGTTTGCAGAGTTGAT	3808	CATTCTTAGCC	CAT
	TGCAGAGTT			
	ACGTCTCAA			
	ACAACAA_____ CTA			
GAM254 TRPS1	TTCTGTTGTTTGCAGAGTTGAT	3808	TCTTAGCC	CI
	TGCAGAGTT			
	ACGTCTCAA			
	ACAACAA_ CT			
GAM254 TRPS1	TTCTGTTGTTTGCAGAGTTGATC	3809	TTTCTTAGCC	C I
	TGCAGAGTT ATC			
	ACGTCTCAA TAG			
	AGACAACAA_ C A			
GAM254 XT3	TCTTCTTTATAACTTGTC	3801	T G II	
	TCTTCTTT TAAT TGT			
	AGAAAGAAA ATTG ACA			
	T A GI			
GAM254 ZNF239	CATTCTTAATCTCCACAGT	3788	GC G G TCA	
	CATTCTTA CT CA AGT			
	GTAAAGAAT GA GT TCA			
	TA G G III			
GAM254 ZNF239	CATTCTTAATCTCCACAGT	3788	GC G G I	
	ATTCTTA CT CA AG			
	TAAAGAAT GA GT TC			
	TA G G I			
GAM255 APLP2	ACCACAGGT-TACCAGAACCTT	3826_	C A	GTI
	CCACAGGT TAC AGAGC			
	GGTGTCCA ATG TCTTG			
	T _ G GAI			
GAM255 APLP2	ACCACAGGT-TACCAGAACCTT	3826	TAAC C A G	
	CACAGGT TAC AGAGC TT			
	GTGTCCA ATG TCTTG AA			
	_____ _ G G			
GAM255 APM1	TTGTGGACA--GGTATTATTTTG	3847_	AA T	I
	TGTGGACA G TATTATTTT			

	ACACCTGT C ATAATAAAA		
	A _ C I		
GAM255 APM1	TTGTGGACA--GGTATTATTTTG 3847 AT	AA T	
	TGTGGACA G TATTATTTTG		
	I		
	ACACCTGT C ATAATAAAAC		
	_ _ C		
GAM255 APPBP2	ATTGTGAGATAAATTTTATTATTTT 3829	_ C G_ GII	
	ATTGTG GA AAA TTATTATTTT		
	II		
	TAACAC CT TTT AATAATAAAA		
	T A AA III		
GAM255 ATP6V1A1	TGTG-ACATATGTCATTATTTTG 3842 ATTGTG	AA_	
	GACA GTTATTATTTTG		
	CTGT CAGTAATAAAAC		
	A_ _ ATA		
GAM255 ATP6V1A1	TGTG-ACATATGTCATTATTTTG 3842 GTG	AA_ I	
	GACA GTTATTATTTT		
	CTGT CAGTAATAAAA		
	CA_ ATA I		
GAM255 C18orf1	ATGGTACACAAAGTTAATGTT 3831 ATT G	TTATTTTG	
	GTG ACAAAGTTA		
	CAT TGTTTCAAT		
	TAC G TACA		
GAM255 C18orf1	ATGGTACACAAAGTTAATGTT 3831 TT G	TTAI	
	GTG ACAAAGTTA		
	CAT TGTTTCAAT		
	C_ G TACA		
GAM255 CLCN6	AACCACAGGGCAAGACCAGAGC 3820 AC	TCTA GI	
	CACAGG CAAGA		
	GTGTCC GTTCT		
	_ C_ GG		
GAM255 CLCN6	AACCACAGGGCAAGACCAGAGC 3820 TA	TCT_ A GTT	
	ACCACAGG AC AGAGC		
	II		
	TGGTGTCC TG TCTCG		
	_ CGTTC G GII		
GAM255 DACH	TAACCACTG--CTACAAGAG 3839	AG T CG	
	TAACCAC G CTACAAGAG		
	I		
	ATTGGTG C GATGTTCTC		
	A_ _ II		
GAM255 DACH	TAACCACTG--CTACAAGAG 3839_	AG T I	
	AACCAC G CTACAAGA		
	I		

	TTGGTG C GATGTTCT			
	A A_ _ I			
GAM255 DDEF1	AACCACAGGATATTTACAA	3817	TC_ _	III
	AACCACAGG TACA			
	TTGGTGTCC ATGT			
	TATAA TII			
GAM255 DDEF1	AACCACAGGATATTTACAA	3817 TA	TC_ _	GAGCGT
	ACCACAGG TACAA			
	TGGTGTCC ATGTT			
	_ TATAA GIIIT			
GAM255 EGR3	TTTTGGCAACAAAGTTATTTTT	3843 TG		ATI
	TG GACAAAGTTATT			
	AC TTGTTTCAATAA			
	CG AAI			
GAM255 EGR3	TTTTGGCAACAAAGTTATTTTT	3843 A TG		ATTTTG
	TTG GACAAAGTTATT			
	AAC TTGTTTCAATAA			
	A CG AAAGII			
GAM255 EHF	ACTATAGGGATACAAGAGC	3825 ACCAC TC		II
	AGG TACAAGAG			
	TCC ATGTTCTC			
	TGATA CT GI			
GAM255 EHF	ACTATAGGGATACAAGAGC	3825 TAACCAC TC		T
	AGG TACAAGAGCG			
	TCC ATGTTCTCGT			
	ATA_ _ CT T			
GAM255 FCN2	CCACCAGGTCTACACGGAGC	3833 _ A_ III		
	CCAC AGGTCTACA GAG			
	GGTG TCCAGATGT CTC			
	G GC GII			
GAM255 FCN2	CCACCAGGTCTACACGGAGC	3833 TAACCA A_ GT		
	CAGGTCTACA GAGC			
	GTCCAGATGT CTCG			
	G_ _ GC AG			
GAM255 FMR2	GTGGAAAAAGA-ATTATTTTG	3836 _ C TT I		
	TGGA AAAG ATTATTTT			
	ACCT TTTC TAATAAAA			
	C T T_ I			
GAM255 HIF1A	TGG-CAAAGCATTATTATTT	3841 A _ II		
	TGG CAAAGT TATTATT			

	ACC GTTTCG ATAATAA		
	— TA AI		
GAM255 HTR1D	AACCACAGGAATC-CCAAGA 3818	— A II	
	AACCACAGG TCT CAAG		
	TTGGTGTCC AGG GTTC		
	TT — TI		
GAM255 HTR1D	AACCACAGGAATC-CCAAGA 3818 TA	— A GCGT	
	ACCACAGG TCT CAAGA		
	TGGTGTCC AGG GTTCT		
	— TT — AIII		
GAM255 IL18R1	ATTTTG-ACAAAGTTAATTATTT 3830 ATTGTG	— TG	
	GACAAAGTTA TTATTT		
	CTGTTTCAAT AATAAA		
	TAAAA_ T II		
GAM255 IL18R1	ATTTTG-ACAAAGTTAATTATTT 3830 TTGTG	— I	
	GACAAAGTTA TTATT		
	CTGTTTCAAT AATAA		
	AAAA_ T I		
GAM255 IL18R1	TTCTTGA-ATAGCTATTATTTT 3845 ATTG CAA	G	
	TGGA AGTTATTATTTT		
	ACTT TCGATAATAAAA		
	AGA_ A_ A		
GAM255 JAG2	AACCACAGGTGCGTCAACAGC 3819 A	CTA_ G I	
	CCACAGGT CAA AG		
	GGTGTCCA GTT TC		
	— CGCA G I		
GAM255 JAG2	AACCACAGGTGCGTCAACAGC 3819 TA	CTA_ G GTT	
	ACCACAGGT CAA AGC		
	TGGTGTCCA GTT TCG		
	— CGCA G GII		
GAM255 KCNJ1	TAACCACAG----AC-AGAGC 3840	GTCT A	
	TAACCACAG ACA GAGC		
	ATTGGTGTC TGT CTCG		
	— —		
GAM255 KCNJ1	TAACCACAG----AC-AGAGC 3840 _	GTCT A	
	AACCACAG ACA GA		
	TTGGTGTC TGT CT		
	A — —		
GAM255 KCNJ6	TTGGTGCCAAA-TTATTATTTT 3846 ATTG ACA_	G	
	TGG AAGTTATTATTTT		

	ACC TTTAATAATAAAA		
	____ ACGG A		
GAM255 KCNJ6	TTGGTGCCAAA-TTATTATTTT	3846 TG	ACA_ I
	TGG AAGTTATTATTT		
	ACC TTTAATAATAAAA		
	A_ ACGG I		
GAM255 LEP	GGGCAAAGTTATTTTATTT	3835 _ A	ATT
	GG CAAAGTTATT		
	CC GTTCAATAA		
	C _ AATAAA		
GAM255 LPHH1	AACCACAGGT---CAAGAG	3821	TAC
	AACCACAGGTC AAGA		
	TTGGTGTCCAG TTCT		

GAM255 LPHH1	AACCACAGGT---CAAGAG	3821 TA	TAC C
	ACCACAGGTC AAGAG		
	TGGTGTCCAG TTCTC		
	_____ A		
GAM255 MAN2A2	TAACCACAGGATTCCCCTAGAGC	3838	__ ACA GTTI
	TAACCACAGG TCT AGAGC		
	ATTGGTGTCC AGG TCTCG		
	TA GGA IIIT		
GAM255 MAN2A2	TAACCACAGGATTCCCCTAGAGC	3838 AA	__ ACA I
	CCACAGG TCT AGAG		
	GGTGTCC AGG TCTC		
	_____ TA GGA I		
GAM255 NAT1	TAACCACAGGCCATCTTTAAAAGA	3837	TAC__ CGTTI
	TAACCACAGGTC AAGAG		
	ATTGGTGTCCGG TTTTC		
	TAGAAA TIIT		
GAM255 NAT1	TAACCACAGGCCATCTTTAAAAGA	3837	TACAAGIIIT
	TAACCACAGGTC		
	ATTGGTGTCCGG		
	TAGAAATTTT		
GAM255 NR4A2	GGACAAAGTTTCCAAGATTTT	3834	ATTATTT
	GGACAAAGTT		
	CCTGTTTCAA		
	AGGTTCTAAA		
GAM255 PEX3	ATT-TGAGACAAATAATTTATTATTTTG	3828 A_ T	G__
	TTG GGACAAA TTATTATTTTG		

	AAC TCTGTTT AATAATAAAAC	
	TA _ ATTA III	
GAM255 PEX3	ATT-TGAGACAAATAATTTATTATTTTG3828 TTGT G__ I	
	GGACAAA TTATTATTTT	
	TCTGTTT AATAATAAAA	
	C__ ATTA I	
GAM255 PPEF1	CACAGGTCTTATTGAAGAGGGTT 3832 ACA AC__ C I	
	GGTCT AAGAG GT	
	CCAGA TTCTC CA	
	__ ATAAC C I	
GAM255 PTPN12	ACATGTCTACAAGCAGCGT 3823 G _ II	
	ACA GTCTACAAG AGCG	
	TGT CAGATGTTC TCGC	
	A G AI	
GAM255 RAP1	ACAAAGTTATATTTATTTT 3822 TATTTIII	
	ACAAAGTTAT	
	TGTTTCAATA	
	TAAATAAA	
GAM255 RNPEPL1	ACCCCAGGAAGCTACAAGAG 3824 A T__ III	
	ACC CAGG CTACAAGA	
	TGG GTCC GATGTTCT	
	G TTC CII	
GAM255 RNPEPL1	ACCCCAGGAAGCTACAAGAG 3824 TAA A T__ _GT	
	CC CAGG CTACAAGAG C	
	GG GTCC GATGTTCTC G	
	__ _ TTC T II	
GAM255 SHANK2	TTGTGGACACAACTCAGTATTT 3844 AT _ G T G	
	TGTGGACA AA TTA TATTTT	
	ACACCTGT TT AGT ATAAAG	
	_ G G C I	
GAM255 SHANK2	TTGTGGACACAACTCAGTATTT 3844 T _ G T I	
	GTGGACA AA TTA TATT	
	CACCTGT TT AGT ATAA	
	_ G G C I	
GAM255 SLC21A3	ATTAGTGAACATT-TTATTATTTTG 3827 ATT_ AAG I	
	GTGGACA TTATTATTTTG	
	CACTTGT AATAATAAAAC	
	TAAT AA_ I	
GAM255 SLC21A3	ATTAGTGAACATT-TTATTATTTTG 3827 TT_ AAG I	
	GTGGACA TTATTATTTT	

	CACTTGT AATAATAAAA			
	AAT AA_ I			
GAM256 AICDA	TGTAAACTCTAA-GAAAGTG 3857	ACAA	TCT	
	TGTAAAC AAGAAAGTG			
	ACATTTG TTCTTTCAC			
	AGA_ III			
GAM256 ANXA4	TGTGAAACACAAAGTAGAAAGT 3854	_ _	GTCTC	
	TGT AAACACAAA AGAAAGT			
	ACA TTTGTGTTT TCTTTCA			
	C CA IICT			
GAM256 BAZ2B	TGGAAACTTCAACAAGAAAGTG 3855	T A_ _	TCTC	
	TG AAAC CAA AAGAAAGTG			
	AC TTTG GTT TTCTTTCAC			
	C AA G IIIC			
GAM256 BCL6	AAAGACAAAAGAACCTATCTC 3853	TGTAAAC	AG	
	ACAAAAGAA TGTCTC			
	TGTTTTCTT ATAGAG			
	C_ GG			
GAM256 CDKN2D	AAACAAGAAGAGAAAGTGTTTC 3851	TGTAAACACAAA	C	
	AGAAAGTGT TC			
	TCTTTCACA AG			
	GTTCTTC_ A			
GAM256 MGA	AAACATCAACTAAAAAGTGTCTC 3850	TGTAAACA A_	I	
	CAA AGAAAGTGTCTC			
	GTT TTTTTCACAGAG			
	GTA_ GA A			
GAM256 PIK3C2B	AAACACAAAAGAGCAAATGT 3852	TGTAAA _	CT	
	CACAAAAGA AAGTGT			
	GTGTTTTCT TTTACA			
	_ CG TT			
GAM256 PROX1	TGGAAA-ACAAAAGAAAATG 3856	TGTAAAC	TCT	
	ACAAAAGAAAGTG			
	TGTTTTCTTTTAC			
	ACCTT_ III			
GAM257 C18orf1	ATTCCAATCCTCAAAACAA 3861	CATTG _ A	CG	
	CCA CC TCAAAACAAG			
	GGT GG AGTTTTGTTT			
	AA_ TA _ II			
GAM257 CASP8	ATTGCCACCAGCTAAAAACA 3860	CA TC_	AGCG	
	TTGCCACCA AAAACA			

	AACGGTGGT TTTTGT	
	___ CGAT AIII	
GAM257 CD2AP	ATTGCTAC-AGCAAAACAAG 3862 CA C CAT CG	
	TTGC AC CAAAACAAG	
	IIII II IIIIIII	
	AACG TG GTTTTGTTC	
	___ A TC_ CI	
GAM257 CYP17	CATTGCCACAAGCTGAAAAAGAAG 3871 CATCAAAAC GCI	
	CATTGCCAC AAGC	
	IIIIIIII IIII	
	GTAACGGTG TTCG	
	_____ ACT	
GAM257 DAG1	GCCAGCCATCAAAAATGAAGCG 3877 CATTGCCA C__ C	
	CCATCAAAA AAGCG	
	IIIIIIII IIII	
	GGTAGTTTT TTCGC	
	C_____ TAC T	
GAM257 DDX11	CATGCCCACCATCACCACA 3872 CAT _ AA AGCG	
	TGCC ACCATCA ACA	
	IIII IIIII III	
	ACGG TGGTAGT TGT	
	GT_ G GG IIIC	
GAM257 DEC1	CATTGGCAGTAGCCATCAAAA 3866 C _____ CAAGCGC	
	CATTG CA CCATCAAAA	
	IIII II IIIIIII	
	GTAAC GT GGTAGTTTT	
	C CATC IIICGCG	
GAM257 FANCC	CATTGCCACATACCAAAATAAG 3867 C_ C CGC	
	CATTGCCAC ATCAAAA AAG	
	IIIIIIII IIIII III	
	GTAACGGTG TGGTTTT TTC	
	TA A III	
GAM257 FLT1	CAGTGCTACAAATCAAAACATGC 3868 T C C_ A GCI	
	CA TGC AC ATCAAAACA GC	
	II III II IIIIIII II	
	GT ACG TG TAGTTTTGT CG	
	C A TT A III	
GAM257 GALNT7	TTGTCACCTAAAAACAAGC 3883 CATTGC ATC	
	CACC AAAACAAGCG	
	III IIIIIII	
	GTGG TTTTGTTCGT	
	CA_____ ATT	
GAM257 GNRHR	TTACCTACATCAAAACTAAG 3881 CATT AC _ CG	
	GCC CATCAAAAC AAG	
	II IIIIIII III	
	TGG GTAGTTTTG TTC	
	_____ AT A AA	
GAM257 IRS1	GCCCCAACCAAAACAAGCG 3879 CATTGCCACC	
	ATCAAAACAAGCG	
	IIIIIIIIII	

		TGGTTTTGTTCGC			
		GT_____			
GAM257 ITGA11		CATTCTACC-TCAAAACAAG	3876	GCC A	CG
		CATT ACC TCAAAACAAG			
		GTAA TGG AGTTTTGTTC			
		AGA _ II			
GAM257 MADH4		CATTGCCACCTTTGCAGAACA	3869	AT_ A	AGCGC
		CATTGCCACC CA AACA			
		GTAACGGTGG GT TTGT			
		AAAC C IIICG			
GAM257 MAOB		ATTTCTACCATCAAAA-AAG	3863	CATTGCC	C CG
		ACCATCAAAA AAG			
		TGGTAGTTTT TTC			
		AAAGA_ _ AI			
GAM257 MARK3		CAATGCGAGGGTCAAAACAA	3874	T CACCA	GCG
		CA TGC TCAAAACAA			
		GT ACG AGTTTTGTT			
		T CTCCC III			
GAM257 MECP2		GCCCACTTTAAACAAGCGC	3880	CATTGCCACCATC	
		AAAACAAGCG			
		TTTTGTTCGC			
		TGAAA_____			
GAM257 PDE4D		CATTGTCCAC-ATCAAAAC	3865	_ C	AAGC
		CATTG CCAC ATCAAAAC			
		GTAAC GGTG TAGTTTTG			
		A _ IIIC			
GAM257 RERE		CATTTTCAACAGACAAAACAAGC	3870	GC C T_	GCI
		CATT CA CA CAAAACAAGC			
		GTAA GT GT GTTTTGTTCG			
		AA T CT III			
GAM257 STX1A		GCCACCATCCCAAACATGC	3878	CATTGCCA A_ A	
		CCATC AAACA GCG			
		GGTAG TTTGT CGT			
		_____ GG A			
GAM257 TRPM7		CATCACCTCATCAAAACAA	3875	TG AC	GCG
		CAT CC CATCAAAACAA			
		GTA GG GTAGTTTTGTT			
		GT GA III			
GAM257 UVRAG		TTGCCACCA-CCTACCAAGC	3882	CATT AAAA	G
		GCCACCATC CAAGC			

	CGGTGGTGG GTTCG			
	_____ ATG_ G			
GAM257 WHSC1L1	ATTGTGACCATTAA--CAAGCGC	3864	CA CC	CAA
	TTG ACCAT AACAGCGC			
	AAC TGGTA TTGTTCGCG			
	__ AC A__			
GAM257 ZNF80	CATTGTATTCATCAAAACA	3873	CCAC	AGCG
	CATTG CATCAAAACA			
	GTAAC GTAGTTTTGT			
	ATAA IIIC			
GAM258 ABCD3	GCTCATTTGGAGTTTAATACCA	3896	A ____	III
	GCTCATTTG AG AATACC			
	CGAGTAAAC TC TTATGG			
	C AAA TII			
GAM258 ABCD3	GCTCATTTGGAGTTTAATACCA	3896	TAGC A ____	CAA
	TCATTTG AG AATACCA			
	AGTAAAC TC TTATGGT			
	_____ C AAA TTI			
GAM258 APLP2	AGCTCATTTAAAAAGGGAATAC	3888		ATAIIIG
	AGCTCATTTGAAGA			
	TCGAGTAAATTTTT			
	CCCTTAT			
GAM258 APLP2	AGCTCATTTAAAAAGGGAATAC	3888	TA ____	CACAA
	GCTCATTTGAA GAATAC			
	CGAGTAAATTT CTTATG			
	_____ TTCC AIIIA			
GAM258 CD164	AGCTCATTTGTAGACTTGCAAAA	3890	A ATAC	CAI
	GCTCATTTG AGA CA			
	CGAGTAAAC TCT GT			
	A GAAC TTI			
GAM258 CD164	AGCTCATTTGTAGACTTGCAAAA	3890	TA A ATAC	CAAI
	GCTCATTTG AGA CA			
	CGAGTAAAC TCT GT			
	_____ A GAAC TTTA			
GAM258 CRIM1	AGCTTTTTTTGAAGAAAACAAAAA	3891	CA T	CACAI
	GCT TTTGAAGAA AC			
	CGA AAACCTTCTT TG			
	AA T TTTTI			
GAM258 CRIM1	AGCTTTTTTTGAAGAAAACAAAAA	3891	TA CA T	CACAAI
	GCT TTTGAAGAA AC			

	CGA AACTTCTT TG		
	__ AA T TTTTG		
GAM258 CYP4F3	TCATTGATGAAGAATAACTCAA	3897 CATT	CCACAI
	TGAAGAATA		
	ACTTCTTAT		
	AACT TGAGTI		
GAM258 CYP4F3	TCATTGATGAAGAATAACTCAA	3897 TAGCTCATT	CCACAAI
	TGAAGAATA		
	ACTTCTTAT		
	AACT_____ TGAGTTA		
GAM258 CYP4F3	GCACATTTTGAAGAA---CACAA	3895 T _	CACI
	GC CATTT GAAGAATAC		
	CG GTAAA CTTCTTGTG		
	T A TTII		
GAM258 CYP4F3	GCACATTTTGAAGAA---CACAA	3895 TAGCTCA	CACA
	TTTGAAGAATAC		
	AACTTCTTGTG		
	TGTA_____ TTTT		
GAM258 DNMT1	ATTTGAAGAAATATTACAA	3892	TACCACAI
	ATTTGAAGAA		
	TAAACTTCTT		
	TATAATGTT		
GAM258 FZD8	TCATT--AAGAATACC-CAA	3898 TG	ACI
	TCATT AAGAATACC		
	AGTAA TTCTTATGG		
	_____ GTT		
GAM258 PCSK1	AGTTCCCTT-AAGAATACCA	3889 G_____	ATTG I
	CTC AAGAATACC		
	GGG TTCTTATGG		
	TCAA AA_____ I		
GAM258 PCSK1	AGTTCCCTT-AAGAATACCA	3889 TAG	ATTG CA
	CTC AAGAATACCA		
	GGG TTCTTATGGT		
	CAA AA_____ TI		
GAM258 SCML2	CATATGAAGAATAAACACA	3893 T	C_ II
	CAT TGAAGAATA CAC		
	GTA ACTTCTTAT GTG		
	T TT TI		
GAM258 SEL1L	AGCTTCTTTTCAATGAATACCACA	3886 GC A G _	I
	TC TTT AA GAATACCAC		

	AG AAA TT CTTATGGTG		
	A_ A G A I		
GAM258 SEL1L	AGCTTCTTTTCAATGAATACCACA 3886 TA	_ A G _	AI
	GCT C TTT AA GAATACCACA		
	CGA G AAA TT CTTATGGTGT		
	_ A A G A GI		
GAM258 TP63	AGCTCATTGTCATGCATGCAAAAA 3887 TA		AAGAATACCACAAI
	GCTCATTG		
	CGAGTAAAC		
	_ GTACGTACGTTTTT		
GAM258 ZNF266	CTCATTGAAG-TTACTCAC 3894	AA _ II	
	CTCATTGAAG TAC CA		
	GAGTAACTTC ATG GT		
	A_ A GI		
GAM258 ZNF266	CTCATTGAAG-TTACTCAC 3894 TAGCTC	AA _ A	
	ATTTGAAG TAC CAC		
	TAACTTC ATG GTG		
	_ A_ A G		
GAM259 BRCA1	TCGCTTGAGCCTAGGAGGTCA 3906 A	AC_	TCI
	TC CTTGGG AGGAGGTCA		
	AG GAACTC TCCTCCAGT		
	C GGA III		
GAM259 BRCA1	TCGCTTGAGCCTAGGAGGTCA 3906 CA	AC_	I
	CTTGGG AGGAGGTC		
	GAACTC TCCTCCAG		
	C_ GGA I		
GAM259 DLEC1	TCACTTGGGCCCAGCAGGCCAT 3903	A_ G	CI
	TCACTTGGG CAG AGGTCAT		
	AGTGAACCC GTC TCCGGTA		
	GG G II		
GAM259 DLEC1	TCACTTGGGCCCAGCAGGCCAT 3903 C	A_ G	I
	ACTTGGG CAG AGGTCA		
	TGAACCC GTC TCCGGT		
	_ GG G I		
GAM259 LZTR1	TCACATCGAACCGCAGGAGGTCAT 3905	_ A_	CII
	TCAC TTGGG CAGGAGGTCAT		
	AGTG AGCTT GTCCTCCAGTA		
	T GGC III		
GAM259 LZTR1	TCACATCGAACCGCAGGAGGTCAT 3905 CAC	A_	I
	TTGGG CAGGAGGTCA		

		AGCTT GTCCTCCAGT			
		T__ GGC I			
GAM259 MYCL2	TCACCTAGGTCAGGAGGTCA	3908	A	TC	
	TCACCTGGG CAGGAGGTCA				
	AGTGGATCC GTCCTCCAGT				
	A II				
GAM259 MYCL2	TCACCTAGGTCAGGAGGTCA	3908	A	I	
	CACTTGGG CAGGAGGTC				
	GTGGATCC GTCCTCCAG				
	A I				
GAM259 RAD52	TCACCTGGGCCCAAGAGGT	3902	A_	CATC	
	TCACCTGGG CAGGAGGT				
	AGTGAACCC GTTCTCCA				
	GG IIIC				
GAM259 RAD52	TCACCTGGGCCCAAGAGGT	3902	A_	II	
	TCACCTGGG CAGGAGG				
	AGTGAACCC GTTCTCC				
	GG AI				
GAM259 SLC21A3	TCACCTGGGAAGCCCAAGGGGTCA	3904	_____ A	TCII	
	TCACCTGGGA CAGG GTCA				
	AGTGAACCCT GTTC CCACT				
	TCGG C IIIC				
GAM259 SLC21A3	TCACCTGGGAAGCCCAAGGGGTCA	3904	CACT _____ A	I	
	TGGGA CAGG GGTC				
	ACCCT GTTC CCACT				
	_____ TCGG C I				
GAM259 TNFAIP2	TCACCTGAACCAGGAGGTC	3907	GA	ATC	
	TCACCTGG CAGGAGGTC				
	AGTGAACCT GTCCTCCAG				
	TG III				
GAM259 TNFAIP2	TCACCTGAACCAGGAGGTC	3907	GA	II	
	TCACCTGG CAGGAGGT				
	AGTGAACCT GTCCTCCA				
	TG GI				
GAM259 WARS	ACTGGGTGACAGGAGGGCA	3901	T _	TCII	
	ACT GG GACAGGAGG				
	TGA CC CTGTCCTCC				
	C A CGTI				
GAM259 WARS	ACTGGGTGACAGGAGGGCA	3901	TCACCTT _	T TC	
	GG GACAGGAGG CA				

	CC CTGTCCTCC GT	
	AC___ A C CT	
GAM260 CELL	AGGTCTTGGCA---CTCTTG 3912 TGAG G TGC	
	GTCTTGG A CTCTTG	
	I	
	CAGAACC T GAGAAC	
	___ G ___	
GAM260 HIP1	TGAGGTCTTGCTATGATGCC 3915 G___ TCTTGC	
	TGAGGTCTTG GATGCC	
	ACTCCAGAAC CTACGG	
	GATA III GCG	
GAM260 PCDH15	TCTTGCCAAGGCTGCCTCTTGC 3914 TGAGGT T A	
	CT GGG TGCCTCTTGCG	
	GG TCC ACGGAGAACGT	
	___ T G	
GAM260 RHO	AGGTCTTGGTGGATGTCCCTT 3911 TGAG ___ C GCG	
	GTCTTGG GATG CTCTT	
	CAGAACC CTAC GGGAA	
	___ AC A GAI	
GAM260 USP6	GGTCTTGGGTTGTGACTTG 3913 TGAGGT A CCT C	
	CTTGGG TG CTTG	
	GAACCC AC GAAC	
	___ A ACT C	
GAM260 ZNF136	TGAGGTCTTGCTATG--TTTTGC 3916 GG CCTC G	
	TGAGGTCTTG ATG TTGC	
	ACTCCAGAAC TAC AACG	
	GA AA___ I	
GAM261 AVP	CCAAGAAGA---GGGTAAG 3921 TACC T_ AAG	
	AAGAAGAG TGGGA	
	TTCTTCTC ATTCT	
	___ CC CII	
GAM261 LPP	AAGAAGTACTCCCCTGGGAAAGCA 3919 TACCAAGAAGAG CI	
	TTGGGAAAGCA	
	GACCCTTTCGT	
	TCATGAGGG___ CG	
GAM261 OGT	CAAGAAGAGTTAG--AAGC 3920 TACCAA AA	
	GAAGAGTTGGG AGC	
	CTTCTCAATCT TCG	

GAM262 ACCN1	CTTCTTTCCAGCACTGGGGCCA 3939 ___ A III	
	CTTCT TAG GCTGGGGCC	

	GAAGA GTC TGACCCCGG		
	AAG G TII		
GAM262 ACCN1	CTTCTTTCCAGCACTGGGGCCA 3939 CAAGTC T A		
	TTCT AG GCTGGGGCCA		
	AAGG TC TGACCCCGGT		
	_____ _ G		
GAM262 ADAM19	CAAGTGT-CTCAGAGCTGGGGC 3937 CT CA		
	CAAGT TCTTAGAGCTGGGGC		
	GTTCA AGAGTCTCGACCCCG		
	C_ II		
GAM262 ADAM19	CAAGTGT-CTCAGAGCTGGGGC 3937_ CT I		
	AAGT TCTTAGAGCTGGGG		
	TTCA AGAGTCTCGACCCC		
	G C_ I		
GAM262 B3GAT1	TCTTCAGTAG-GCTGGGGCC 3944 T_ A II		
	TCTTC TAG GCTGGGGC		
	AGAAG ATC CGACCCCG		
	TC _ GI		
GAM262 B3GAT1	TCTTCAGTAG-GCTGGGGCC 3944 CAAGTCTTCT A		
	TAG GCTGGGGCC		
	ATC CGACCCCGG		
	GTC_____ _		
GAM262 B4GALT3	GTCTTCTTAGGGATCATGGGG 3942 AGC_ III		
	GTCTTCTTAG TGGG		
	CAGAAGAATC ACCC		
	CCTAGT CII		
GAM262 B4GALT7	TCCTGTCAGAGCTGGGCCCA 3946 C G I		
	CTT TTAGAGCTGGG CC		
	GGA AGTCTCGACCC GG		
	C G I		
GAM262 B4GALT7	TCCTGTCAGAGCTGGGCCCA 3946 CAAGTCTTC G		
	TTAGAGCTGGG CC		
	AGTCTCGACCC GG		
	C_____ G		
GAM262 CSF1R	CAAGT-TTC--AGAGCTGGG 3936 CTTC GC		
	CAAGT TTAGAGCTGGG		
	GTTCA AGTCTCGACCC		
	A_ II		
GAM262 CSF1R	CAAGT-TTC--AGAGCTGGG 3936_ CTTC		
	AAGT TTAGAGCTGG		

	TTCA AGTCTCGACC	
	G A__	
GAM262 EXT1	AGTGCATCTTGCAGCTGGGGC 3930_ CT AG I	
	GT TCTT AGCTGGGG	
	CG AGAA TCGACCCC	
	A T_ CG I	
GAM262 EXT1	AGTGCATCTTGCAGCTGGGGC 3930 CAA CT AG CA	
	GT TCTT AGCTGGGGC	
	CG AGAA TCGACCCCG	
	A__ T_ CG CG	
GAM262 HPRT1	CAAACTTCTTAGATGCTG 3935 T _ GGGCC	
	CAAG CTTCTTAGA GCTG	
	GTTT GAAGAATCT CGAC	
	T A AC	
GAM262 HPRT1	CAAACTTCTTAGATGCTG 3935 T _	
	CAAG CTTCTTAGA GCT	
	GTTT GAAGAATCT CGA	
	T A CI	
GAM262 IL17R	AAGT-TCCTTCATGGCTGGGGCCA 3924 C AGA_ I	
	AGT TTCTT GCTGGGGCC	
	TCA AGGAA CGACCCCGG	
	_ GTAC I	
GAM262 IL17R	AAGT-TCCTTCATGGCTGGGGCCA 3924 CAAG TTAGA I	
	TCTTC GCTGGGGCCA	
	GGAAG CGACCCCGGT	
	TCAA TAC__ A	
GAM262 IL1F5	AGCCTTCTTAGAGACTGGATCCA 3931 CAAGT _ GG I	
	CTTCTTAGAG CTGG CCA	
	GAAGAATCTC GACC GGT	
	G__ T TA T	
GAM262 IL1F5	AGCCTTCTTAGAGACTGGATCCA 3931 GT _ GG I	
	CTTCTTAGAG CTGG CC	
	GAAGAATCTC GACC GG	
	G_ T TA I	
GAM262 ITGA5	AAGGCTTCAGGGAGGCTGGGGCC 3925 A T TTA _ I	
	G CTTC GAG CTGGGGC	
	C GAAG CTC GACCCCG	
	C_ TCC C I	
GAM262 ITGA5	AAGGCTTCAGGGAGGCTGGGGCC 3925 CA T TTA _ AI	
	AG CTTC GAG CTGGGGCC	

	TC GAAG CTC GACCCCGG	
	__ C TCC C AI	
GAM262 MLLT2	CAA-TCTGTTTTAGAGCTGG 3934 CA TC_ GGCC	
	AGTCT TTAGAGCTGG	
	TTAGA AATCTCGACC	
	G_ CAA IIIA	
GAM262 MLLT2	CAA-TCTGTTTTAGAGCTGG 3934 CA TC_ II	
	AGTCT TTAGAGCTG	
	TTAGA AATCTCGAC	
	G_ CAA CI	
GAM262 MMP19	AGCCCTCGTAGA-CTGGGGCCA 3932 _ T G I	
	GTCTTC TAGA CTGGGGCC	
	CGGGAG ATCT GACCCCGG	
	T C _ I	
GAM262 MMP19	AGCCCTCGTAGA-CTGGGGCCA 3932 CAAGT T G	
	CTTC TAGA CTGGGGCCA	
	GGAG ATCT GACCCCGGT	
	G_ C _	
GAM262 MX2	GTCTCCCTGTCAGAGCTGGGG 3941 _ III	
	GTCTTCT TAGAGCTGGG	
	CAGAGGG GTCTCGACCC	
	ACA CII	
GAM262 MX2	GTCTCCCTGTCAGAGCTGGGG 3941 CAAG C CCA	
	TCTT TTAGAGCTGGGG	
	GGA AGTCTCGACCCC	
	A_ C CTA	
GAM262 MYO1D	CAAGGCCTTCTCAGCAGCTGGGGC 3933 _ _ CAI	
	CAAG TCTTCTTAG AGCTGGGGC	
	GTTC GGAAGAGTC TCGACCCCG	
	C G III	
GAM262 MYO1D	CAAGGCCTTCTCAGCAGCTGGGGC 3933 AA _ I	
	GTCTTCTTAG AGCTGGGG	
	CGGAAGAGTC TCGACCCC	
	C_ G I	
GAM262 PLCG1	CTTCATCCAGAGCTGGGGC 3940 _ III	
	CTTC TTAGAGCTGGGG	
	GAAG GGTCTCGACCCC	
	TA GII	
GAM262 PLCG1	CTTCATCCAGAGCTGGGGC 3940 CAAGTCTTC C	
	TTAGAGCTGGGGC	

		GGTCTCGACCCCG		
		A _____ T		
GAM262 PPP1R12B		AAGTCTTCTTAAACTTGGGG	3928	GC I
		AGTCTTCTTAGA TGGG		
		TCAGAAGAATTT ACCC		
		GA I		
GAM262 PPP1R12B		AAGTCTTCTTAAACTTGGGG	3928 CA	GC CC
		AGTCTTCTTAGA TGGGG		
		TCAGAAGAATTT ACCCC		
		_____ GA AI		
GAM262 PRKG2		AAGT-TGCTGAGAGCTGGGG	3927 _ CTT T	I
		AGT CT AGAGCTGGG		
		TCA GA TCTCGACCC		
		T AC_ C I		
GAM262 PRKG2		AAGT-TGCTGAGAGCTGGGG	3927 CA CTT T	CC
		AGT CT AGAGCTGGGG		
		TCA GA TCTCGACCCC		
		_____ AC_ C TI		
GAM262 PROS1		AAG-CTTTTCGGAGCTGGGG	3926 _ T C TA	I
		AG CTT T GAGCTGGG		
		TC GAA A CTCGACCC		
		T _ A GC I		
GAM262 PROS1		AAG-CTTTTCGGAGCTGGGG	3926 CA T C TA	CC
		AG CTT T GAGCTGGGG		
		TC GAA A CTCGACCCC		
		_____ A GC CI		
GAM262 RFX2		TCTTAAAGGGACTGGGGCCA	3943 _____	
		TCTTAGAG CTGGGGCC		
		AGAATTC GACCCCGG		
		CCT TII		
GAM262 RFX5		CAAGTCTTC---ACCTGGAGCCA	3938	TTAGAG
		CAAGTCTTC CTGGGGCC		
		GTTCAGAAG GACCTCGG		
		TG_____		
GAM262 RFX5		CAAGTCTTC---ACCTGGAGCCA	3938 _	TTAGAG
		AAGTCTTC CTGGGGCC		
		TTCAGAAG GACCTCGG		
		G TG_____		
GAM262 SLC29A1		TCATCTCGGGGCTGGGGCCA	3945 CT AGA	I
		TCTT GCTGGGGCC		

	AGAG CGACCCCGG			
	GT CCC I			
GAM262 STK4	AAGCCTGGGTGGAGCTGGGGCC	3929	TCTTA	I
	AGTCT GAGCTGGGGC			
	TCGGA CTCGACCCCG			
	CCCAC I			
GAM262 STK4	AAGCCTGGGTGGAGCTGGGGCC	3929 CA	TCTTA	A
	AGTCT GAGCTGGGGCC			
	TCGGA CTCGACCCCG			
	— CCCAC G			
GAM263 AANAT	GATACCCAGTGTTCCTCCA	3959 AGAA	ACGA	T
	ACC GTTCCCTCCAT			
	TGG CAAGGGAGGTG			
	TA__ GTCA I			
GAM263 APC	AGGAAGGAAGACTTCCCTCCA	3953 AGAAACCAC	G	TTT
	GA TTCCCTCCA			
	CT AAGGGAGGT			
	TCCTTCCTT G			
GAM263 AQP6	AGAAAGTA--AGTTCCCTCC	3951	CCAC	AT
	AGAAA GAGTTCCCTCC			
	TCTTT TTCAAGGGAGG			
	CA__			
GAM263 CASP8	GAAAACAC---TTCCCTCCA	3957 A	C GAG	T
	GAAAC AC TTCCCTCCA			
	TTTTG TG AAGGGAGGT			
	— — — C			
GAM263 DAXX	AACCTCGCATGGTTCCCTCC	3949 AGAAACCACGA		ATT
	GTTCCCTCC			
	CAAGGGAGG			
	GAGCGTAC__ CGG			
GAM263 FGFR3	GAATTCACGGCTTCCCTCCA	3958 AGAAAC	AG	TT
	CACG TTCCCTCCA			
	GTGC AAGGGAGGT			
	TTAA__ CG TI			
GAM263 OPA1	AGAAATGAAGATCTCCCTCCAT	3954	CCAC G	TT
	AGAAA GA TTCCCTCCAT			
	TCTTT CT GAGGGAGGTA			
	ACTT A			
GAM263 PAICS	GAAA--ATGAGTTCCCTTCAT	3960 AGAAACCAC		C T
	GAGTTCCCT CAT			

	CTCAAGGGA GTA		
	TTTTA___ A C		
GAM263 RAD54B	AGAAACCACTGG--CCCTGCA 3952	GAGTT C TT	
	AGAAACCAAC CCCT CA		
	TCTTTGGTG GGA GT		
	ACC__ C II		
GAM263 RTDR1	AGAAACCACTCACTGCCTCC 3950	GAGTTC ATT	
	AGAAACCAAC CCTCC		
	TCTTTGGTG GGAGG		
	AGTGAC III		
GAM263 WIF1	AGAAAC----AGGTCCCTCCATT 3955	CACG T	
	AGAAAC AG TCCCTCCATT		
	TCTTTG TC AGGGAGGTAA		
	___ C		
GAM263 WT1	GAAA--ATGAATTCCTCCATTT 3956	AGAAACCAAC _	
	GAGTTCCC TCCATTT		
	CTTAAGGG AGGTAAA		
	TTTTA___ G		
GAM264 AKAP13	CAGGTTCACTACTGCCCTCC 3965	___ G III	
	CAGGTTCACTA GCC TC		
	GTCCAAGTCAT CGG AG		
	GA G GII		
GAM264 AKAP13	CAGGTTCACTACTGCCCTCC 3965	TGCCAGG ___ G CC	
	GTTCAGTA GCC TCC		
	CAAGTCAT CGG AGG		
	___ GA G AC		
GAM264 AOC3	AGGTTCACT----GTCCCC 3963	AGCC	
	AGGTTCACT GTCCC		
	TCCAAGTCA CAGGG		

GAM264 BDKRB2	CCAGGTTCACT--CCCTCC 3967	GTAG G I	
	CCAGGTTCA CC TC		
	GGTCCAAGT GG AG		
	AA__ G G		
GAM264 BDKRB2	CCAGGTTCACT--CCCTCC 3967	TGCC GTAG G C	
	AGGTTCA CC TCC		
	TCCAAGT GG AGG		
	___ AA__ G T		
GAM264 BDKRB2	TGCCAGGTTCC--TAGCCCTCC 3974	AG G CC	
	TGCCAGGTTCC TAGCC TCC		

	ACGGTCCAAG ATCGG AGG	
	___ G II	
GAM264 BDKRB2	TGCCAGGTTC--TAGCCCTCC 3974_ AG G I	
	GCCAGGTTC TAGCC TC	
	II	
	CGGTCCAAG ATCGG AG	
	A ___ G I	
GAM264 C4B	CCAGGTTCAGGTTCC-TCCC 3968_ TAG G I	
	CAGGTTTCAG CC TCC	
	GTCCAAGTC GG AGG	
	G CAA _ I	
GAM264 C4B	CCAGGTTCAGGTTCC-TCCC 3968 TGCC TAG G C	
	AGGTTTCAG CC TCCC	
	TCCAAGTC GG AGGG	
	___ CAA _ T	
GAM264 CDY2	TGACAGCTTGCTCAGTAGCC 3972 T___ CAG III	
	GC GTTCAGTAGC	
	II	
	CG CGAGTCATCG	
	ACTGT AA_ GII	
GAM264 GNB5	GCC-GCTCCAGCAGCCGTCCCC 3970_ AGG I	
	CC TTCAGTAGCCGTCCCC	
	II	
	GG AGGTCGTCTGGCAGGG	
	C CG_ I	
GAM264 GORASP1	CAGGTGATGAGGGGCCGTCCCC 3964 A_ TC TA I	
	GGT AG GCCGTCCC	
	III II	
	CTA TC CGGCAGGG	
	CA C_ CC I	
GAM264 GORASP1	CAGGTGATGAGGGGCCGTCCCC 3964 TGCCA TC TA C	
	GGT AG GCCGTCCCC	
	III II	
	CTA TC CGGCAGGGG	
	CA___ C_ CC T	
GAM264 IL6R	TTAAGTAAAGCCGTCCCC 3976 TTC ___ III	
	AGT AGCCGTCCC	
	III	
	TCA TCGGCAGGG	
	AAT TTT GII	
GAM264 MECP2	CAGGTTCAGAAGCCATGTCC 3966 T CIII	
	CAGGTTTCAG AGCCGT	
	GTCCAAGTC TCGGTA	
	T CAGG	
GAM264 MECP2	CAGGTTCAGAAGCCATGTCC 3966 TGCCAG T ___ CC	
	GTTCAG AGCC GTCC	

	CAAGTC TCGG CAGG	
	_____ T TA AG	
GAM264 MPDU1	TGCCTGAGTCATTCTCCGTCCCC 3975	A GT GTAG I
	TGCC G TCA CCGTCCCC	
	ACGG C AGT GGCAGGGG	
	A TC AAGA I	
GAM264 MPDU1	TGCCTGAGTCATTCTCCGTCCCC 3975	A GT GTAG I
	GCC G TCA CCGTCCCC	
	CGG C AGT GGCAGGGG	
	A TC AAGA I	
GAM264 PLCB2	GCCAGGG--AGTGGCCGTCCCC 3971_	TTC A I
	CCAGG AGT GCCGTCCC	
	GGTCC TCA CGGCAGGG	
	C C__ C I	
GAM264 PLCB2	GCCAGGG--AGTGGCCGTCCCC 3971 TG	TTC A
	CCAGG AGT GCCGTCCCC	
	GGTCC TCA CGGCAGGG	
	__ C__ C	
GAM264 TCF1	GCCAGGTTCTCAGCAGCAGGCC 3969 CC	__ C_ CI
	AGGT TCAGTAGC GTC	
	TCCA AGTCGTCG CGG	
	__ AG TC II	
GAM264 TCF1	GCCAGGTTCTCAGCAGCAGGCC 3969 TG	__ C_ CCCI
	CCAGGT TCAGTAGC GTCC	
	GGTCCA AGTCGTCG CGGG	
	__ AG TC TIII	
GAM264 ZNF180	TGCCAGGTTGAAAAGTCGT 3973	C T C CCCC
	TGCCAGGTT AG AG CGT	
	ACGGTCCAA TT TC GCA	
	C T A IIIC	
GAM264 ZNF180	TGCCAGGTTGAAAAGTCGT 3973	C T C II
	TGCCAGGTT AG AG CG	
	ACGGTCCAA TT TC GC	
	C T A AI	
GAM265 ABCA1	TAATTTGAAATC---TGAA 3982 TGTA	AGT
	ATTTGAAATC TGAA	
	TAAACTTTAG ACTT	
GAM265 AS3	TAATTTGAAATTGGTTTGAA 3981 TGTA	CAG_ TT
	ATTTGAAAT TTGAA	

	TAAACTTTA AACTT		
	_____ ACCA TA		
GAM265 CPNE3	TGTAATTTGATGAATTA-TTCAA 3984	AATCAGT	T
	TGTAATTTGA TGAATT		
	ACATTAAACT ACTTAA		
	_____ T		
GAM265 DDX15	TAATTTATGAAATCAGAATGGAAT 3980	TGTAATT	TT__ TTI
	TGAAATCAG GAAT		
	ACTTTAGTC CTTA		
	TAAAT__ TTAC TAI		
GAM265 DIAPH2	TGTAATTTGAAAGCAGATTAAGTT 3987	T TTG	I
	TGTAATTTGAAA CAG AATTT		
	ACATTAAAGTTT GTC TTGAA		
	C TAA I		
GAM265 KLRC4	TATTATGAAGTCAGTTGAAT 3983	TGTAATT A	T
	TGAA TCAGTTGAAT		
	ACTT AGTCAACTTA		
	AAT__ C T		
GAM265 TEM8	TGTAATTTGAGAAGGATTGTGAA 3985	AATCA	AATTTI
	TGTAATTTGA GTTG		
	ACATTAAACT TAAC		
	CTTCC ACTTII		
GAM265 TNC	GTAGACTTCAAATCAGTTG 3979	TGTA G	AATT
	ATTT AAATCAGTTG		
	TGAA TTTAGTCAAC		
	ATC_ G AIII		
GAM265 TRPM6	TGAAATTTGAAATCCAAATGTATTT 3986	T AGT_ A	II
	TG AATTTGAAATC TG ATTT		
	AC TTAAACTTTAG AC TAAA		
	T GTTT A II		
GAM266 ATP11B	TTAACTTTTC-CCATGAAA 3996	TT G	CA
	TAACTTTTC CCATGGAA		
	ATTGAAAAG GGTACTTT		
	_____ TI		
GAM266 B4GALT5	GCCATGCT-GA---TGAAAAG 3994	TTGC	GAAC
	CATGCTG GTGAAAA		
	GTACGAC TACTTTT		

GAM266 BCL2	CCATGCTCCA-CGTGAAAA 3991	TTGCCA	GGA
	TGCT ACGTGAAAA		

	ACGA TGCAC TTTT			
	_____ GG_			
GAM266 CLN5	TTTAACTTTTATGCACCAAGGAAGAA 4003	T__ T	CAACII	
	TTTAACTTT CGCCA GGAA			
	AAATTGAAA GTGGT CCTT			
	TAC T CTTIII			
GAM266 CSNK1A1	TTAACTTTTCCACTTGAAAAAA 3998 TT	_ CA	CAAC	
	TAAC TTTTC GC TGGAA			
	ATTGAAAAG TG ACTTT			
	_____ G A_ TTTA			
GAM266 EIF2C1	CCATGCTGG-ACTTGAGAGGG 3993 TTGCCA	ACG	AA	
	TGCTGGA TGA AG			
	ACGACCT ACT TC			
	_____ GA_ C_			
GAM266 GPC4	TTTAACTTTTGG--AT-GAACA 4006	CGCCATG	A	
	TTTAACTTTT GAACA			
	AAATTGAAAA CTTGT			
	ACTA_____ I			
GAM266 IL1RN	TTGCCATGCAAGAATGGGAACAGG 4000	T CGT	A I	
	TTGCCATGC GGAA GAA AGG			
	AACGGTACG TCTT CTT TCC			
	T ACC G I			
GAM266 IMPA1	TGGCATGGT--AACGTGAAA 3995 TTGCCAT	_ _	A	
	GC TGG AACGTGAAA			
	CG ACC TTGCACTTT			
	C_____ T A A			
GAM266 MEN1	TTTAACTTTTATCTACCTGAAACA 4002	C__ A	ACI	
	TTTAACTTTT GCC TGGAAACA			
	AAATTGAAAA TGG ACTTTGT			
	TAGA _			
GAM266 NXF3	CCATACTTTATTGTGAAAAGG 3992 TTGCCA	GGAAC		
	TGCT GTGAAAAGG			
	ATGA CACTTTTCC			
	_____ AATAA			
GAM266 OGT	AACTTAGTTGACCATGGAAC 3990 TTTAACTTTTC	AA		
	GCCATGGAAC			
	TGGTACCTTG			
	AATCAAC_____ AG			
GAM266 PCDHB4	TTTAA-TATTAGCATTTCATGGAACA 4004 TTTAACTTTTC	_____	ACI	
	GC CATGGAACA			

	CG GTACCTTGT		
	AAATTATAAT_ TAA III		
GAM266 PPARBP	TTTAACTTTTCTTTCTGGCACAGGAACAA4001	C_____ T	CIII
	TTTAACTTTT GC CA GGAACAA		
	AAATTGAAAG CG GT CCTTGT		
	AAAGAC T _ IIIC		
GAM266 RRM2B	TTTAACTTTTTACAAAGGAGCA 4005	CG CAT A AC	
	TTTAACTTTT C GGA CA		
	AAATTGAAAA G CCT GT		
	AT TTT C II		
GAM266 SPTBN1	TTGC-ATGCTGGAATTTCACTGAAAAGG3999	C _____ III	
	TTGC ATGCTGGAA CG TGAAGG		
	AACG TACGACCTT GT ACTTTTCC		
	_ AAA G III		
GAM266 SRY	TTAACTTTT-GTAATGAAAC 3997 TT	CGCC AA	
	TAAC TTTT ATGGAAC		
	ATTGAAAA TACTTTG		
	_ CAT_ AI		
GAM267 APOL1	GGTAAGAGCGATGGGACTGT 4013 _	A TCAT GT	
	TGGGA GT TGGGACTGT		
	ATTCT CG ACCCTGACA		
	C _ CT_ AI		
GAM267 APOL1	GGTAAGAGCGATGGGACTGT 4013 GG	TTCAT I	
	AAG TGGGACTG		
	TTC ACCCTGAC		
	CA TCGCT I		
GAM267 C21orf33	TGGGAAGTTGCCATTTTGGGA 4014	_ _ CTGTGTC	
	TGGGAAGT TCAT TGGGA		
	ACCCTTCA GGTA ACCCT		
	AC AA IICTGT		
GAM267 C21orf33	TGGGAAGTTGCCATTTTGGGA 4014	_ _ IIIT	
	TGGGAAGT TCAT TGGG		
	ACCCTTCA GGTA ACCC		
	AC AA TIII		
GAM267 KLRC4	TGTGATGT-CA--GGGACTGTG 4017 GG_ A T TT		
	GA GT CA GGGACTGT		
	CT CA GT CCCTGACA		
	ACA A _ _		
GAM267 KLRC4	TGTGATGT-CA--GGGACTGTG 4017 TGG A T TT	T	
	GA GT CA GGGACTGTG		

	CT CA GT CCCTGACAC		
	ACA A _ _ I		
GAM267 NR2E1	GAAGTTCATCTGATACTGT 4011	GGG_ II	
	GAAGTTCATT ACTG		
	CTTCAAGTAG TGAC		
	ACTA AI		
GAM267 NR2E1	GAAGTTCATCTGATACTGT 4011	TGGGAA GGG_ G	
	GTTCACT ACTGT T		
	I		
	CAAGTAG TGACA G		
	_____ ACTA G		
GAM267 PIGN	TGGGAAGTT--GTGCGACTG 4015	CAT G TG	
	TGGGAAGTT TG GACTG		
	ACCCTTCAA AC CTGAC		
	C_ G II		
GAM267 PIGN	TGGGAAGTT--GTGCGACTG 4015_	CAT G I	
	GGGAAGTT TG GACT		
	CCCTTCAA AC CTGA		
	A C_ G I		
GAM267 RBP3	AAGCTCCCTGG-ACTGTGT 4009	ATTG I	
	AAGTTC GGA CTGTG		
	TTCGAG CCTGACAC		
	GGA_ A		
GAM267 TCF12	GGAAGTTCAAAGTGATTATGTC 4012	TT _ C I	
	GAAGTTCA GG GA TGTGT		
	CTTCAAGT TC CT ATACA		
	T_ A A I		
GAM267 TCF12	GGAAGTTCAAAGTGATTATGTC 4012	TGGG TT _ C	
	AAGTTCA GG GA TGTGTC		
	TTCAAGT TC CT ATACAG		
	_____ T_ A A		
GAM267 TCIRG1	TGGGAAGTTC--CGGGCCTG 4016	AT A TG	
	TGGGAAGTTC TGGG CTG		
	ACCCTTCAAG GCCC GAC		
	_ G II		
GAM267 TCIRG1	TGGGAAGTTC--CGGGCCTG 4016	AT ACI	
	TGGGAAGTTC TGGG		
	ACCCTTCAAG GCCC		
	_ GGA		
GAM267 USP6	AAGTTCATTTGCA-TGTGT 4010	GGGAC I	
	AAGTTCATT TGTG		

	TTCAAGTAA ACAC	
	ACGT_ A	
GAM268 ACOX3	AATCTGCAATTT--CTTTT 4030 TGAAAT GA	
	CTGCAATTT CTTTT	
	GACGTTAAA GAAAA	
GAM268 ARCN1	_____ _	
	TGAAAT-TA-AACTTGACTTTTA 4035 C C G	
	TGAAAT TG AATTTGACTTTTA	
	ACTTTA AT TTGAACTGAAAAT	
GAM268 B3GAT1	- - I	
	AAAAGTGA-TTTGACTTTTA 4024 TGAAAT CA	
	CTG ATTTGACTTTTA	
	GAC TAACTGAAAAT	
	TT____ A_	
GAM268 CUL3	GAAATCTGC-ATTT--CTTTT 4031 TG A GA	
	AAATCTGCA TTT CTTTT	
	TTTAGACGT AAA GAAAA	
GAM268 DGKB	_____ _ _	
	AATCTGCAATTATGATCATTGTAG 4028 TGAAAT _ CTTTTAGI	
	CTGCAATT TGA	
	GACGTTAA ACT	
	_____ T AGTAACAT	
GAM268 LAMP2	GAAATCTGC-ATT--AATTTTAG 4032 TG AT C	
	AAATCTGCA TTGA TTTTA	
	TTTAGACGT AATT AAAAT	
GAM268 NEBL	_____ _ _	
	AAATATGTA--TTGACTTTTA 4025 TGAAATCTGCAAT	
	TTGACTTTTA	
	AACTGAAAAT	
	TATACAT_____	
GAM268 PMCHL1	TGAGAATCTGCAATTT-ACT 4034 _ ACTTTTA	
	TGA AATCTGCAATTTG	
	ACT TTAGACGT TAAAT	
	C GAIIGA	
GAM268 PTER	TGTAATAT--ATTTTGACTTTTA 4036 TGAAATCTGCAA G	
	TTTGACTTTTA	
	AACTGAAAAT	
	ACATTATATA__ I	
GAM268 RAB6A	AAATCTGCATAATATTGAGTTTTA 4021 TGAA AT__ C GI	
	ATCTGCA TTGA TTTTA	

		TAGACGT AACT AAAAT		
		____ ATTAT C AA		
GAM268 RANBP2		AAGCTGCAATTTTACATTT 4029 TGAAAT	G T A	
		CTGCAATTT AC TTT		
		GACGTTAAA TG AAA		
		____ A T C		
GAM268 RGS5		AAATCTGCACTTTTGACTGTAAG 4022 TGAA	A_ TTTAGI	
		ATCTGCA TTTGACT		
		TAGACGT AAAGTGA		
		____ GA CATTCA		
GAM268 SGC8		GAAATCTGCATCTTTCCTTTTAG 4033 TG	A GA I	
		AAATCTGCA TTT CTTTTAG		
		TTTAGACGT GAA GAAAATC		
		____ A AG T		
GAM268 SLC4A7		AAATCACCTGCAATTTTACTT 4020 TGAA	G TTAG	
		ATCTGCAATTT ACTT		
		TGGACGTTAAA TGAA		
		TAG_ A CAII		
GAM268 SOCS5		AAATCTGCAATTTAGGTTTCAG 4026 TGAA	AC	
		ATCTGCAATTTG TTTTAG		
		TAGACGTTAAAT AAAGTC		
		____ CC		
GAM268 SOCS5		AAACTGAAACATGTGACTTTTAG 4027_ C CAATT	I	
		TGAAAT TG TGAATTTTAG		
		ACTTTG AC ACTGAAAATC		
		G T _____ G		
GAM268 SORCS3		TGAAGGCAGACATTTGACTTTAAG 4037 ATCT	_____ TAGI	
		TGAA GCA ATTTGACTTT		
		ACTT CGT TAAACTGAAA		
		C_ CTG TTCI		
GAM268 UBL3		AAATCAGCT-TTTGACTTT 4023 TGAA T AA	T	
		ATC GC TTTGACTTT		
		TAG CG AAAGTGA		
		____ T A_ T		
GAM269 CDH11		TCACGCAGA-CCTC-TCTTGGG 4047	CGCA _ C T	
		TCACGCAGATC TC CT GG		
		AGTGCGTCTGG AG GA CC		
		____ A A C		
GAM269 CDKN1A		CGC-GAACACGCATCCTCG 4044 TCACGCA TC	G	
		GA CGCATCCTCG		

	TT GCGTAGGAGC	
	C_____ GT G	
GAM269 IDH3G	CACGCAGATACGC-T-CTCG 4043 TC C ATC G	
	ACGCAGAT CGC CTCG	
	TGCGTCTA GCG GAGC	
	__ T A__ G	
GAM269 IGFBP4	CGCTGCGCCGCATCCTCGG 4045 TCAC AGAT	
	GC CCGCATCCTCGGT	
	CG GGCGTAGGAGCCG	
	A__ C__	
GAM269 NEK6	TCACAGCAGATCCGAGTCCACGTGTG 4046 _ CA T _	
	TCAC GCAGATCCG TCC CG GTG	
	AGTG CGTCTAGGC AGG GC CAC	
	T TC T A	
GAM269 NLGN2	TCACGGATATC-G--TCCTCGGTG 4051 CAG CGCA	
	TCACG ATC TCCTCGGTG	
	AGTGC TAG AGGAGCCAC	
	CTA C__	
GAM269 SLC38A2	TCACGCAGA--CG--TCTTCAGTG 4049 CCGCA C	
	TCACGCAGAT TC TCGGT	
	AGTGCGTCTG AG AGTCA	
	C__ A	
GAM269 TGFB1	CACAGAGATCCGCAGTCCTC 4042 TC C _ GGT	
	ACG AGATCCGCA TCCTC	
	TGT TCTAGGCGT AGGAG	
	_ C C All	
GAM269 TXN	TCACGCAGAT-GGCA-ACTGGGT 4048 CC TC C G	
	TCACGCAGAT GCA CT GGT	
	AGTGCGTCTA CGT GA CCA	
	C_ T_ C I	
GAM269 UCN	TCACGCAGA-CAGTGCCCT-GGTG 4050 CC_ AT C	
	TCACGCAGAT GC CCT GGTG	
	AGTGCGTCTG CG GGA CCAC	
	TCA _ _	
GAM269 VENTX2	CACTGCAGGGCCCCAGCATCCTCG 4041 TCAC A__ _ GTGI	
	GCAG TCC GCATCCTCG	
	CGTC GGG CGTAGGAGC	
	TGA_ CCG T G	
GAM269 ZNF264	ACGCAGGGCCGCGCCTCCTCGGTG 4040 TCAC AT__ A	
	GCAG CCGC TCCTCGGTG	

	CGTC GGCG AGGAGCCAC			
	____ CCGGC G CG			
GAM270 BRF2	AGCCTTCAG-AGACTCCTG 4054 TCAG	C C C		
	CCTTCAG AG CTCCTG			
	GGAAGTC TC GAGGAC			
	____ _ T C			
GAM270 CA11	TCAGCCTTCTGCTGCCCCC 4062	A A TGCC		
	TCAGCCTTC GC GCCTCC			
	AGTCGGAAG CG CGGGGG			
	A A IIIC			
GAM270 CD3E	TTCACCATGAGGCTGAG-GAA 4067 TCATTG T C			
	ACC TGAGGCTGAG GA			
	TGG ACTCCGACTC CT			
	____ T _			
GAM270 COL9A1	CAGCCTTGGTC--CCTCCTGCCC 4057 TC CAGCAG			
	AGCCTT CCTCCTGCCC			
	TCGGAA GGAGGACGGG			
	_ CCAG_			
GAM270 EN2	TCAGCCTTCGGC--CCTCCCGC 4063	A AG C		
	TCAGCCTTC GC CCTCCTGC			
	AGTCGGAAG CG GGAGGGCG			
	C _ I			
GAM270 GJB3	CACTG-CCT-GAGGCTGAGGGA 4059 TC A T C			
	ATTG CCT GAGGCTGAG GA			
	TGAC GGA CTCCGACTC CT			
	_ _ _ C			
GAM270 HSPB3	CAGCCTTGAACAGCCTCCT 4056 TC C GCC			
	AGCCTT AGCAGCCTCCT			
	TCGGAA TTGTCTGGAGGA			
	_ C AII			
GAM270 KCNF1	GCCCTC-GCAGCCTCC-GCCC 4061 TCAGCCTTCA T			
	GCAGCCTCC GCC			
	CGTCGGAGG CGG			
	GAG_____ _			
GAM270 KCNMB4	CAGCCGCTTCAG-AGCCTCCTGC 4055 TC _ C CC			
	AGCC TTCAG AGCCTCCTGC			
	TCGG AAGTC TCGGAGGACG			
	_ CG _ TI			
GAM270 LSS	TCACT-ACCTTGAGGCCGTGC 4064 A A GA			
	TCATTG CCTTGAGGCTG GC			

AGTGAT GGAAC TCCGGC CG

— A II

GAM270 PPP1R12B CTTCATCCAGACTCCTGCCC 4060 TCAGCCTTCAG C
CAG CTCCTGCC
||| |||||
GTC GAGGACGG

AG — T

GAM270 PRSS11 CATTGACCTTTGGGTGCTGA 4058 TC GAG — GCGA
ATTGACCTT GCTGA
||||| ||||
TAACTGGAA C GACT

— ACCCA GIII

GAM270 TIAL1 TTGTCCTTGGGGAGGCTGAGC 4066 TCATTGA — AA
CCTT GAGGCTGAGCG
||| |||||
GGAA CTCCGACTCGT

A — CCC GG

GAM270 TNFRSF10B TGAGCCCTGAGGCTGAGCG 4065 TCATTGA A
CCTTGAGGCTGAGCG
|||||||
GGGACTCCGACTCGC

— A

GAM271 A1BG CAGCC-CAC--TCAGCCCTG 4079 T CT I
CAGCC CAC TCAGCCC
|||| | |||||
GTCGG GTG AGTCGGG

— — A

GAM271 A1BG CAGCC-CAC--TCAGCCCTG 4079 TC T CT
AGCC CAC TCAGCCCTG
|||| | |||||
TCGG GTG AGTCGGGAC

— — —

GAM271 ALDH3A2 CAGGATGATAAAGAATG-AAT 4088 T CAATTC
CAGGATGAT GAGGATG
||||| |||||
GTCCTACTA TTCTTAC

T TTAIII

GAM271 ALK CAGCCTCACCTTC-GCTCT 4075 CA CCII
CAGCCTCACCTT GC
||||||| ||
GTCGGAGTGGGA CG

AG AGAI

GAM271 ALK CAGCCTCACCTTC-GCTCT 4075 TC CA C GT
AGCCTCACCTT GC CT
||||||| |||
TCGGAGTGGGA CG GA

— AG A GI

GAM271 ATM CAGGAGG-TTGAGGATGCA 4086 TGA ATT
CAGGA TTGAGGATGCA
|||| |||||

	GTCCT AACTCCTACGT			
	CC_ III			
GAM271 BAK1	CAGCCACCCCTTCAGCCTCCTGT	4076 G TCA	_ GI	
	CC CCTTCAGCC CT			
	II IIIIIII II			
	GG GGAAGTCGG GG			
	_ TGG A AI			
GAM271 BAK1	CAGCCACCCCTTCAGCCTCCTGT	4076 TC TCA	_ II	
	AGCC CCTTCAGCC CTGT			
	III IIIIIII III			
	TCGG GGAAGTCGG GACA			
	_ TGG AG AI			
GAM271 BPHL	CAGGTTGGAGTGCAGTGATGCAATT	4083 AT_ T _ _	CGII	
	CAGG GA TG AG GATGCAATT			
	III II II IIIIIII			
	GTCC CT AC TC CTACGTAA			
	AAC C G A IIII			
GAM271 BUB3	CAGGATGATTAGGTGGACCTGCAAT	4084 A_ _	TCGII	
	CAGGATGATTG GGA TGCAAT			
	IIIIIIII III IIIII			
	GTCCTACTAAT CCT ACGTTA			
	CCA GG IIIIC			
GAM271 C1orf1	CAGGACTCAATAAGGGATGCAATT	4082 GAT_ _	CGI	
	CAGGAT TGAGG ATGCAATT			
	IIIII IIII IIIIIII			
	GTCCTG ATTCC TACGTAA			
	AGTT C III			
GAM271 CKMT1	CAGG--GAGGGAGGATGCAA	4087 AT TT TT		
	CAGG GA GAGGATGCAA			
	III II IIIIIII			
	GTCC CT CTCCTACGTT			
	_ CC II			
GAM271 CYP3A4	GGGTG-TTGAGGATGGAAT	4094 CAGGA A	C T	
	TG TTGAGGATG AAT			
	II IIIIIII III			
	AC AACTCCTAC TTA			
	C_ _ C C			
GAM271 DIAPH2	AGGA-GATAATGGATGCAATT	4071 CA T TGA	C	
	GGA GAT GGATGCAATT			
	III III IIIIIII			
	CCT CTA CCTACGTAA			
	_ _ TTA T			
GAM271 ELAVL4	GGATGATTG-TAAAGCAAATC	4095 CAGG	AG T T	
	ATGATTG GA GCAA TC			
	IIIII II III II			
	TACTAAC TT CGTT AG			
	_ _ AT _ T			
GAM271 EXT2	CAGCCTCACATTCAGACCT	4078 TC	C C GT	
	AGCCTCAC TTCAG CCT			
	IIIIII IIII III			

	TCGGAGTG AAGTC GGA			
	___ T T GI			
GAM271 EXT2	CAGCCTCACATTCAGACCT 4078	C	_	CII
	CAGCCTCAC TTCAG CC			
	GTCGGAGTG AAGTC GG			
	T T AII			
GAM271 FCN2	TCACCCCCACCTTCAGCTCCTG 4102	G	_	TI
	TCA CCTCACCTTCAGC CCTG			
	AGT GGGGTGGAAGTCG GGAC			
	G A II			
GAM271 FCN2	TCACCCCCACCTTCAGCTCCTG 4102	CAG	_	I
	CCTCACCTTCAGC CCT			
	GGGGTGGGAAGTCG GGA			
	TG_ A I			
GAM271 FCRH3	TCAGCCTCACATACCCTGCAGCCC 4097	_____	_	TGTII
	TCAGCCTC ACCTT CAGCCC			
	AGTCGGAG TGGGA GTCGGG			
	TGTA C IIITG			
GAM271 FCRH3	TCAGCCTCACATACCCTGCAGCCC 4097	_____	_	IIIG
	TCAGCCTC ACCTT CAGCC			
	AGTCGGAG TGGGA GTCGG			
	TGTA C GIII			
GAM271 FOLH1	GCCTCGCTTATCAGCCCTG 4090	ACCT_		II
	GCCTC TCAGCCCT			
	CGGAG AGTCGGGA			
	CGAAT CI			
GAM271 FOLH1	GCCTCGCTTATCAGCCCTG 4090	TCA CTCACCT		
	GC TCAGCCCTGT			
	CG AGTCGGGACG			
	AG_ AAT_____			
GAM271 HAL	TCAGGTCTCTCCTTCAGCC 4096	C_ A		CTGT
	TCAG CTC CTTTCAGCC			
	AGTC GAG GGAAGTCGG			
	CA A IIIT			
GAM271 HAL	TCAGGTCTCTCCTTCAGCC 4096	C_ A		II
	TCAG CTC CTTTCAGC			
	AGTC GAG GGAAGTCG			
	CA A GI			
GAM271 HSPA8	TCAGCCTCATCCTCCCCAGGACCCCTGT4098	_	AG_____	III
	TCAGCCTCA CCTTC CCCTGT A			

	AGTCGGAGT GGAGG GGGACA T
	A GGTCTG III
GAM271 HSPA8	TCAGCCTCATCCTCCCCAGGACCCCTGT4098 AG_ A TCA GI
	CCTC CCT GCCCT
	III
	GGAG GGG TGGGG
	GTA _ TCC AI
GAM271 MAFG	GCTTCACCTTCAAGGCCTTGT 4091 C _ C III
	GC TCACCTTCA GCC TG
	III
	CG AGTGGAAGT CGG AC
	A TC A AII
GAM271 MAFG	GCTTCACCTTCAAGGCCTTGT 4091 TCAGCC _ C I
	TCACCTTCA GCC TGT
	III
	AGTGGAAGT CGG ACA
	_ TC A A
GAM271 MEN1	TCGGCCTCACCTCTCTGCTCCTGT 4101 A _ A _ II
	TC GCCTCACCT TC GC CCTGT
	AG CGGAGTGGA AG CG GGACA
	C G A A II
GAM271 MEN1	TCGGCCTCACCTCTCTGCTCCTGT 4101 CA _ A _ I
	GCCTCACCT TC GC CCTG
	CGGAGTGGA AG CG GGAC
	_ G A A I
GAM271 PFAH1B1	ATCATCTGAGGATGCAATTC 4072 CAGGATGA
	TTGAGGATGCAATTC
	GACTCCTACGTTAAG
	A _
GAM271 PDE4B	CAGCAACAGCTTCAGCCCT 4077 CT C II
	CAGC CA CTTCAGCCC
	GTCG GT GAAGTCGGG
	TT C AI
GAM271 PDE4B	CAGCAACAGCTTCAGCCCT 4077 TC CT C GT
	AGC CA CTTCAGCCCT
	TCG GT GAAGTCGGGA
	_ TT C GI
GAM271 PHLDA3	CATCTTCATCCTCAGCCCTG 4080 AGCC C I
	TCA CTTCAGCCCT
	AGT GGAGTCGGGA
	TAGA A I
GAM271 PHLDA3	CATCTTCATCCTCAGCCCTG 4080 TCAGCC C
	TCA CTTCAGCCCTGT

	AGT GGAGTCGGGACG			
	TAGA__ A			
GAM271 PRX	AGCCTCACCATCCACCTCTG	4070	T A _ II	
	AGCCTCACC TC GCC CT			
	II III II			
	TCGGAGTGG AG TGG GA			
	T G A CI			
GAM271 PRX	AGCCTCACCATCCACCTCTG	4070 TCAG	T A _ T	
	CCTCACC TC GCC CTG			
	II III III			
	GGAGTGG AG TGG GAC			
	_____ T G A C			
GAM271 PRX	TCAGCCTCAGCCCCACCC	4100	_ G TGT	
	TCAGCCTCA CCTTCA CCC			
	III			
	AGTCGGAGT GGGGGT GGG			
	C _ III			
GAM271 PRX	TCAGCCTCAGCCCCACCC	4100	_ GCII	
	TCAGCCTCA CCTTCA			
	AGTCGGAGT GGGGGT			
	C GGGI			
GAM271 PRX	TCAGCCTCAGC-CCA-CCCT	4103	_ TCA G	
	TCAGCCTCA CCT GCCCT			
	III			
	AGTCGGAGT GGG TGGGA			
	C _ _ I			
GAM271 PRX	TCAGCCTCAGC-CCA-CCCT	4103 _	_ TCA I	
	CAGCCTCA CCT GCCC			
	III			
	GTCGGAGT GGG TGGG			
	A C _ _ I			
GAM271 RB1	CAGAATAATTTTGAGATGCAATT	4085	GA_ CGI	
	CAGGATGATT GGATGCAATT			
	GTCTTATTAA TCTACGTAA			
	AAC III			
GAM271 RLBP1	ATGATTGAGAAAATG-AATTCTG	4073 CAGGA TT	C	
	TGA GAGGATG AATTCTG			
	III			
	ACT CTTTTAC TTAAGC			
	A _ _ _			
GAM271 RNTRE	CAGG-TCAGTGATGATGCAATT	4089	ATGAT G CG	
	CAGG TGA GATGCAATT			
	III			
	GTCC ACT CTACGTAA			
	AGTC_ A II			
GAM271 RUNX1	TCAGCCTCACCCTCTAGCCCT	4099	_ _ GTI	
	TCAGCCTCACCT TC AGCCCT			

	AGTCGGAGTGGG AG TCGGGA		
	G A III		
GAM271 RUNX1	TCAGCCTCACCCCTCTAGCCCT 4099 CA	_ _	I
	GCCTCACCT TC AGCCC		
	CGGAGTGGG AG TCGGG		
	_ G A I		
GAM271 SFRS1	GGAT-ATTACAAGAATGCAATTC 4093 CAGGATGATT		
	GAGGATGCAATTCG		
	TTCTTACGTTAAGT		
	TATAATG_		
GAM271 SMAC	CAGGAACCTAAATGAGGATGCA 4081	_ T	ATTCG
	CAGGA TGA TGAGGATGCA		
	GTCCT ATT ACTCCTACGT		
	TGG T IIIGC		
GAM271 SPAG4	GCCTC--CTTCAGCCGCTG 4092 CA	_ I	
	GCCT CCTTCAGCC CT		
	CGGA GGAAGTCGG GA		
	_ C C		
GAM271 SPAG4	GCCTC--CTTCAGCCGCTG 4092 TCAGCCTCA	_	
	CCTTCAGCC CTG		
	GGAAGTCGG GAC		
	A_ C		
GAM271 TP63	ATGATACAGTGATGCAATT 4074 CAGGATGATTG	_	C
	AG GATGCAATT		
	TC CTACGTAA		
	ATG_ A A		
GAM272 ABCB8	TGTGAGCAGGAGCAGCCGC 4120	TCCAC	CCT
	TGTGAGCAGG CGGCC		
	ACACTCGTCC GTCGG		
	TC_ CGI		
GAM272 ACP5	TGTGAGCAGGGTC--CCGGC 4115	TCCA	CCC
	TGTGAGCAGG CCGGC		
	ACACTCGTCC GGCCG		
	CAG_ III		
GAM272 ASTN	TGTGAGCAGGGCCA-AGGCTCC 4124	T CC	C TA
	TGTGAGCAGG CCA GGC CC		
	ACACTCGTCC GGT CCG GG		
	C T_ A II		
GAM272 B4GALT5	TGTGAGCA-GTGCACCTGGGCTCT 4119	GTC _	CCCTAI
	TGTGAGCAG CACC GGC		

	ACACTCGTC GTGG CCG			
	AC_ AC AGAIII			
GAM272 CSK	GTGAGCAGGGGCACCAGGTCC 4113 TG TC CC TA			
	TGAGCAGG CACCGG CC			
	II			
	ACTCGTCC GTGGTC GG			
	_ CC CA TI			
GAM272 GNGT2	TGAGGCAAGTCCTAGACCGGCCCTA 4114 TGTGA _ II			
	GCAGGTCC ACCGGCCCCTA			
	CGTTCAGG TGGCCGGGGAT			
	TC_ ATC TG			
GAM272 HIVEP3	GAGCAGGTCATCAGGGCCC 4108 TGTGAG CACC_ CT			
	CAGGTC GGCCC			
	GTCCAG CCGGG			
	_ TAGTC TG			
GAM272 HOXB6	GAGCAGGTCTCCTGGCTCC 4109 TGTGAG CA _ _			
	CAGGTC CC GGC CCCT			
	GTCCAG GG CCG GGGG			
	_ A_ A A			
GAM272 KCNA5	AGC-GGTCGGCCGGCCCCT 4106 TGTGAGCAG CA			
	GTC CCGGCCCC			
	CAG GGCCGGGG			
	_ CC			
GAM272 LAPTM5	TGTGAGCAGCT-CACAGGCC 4122 G C C CT			
	TGTGAGCAG TC AC GGCCC			
	ACACTCGTC AG TG CCGGG			
	G _ T II			
GAM272 MYO15A	TGTGAGCAGACCCGACTGGCCC 4117 GT _ C CTA			
	TGTGAGCAG CC AC GGCCC			
	ACACTCGTC GG TG CCGGG			
	TG C A III			
GAM272 PTGIR	GAGCAGGTCCGCCAGGCCACT 4107 TGTGAG CA _ C A			
	CAGGTC CC GGCC CT			
	GTCCAG GG CCGG GA			
	_ CC T T C			
GAM272 PTHR1	TGTCAGCAGGTCCA--GCCCC 4123 G CCG T			
	TGT AGCAGGTCCA GCCCC			
	ACA TCGTCCAGGT CGGGG			
	G _ I			
GAM272 PTTG1IP	GTGGGCAGGTCCAGCAGTGCCACT 4110 TG A CCG_ C AI			
	TG GCAGGTCCA GCC CT			

	AC CGTCCAGGT CGG GA	
	__ C CGTCA T CI	
GAM272 RAD9	TGTGAGCAGGATCCTGGGGCC 4116	_ ACC CCTA
	TGTGAGCAGG TCC GGCC	
	ACACTCGTCC AGG CCGG	
	T ACC IIIA	
GAM272 SLC17A5	GTGAGCAGGTGTACTCGCCACCT 4111 TG	CC CG _ AI
	TGAGCAGGT AC GCC CCT	
	ACTCGTCCA TG CGG GGA	
	__ CA AG T CI	
GAM272 SMOH	TGGGAGCAGGTCCTTCCAGCCCC 4118 T	A_ TAI
	TG GAGCAGGTCC CCGGCCCC	
	AC CTCGTCCAGG GGTCGGGG	
	C AA III	
GAM272 TLR4	TGTGAGCAG--CAGTGGCCC 4121	GTC CC C
	TGTGAGCAG CA GGCCC	
	ACACTCGTC GT CCGGG	
	__ CA I	
GAM272 TRPV1	GTGAGCAGGCCTAGCAGGGGCC 4112 TG	CACC__ CTA
	TGAGCAGGTC GGCCC	
	ACTCGTCCGG CCGGG	
	__ ATCGTC TII	
GAM273 AGM1	AGTACTGCCATTATTATTG 4127 G G	II
	AG AC GCCATTATTGTT	
	TC TG CGGTAATAATAA	
	A A CI	
GAM273 AGM1	AGTACTGCCATTATTATTG 4127 TATGAGGACG	
	GCCATTATTGTTG	
	CGGTAATAATAAC	
	GA_____	
GAM273 CASQ2	TATGA--ACTCCAATTATTGTTG 4134 ATGA GG _ I	
	GGAC CCA TTATTGTT	
	CTTG GGT AATAACAA	
	ATA_ A_ T I	
GAM273 CASQ2	TATGA--ACTCCAATTATTGTTG 4134 TATGA GG _ G	
	GGAC CCA TTATTGTTG	
	CTTG GGT AATAACAAC	
	ATA_ A_ T I	
GAM273 CLASP1	TATGAGGACGTCCAGCAATGTT 4133	G T T GG
	TATGAGGACG CCA TA TGTT	

	ATACTCCTGC GGT GT ACAA		
	A C T II		
GAM273 CLASP1	TATGAGGACGTCCAGCAATGTT 4133	G T T I	
	ATGAGGACG CCA TA TGT		
	TACTCCTGC GGT GT ACA		
	A C T I		
GAM273 ESR1	GAGGACGGCCAGGGACTGTTG 4129	TATGAG TT_ G	
	GACGGCCA ATTGTTG		
	CTGCCGGT TGACAAC		
	_____ CCC G		
GAM273 ESR1	GAGGACGGCCAGGGACTGTTG 4129	A TT_ I	
	GGACGGCCA ATTGTT		
	CCTGCCGGT TGACAA		
	_ CCC I		
GAM273 GAS7	TGACGACAGGGCCATTATAGT 4135	G _ TGIII	
	TGA GAC GGCCATTAT		
	ACT CTG CCGGTAATA		
	G TC TCAII		
GAM273 GAS7	TGACGACAGGGCCATTATAGT 4135	TATGAG _ T TGG	
	GAC GGCCATTAT GT		
	CTG CCGGTAATA CA		
	TG_ TC T CAI		
GAM273 IL17BR	TGAAGATG--CTTTATTGTTG 4136	_ CG CA I	
	GAGGA GC TTATTGTT		
	CTTCT CG AATAACAA		
	A A_ A_ I		
GAM273 IL17BR	TGAAGATG--CTTTATTGTTG 4136	TATG CG CA	
	AGGA GC TTATTGTTG		
	TTCT CG AATAACAAC		
	_____ A_ A_		
GAM273 PCDHA9	TAGGAGGAGCTTCATTATTGTT 4132	AT CG _ I	
	GAGGA GC CATTATTGT		
	CTCCT CG GTAATAACA		
	TC _ AA I		
GAM273 PCDHA9	TAGGAGGAGCTTCATTATTGTT 4132	TAT CG _ GG	
	GAGGA GC CATTATTGTT		
	CTCCT CG GTAATAACAA		
	ATC _ AA II		
GAM273 SHANK2	TATGAGGACTGGAATTTT 4131	_ CCATTATII	
	TATGAGGAC GG		

	ATACTCCTG CC			
	A TTA AAAA II			
GAM273 SLC17A4	TATCATGATGGAATCATTATTGTT 4130	_ _	CGGC	I
	ATGA GGA CATTATTGT			
	TACT CCT GTAATAACA			
	G A TA_ I			
GAM273 SLC17A4	TATCATGATGGAATCATTATTGTT 4130	___ _	CGGC	GGI
	TATGA GGA CATTATTGT			
	G TACT CCT GTAATAACAA			
	ATA A TA_ III			
GAM273 UGT1A1	ATGAGGACTGACCATTATTG 4128	_	II	
	ATGAGGAC GGCCATTATT			
	TACTCCTG CTGGTAATAA			
	A CI			
GAM273 UGT1A1	ATGAGGACTGACCATTATTG 4128 TA	_	TTG	
	TGAGGAC GGCCATTATTG			
	ACTCCTG CTGGTAATAAC			
	_ A CII			
GAM273 UGT1A4	ATGAGGACTGACCATTATTG 4128	_	II	
	ATGAGGAC GGCCATTATT			
	TACTCCTG CTGGTAATAA			
	A CI			
GAM273 UGT1A4	ATGAGGACTGACCATTATTG 4128 TA	_	TTG	
	TGAGGAC GGCCATTATTG			
	ACTCCTG CTGGTAATAAC			
	_ A CII			
GAM273 UGT1A9	ATGAGGACTGACCATTATTG 4128	_	II	
	ATGAGGAC GGCCATTATT			
	TACTCCTG CTGGTAATAA			
	A CI			
GAM273 UGT1A9	ATGAGGACTGACCATTATTG 4128 TA	_	TTG	
	TGAGGAC GGCCATTATTG			
	ACTCCTG CTGGTAATAAC			
	_ A CII			
GAM274 GFRA1	GTAATCTTCGAGAGCTCGAA 4140	_ T	GGAI II	
	GTAATCTTC AG GT			
	CATTAGAAG TC CG			
	C T AGCTTI			
GAM274 ZFP161	TCAGAGTAACTCTGATCAG 4141	_ _	TGTGGAA	
	TCAGAGTAA TCT TCAG			

	AGTCTCATT AGA AGTC			
	G CT IIITAAG			
GAM274 ZFP161	TCAGAGTAACTCTGATCAG	4141	T CAIII	
	TCAGAGTAA CTT			
	III			
	AGTCTCATT GAG			
	_ ACTAG			
GAM274 ZNF80	AAGCTTCCACAGTGTGGAA	4139	AA__ T III	
	TCT CAGTGTGGA			
	III			
	AGG GTCACACCT			
	TTCGA T TII			
GAM275 ANK1	TCTAATGTG--CAGACTGCA	4154	ATA CG	
	TCTAATGTG AGGCTGCA			
	AGATTACAC TCTGACGT			
	G__ II			
GAM275 ATP11A	TGTGCAGGAGGCTGCACGTT	4156	TCTAATGTGATA	
	AGGCTGCACGT			
	TCCGACGTGCA			
	TCC_____			
GAM275 CORO2B	TCTAC-GTGCATAAGGCTGAAAGT	4153	A _ CACGTTI	
	TCTA TGTG ATAAGGCTG			
	AGAT GCAC TATTCCGAC			
	_ G TTTCAII			
GAM275 KCNJ3	ATGTGATAATACATGCCCGTT	4145	TCTAATGT G _ A	
	GATAA GC TGC CGTT			
	CTATT TG ACG GCAA			
	_____ A T G			
GAM275 KCNK2	TCTTAGGTAA-AAGGCTGCA	4155	AAT T CGT	
	TCT GTGA AAGGCTGCA			
	AGA CATT TTCCGACGT			
	ATC _ III			
GAM275 MOCS1	TAAGCTGA-AAGGCTGCAAGT	4151	TCTAAT GAT C	
	GT AAGGCTGCA GT			
	CG TTCCGACGT CA			
	T_____ ACT T			
GAM275 MYO3A	TACTGTGTCCAGGCTGCAC	4150	TCTAA ATA GT	
	TGTG AGGCTGCAC			
	ACAC TCCGACGTG			
	G_____ AGG AC			
GAM275 NLGN1	CTTATGTGATAATGGTGTAC	4149	TCTA _ C C GT	
	ATGTGATAA GG TG AC			

	TACACTATT CC AC TG			
	AA__ A _ A GI			
GAM275 NOTCH3	TCTATTCTGCCATAAGGCTG	4152	A__ G	CACGT
	TCTA TGT ATAAGGCTG			
	AGAT ACG TATTCCGAC			
	AAG G IIIT			
GAM275 PFKL	AAGGTGACAGGTGCTGCACGT	4144	TCTAAT	AG_ T
	GTGATA GCTGCACGT			
	CACTGT CGACGTGCA			
	_____ CCA C			
GAM275 PITPNB	CTAATGTGATTTGACTGCA	4148	TC	AA CGT
	TAATGTGAT GGCTGCA			
	ATTACACTA CTGACGT			
	___ AA CII			
GAM275 SLC21A3	ATGTAACAAACCTGCACGTT	4146	TCTAATGT	G
	GATAAG CTGCACGT			
	TTGTTT GACGTGCA			
	_____ G			
GAM275 SPARC	CTAATGTGAAAAGAACTGCAC	4147	TC	T __ GTT
	TAATGTGA AAG GCTGCAC			
	ATTACACT TTC TGACGTG			
	___ T TT AII			
GAM276 CAPZA1	TGAGGAAGAGTAA---TTTGAAA	4165	_ CCT	C
	TGAGGAAGA TAAT TTGAAA			
	ACTCCTTCT ATTA AACTTT			
	C ___ I			
GAM276 COX7A2L	TGAGGCAAATAACCCTTTGAAA	4175	A	CA
	TGAGG AGATAATCCTTTGAAA			
	ACTCC TTTATTGGGAACTTT			
	G II			
GAM276 CYP7A1	TGAGGAAGAAAAT-CTCTGA	4172	T C	AAC
	TGAGGAAGA AATC TTTGA			
	ACTCCTTCT TTAG AGACT			
	T _ III			
GAM276 ECT2	TGTGAAAGATA-TCACACTTTGAAACA	4169	TGA	__ TC II
	GGAAGATA A CTTTGAAACA			
	I			
	CTTTCTAT T GAACTTTGT			
	ACA AG GT II			
GAM276 FBXL5	TGAGGAAGAAAATCTCTTGTA	4174	T C	AAACA
	TGAGGAAGA AATC TTTG			

ACTCCTTCT TTAG GAAC
 T A ATTII
 GAM276 FMR1 GAGGAAGATCAAACCTTTATTGAAAC 4163 TG AATC ____ AII
 AGGAAGAT CTT TGAAAC
 ||||| || |||||
 TCCTTCTA GAA ACTTTG
 ____ GTTT ATA AII
 GAM276 GOLGA5 AGCAGGATAATCCTATTGGCAAAC 4160 TGAGGAA _ _ AI
 GATAATCCT TTG AAAC
 ||||| || |||||
 CTATTAGGA AAC TTTG
 GTC____ T CG GA
 GAM276 HTR4 TGAGGAGGGTCGTTTCCTTTGAAACA 4168 AGATAA_ II
 TGAGGA TCCTTTGAAACA
 |||| | |||||
 ACTCCT AGGAACTTTGT
 CCCAGCA II
 GAM276 IL10RA TGAGCAA-ATAATCCTTTATGATACA 4170 GA _ A II
 TGAG AGATAATCCTT TGA ACA
 ||| ||||| || |||
 ACTC TTTATTAGGAA ACT TGT
 G_ AT A II
 GAM276 IRTA2 TGAGGAAGAATAAGCCCTTTTGTTACA4164 _ _ GAA_ III
 TGAGGAAGA TAA TCCTTT ACA
 ||||| || ||||| |||
 ACTCCTTCT ATT GGGAAA TGT
 T C ACAA III
 GAM276 ITPKA TGAGGAAGA-AGCCCTTTG 4171 TAA AAA
 TGAGGAAGA TCCTTTG
 ||||| |||||
 ACTCCTTCT GGGAAAC
 TC_ III
 GAM276 MSX2 GAGGGAGAGGAAACCCTTTGAAACA 4162 T____ GATA II
 GAGGAA ATCCTTTGAAACA
 |||| | |||||
 CTCCTT TGGGAACTTTGT
 TCCCT ____ TI
 GAM276 MTF1 TGAGGAAGAAAATACCATTAAAA 4167 T _ T CAI
 TGAGGAAGA AAT CC TTGAAA
 ||||| || || |||||
 ACTCCTTCT TTA GG AATTTT
 T T T III
 GAM276 NDUFA5 AGAAATATCATC-TTTGAAACA 4161 TGAGGAAGATAATC
 CTTTGAAACA
 |||||
 GAAACTTTGT
 TTTATAGTA____
 GAM276 PIR51 TGAG-AAGATAATTCTTATAAACA 4176 G C TG I
 TGAG AAGATAAT CTT AAACA
 ||| ||||| || |||||

	ACTC TTCTATTA GAA TTTGT		
	— A TA I		
GAM276 SMOH	TGAGGAAGAAGAGCC-TTGAA 4173	TAATC	AC
	TGAGGAAGA CTTTGAA		
	ACTCCTTCT GGA ACTT		
	TCTC_ II		
GAM276 UBE2V1	AAGATAAATTCCTTTGAA 4159	TGAGGAAGATAA	AC
	TCCTTTGAA		
	AGGAAACTT		
	TTTAA_____ AC		
GAM276 ZNF80	TGAGGAAGATATTCCTGTG 4166	A_ T AAAC	
	TGAGGAAGATA TCCT TG		
	II		
	ACTCCTTCTAT AGGA AC		
	AA C IIIA		
GAM277 CAPN5	CCAGGGAGGGGAGGGGGAA 4185	T CCA CAAAT A	
	GG GGGAGGG GGAA		
	II		
	CC CCCTCCC CCTT		
	C TC_ _____ G		
GAM277 CDK5R2	AGGAACGGA AATGGAAAG 4179	TGGCCA_ AATGGAAA	
	GGGAGGGCA		
	CCTTTCCGT		
	GCCTTTTA CCIIGAA		
GAM277 DLX4	TGGCCAGGGCCCGGGCAGAAGG 4197	A_ AAT AAAG	
	TGGCCAGGG GGGCA GG		
	II		
	ACCGGTCCC CCCGT CC		
	GGG CTT IIIG		
GAM277 FZD8	GCCAGGGAGGGCTCCAAAT 4189	TGGC AAATGGAAA	
	CAGGGAGGGC		
	GTCCCTCCCG		
	_____ AGGTTTAGA		
GAM277 GGT2	GGCCAGGGAGGCCACCTGGA 4193	TG G AA AA	
	GCCAGGGAGG CA TGGA		
	II		
	CGGTCCCTCC GT ACCT		
	_____ G GG CI		
GAM277 GPRC5B	GCCAGGGA-GGCAAATCGGTAAG 4190	TGGC G _ A	
	CAGGGAGG CAAAT GG AAG		
	II		
	GTCCCTCC GTTTA CC TTC		
	_____ _ G A		
GAM277 HPCAL1	GCCAGGGAGGGAGCAAGGTGGA 4188	TGGC _ A_ AAG	
	CAGGGAGG GCAA TGGA		

	GTCCCTCC CGTT ACCT		
	_____ CT CC CCI		
GAM277 MAG	TGGC-AGGGAGGGGCAGCTGGGAAG 4198	C	_ AA A I
	TGGC AGGGAGGG CA TGG AAG		
	ACCG TCCCTCCC GT ACC TTC		
	_ C CG C I		
GAM277 NGFR	GGCCAGGGAGGG--GGTGGAAAG 4195 TG		CAAA
	GCCAGGGAGGG TGGAAAG		
	CGGTCCCTCCC ACCTTTC		
	_____ CC_		
GAM277 PCSK2	TGGGGAGGGAGGGCGGTGGGAAAG 4201	CC	AAAT I
	TGG AGGGAGGGC GGAAAG		
	ACC TCCCTCCCG CCTTTC		
	CC CCAC I		
GAM277 PGR	CCAGGGAGGAGGGAAAAGGGAAG 4183 T	CCA	C T AGI
	GG GGGAGGG AAA GGAA		
	CC TCCTCCC TTT CCTT		
	C _ T C CCT		
GAM277 PKD2L1	GCCAGCAGAGAGCAAATGGAAAG 4187 T	CAG	I
	GGC GGAGGGCAAATGGAAAG		
	TCG TCTCTCGTTTACCTTTC		
	G _ C		
GAM277 POLR2E	GGCCAGGGAGGGGACAGAGAGAG 4196 TG		CAA AAGI
	GCCAGGGAGGG ATGGA		
	CGGTCCCTCCC TGTCT		
	_____ C_ CTCT		
GAM277 PTN	CAGGGAGGGAACGGAAGGGAAA 4180 T_	CCA	C AAG
	GG GGGAGGG AAATGGA		
	CC CCTTCCC TTTACCT		
	CTC TTG _		
GAM277 SLC8A2	TGGC-ACTGAGGGCAAAAGGAA 4199	CAGG	T AG
	TGGC GAGGGCAAA GGAA		
	ACCG CTCCCGTTT CCTT		
	TGA_ T		
GAM277 SNAP25	CAGGGAGGG-AA--GGAAAG 4181 T_	CC	AATGGAA
	GG AGGGAGGGCA		
	CC TCCTTTCTGT		
	CT CT CIIIGAA		
GAM277 SOX11	TGGAAAGGGAGGGCAGAGAGAAAG 4200	CC	AAT I
	TGG AGGGAGGGCA GGAAAG		

	ACC TCCCTCCCGT TCTTTC	
	TT CTC I	
GAM277 SUFU	CAGGGAGGG-AAA--GAAAG 4182 TGGCC C T AA	
	AGGGAGGG AAA GG	
	TCCCTTTC TTT CC	
	C_____ _ C AT	
GAM277 SUPT5H	CCAGGGAGGGAAAAAGATGGAAA 4184 TGGCCA C _	
	GGGAGGG AA ATGGAAAG	
	CCCTCCC TT TACCTTTT	
	_____ T TC	
GAM277 TGM7	GCCAGGGAGGGCAGCTGGA 4191 TGGC AA AA	
	CAGGGAGGGCA TGGA	
	GTCCCTCCCGT ACCT	
	_____ CG CC	
GAM277 THRA	GGCCAGGGAGTGGCAGGTGG 4192 TG _ AA AAA	
	GCCAGGGAG GGCA TGG	
	CGGTCCCTC CCGT ACC	
	_____ A CC CII	
GAM277 TULP3	GGGCAGGGAGGGGAAGGGGA 4194 T C C AT AA	
	GGC AGGGAGGG AA GGA	
	CCG TCCCTCCC TT CCT	
	_____ C CC CI	
GAM277 USP18	CCAGGAACGG-AAATGGAAA 4186 TGGCCA G C	
	GGGA GG AAATGGAAA	
	CCTT CC TTTACCTT	
	_____ G _	
GAM278 ALEX2	TGAAATTTCTTCAAGTCTTTTGA 4218 TTGC _ A AI	
	AGTTTCTTCAA TCTT TGA	
	TTAAAGAAGTT AGAA ACT	
	CT_____ C A GI	
GAM278 ANKH	TTATAGCCTAAAATAAATTACATAA 4223 A _ TTI	
	GGTT AAATAAATTGC	
	TCGG TTTATTTAATG	
	A AT	
GAM278 ANKH	TTATAGCCTAAAATAAATTACATAA 4223 T_ AGGTT TTAII	
	TAG AAATAAATTGC	
	ATC TTTATTTAATG	
	AAT GGAT_ TATTII	
GAM278 AREG	TTAAATATTAAATAAATTATTA 4227 G C AI	
	TTAGA GTTAAATAAATTG TTA	

	AATTT TAATTTATTTAAT AAT		
	A A II		
GAM278 AREG	TTAAATATTAAATAAATTATTTA 4227 G	CTTI	
	TAGA GTTAAATAAATTG		
	ATTT TAATTTATTTAAT		
	A AAAI		
GAM278 ATRX	GTTTCTTCAGATTCTTCTGA 4214 TTG T	AATCTT	
	CAG TTCTTC ATGA		
	GTC AAGAAG TACT		
	AA_ T AC__		
GAM278 CCR2	TTGCAGTTTTTCAGCTTTAATTTTAT 4229	CT ATCTTATGAII	
	TTGCAGTTT TCA		
	AACGTCAAA AGT		
	__ CGAAATTAAAT		
GAM278 CTBP2	TGTACTGTCTTCAATCCTATG 4220 TTGCAGTT	AA	
	TCTTCAATCTTATG		
	AGAAGTTAGGATAC		
	CATGAC__ GI		
GAM278 DIO3	TTGCAGTTTACCTCAAGCCTTTAT 4230	_ _ ATGAII	
	TTGCAGTTT CTTCAA TCTT		
	AACGTCAAA GGAGTT GGAA		
	T C ATAI		
GAM278 F2R	TTAGGAGGTTAAA-AAA-TGCTT 4222 TA__	TAAAT I	
	GAGGTTAAA TGCT		
	CTCCAATTT ACGA		
	AATC TTT__ I		
GAM278 F2R	TTAGGAGGTTAAA-AAA-TGCTT 4222 TTA_	TAAAT AA	
	GAGGTTAAA TGCTT		
	CTCCAATTT ACGAA		
	AATC TTT__ II		
GAM278 FLOT1	TTAGGAAGTTAAATAAGTTG 4221 TTA_	A CTTA	
	GAGGTTAAATAA TTG		
	CTTCAATTTATT AAC		
	AATC C IIIA		
GAM278 FLOT1	TTAGGAAGTTAAATAAGTTG 4221 TTA_	ATTII	
	GAGGTTAAATAA		
	CTTCAATTTATT		
	AATC CAACI		
GAM278 GCNT2	TGCAGTTTCCCTTCAGTC--ATGA 4215 TT	CAATC A	
	GCAGTTTCTT TTATGA		

		CGTCAAAGGG AGTACT		
		___ AAGTC C		
GAM278 GEMIN5		GCAGTTTCTTCAAGGTGTGTGAA 4213 TTGC		TCTTATGAAI
		AGTTTCTTCAA		
		TCAAAGAAGTT		
		___ CCACACACTT		
GAM278 GPR48		TTAGAT-TTA--TAAATTGCTTAA 4228 TAG AA		
		AGGTT ATAAATTGCTTA		
		TCTAA TATTTAACGAAT		
		AA_ A_		
GAM278 GPR48		TTAGAT-TTA--TAAATTGCTTAA 4228 TTAG AA		
		AGGTT ATAAATTGCTTAA		
		TCTAA TATTTAACGAATT		
		AA_ A_		
GAM278 HIS1		AGTTTGA-CAATCTTATGAA 4208 TTGCAGTTTCTT		
		CAATCTTATGA		
		GTTAGAATACT		
		ACT_____		
GAM278 HNRPDL		CATTTTGTTC AATCTTGTG 4211 TTGCAGTTTC		A A
		TTCAATCTT TG		
		AAGTTAGAA AC		
		AAAC_____ C C		
GAM278 IARS		AGAGGTCTCAAATAAATT--TTAA 4204		___ GCTTAI
		GAGGTT AAATAAATT		
		CTCCAG TTTATTTAA		
		AG AAT		
GAM278 MYD88		GAGGGTAAAGTATAAATTGCT 4212 T		___
		GAGG TAA ATAAATTGC		
		CTCC ATT TATTTAACG		
		C TCA A		
GAM278 MYD88		GAGGGTAAAGTATAAATTGCT 4212 TTA TAA		AA
		GAGGT ATAAATTGCTT		
		TTTCA TATTTAACGAG		
		CCA _____ AC		
GAM278 NARS		TTACAAATTCTTCAATTTCTATG 4232 T		C_ AAI
		TTGCAG TTCTTCAAT TTATG		
		AATGTT AAGAAGTTA GATAC		
		T AA		
GAM278 NEB		TTAGAGGTTTTATTAGTTGCT 4224		AAATAAA I
		TAGAGGTT TTGC		

	ATCTCCAA	AACG		
	AATAATC	I		
GAM278 NEB	TTAGAGGTTTTATTAGTTGCT	4224	AAATAAA	TAA
	TTAGAGGTT	TTGCT		
	AATCTCCAA	AACGA		
	AATAATC	III		
GAM278 NEDD4	AGAGGTTAAGTAAGCTGCTT	4206	A A	I
	GAGGTAA	TAA TTGCT		
	CTCCAATT	ATT GACGA		
	C C	I		
GAM278 NEDD4	AGAGGTTAAGTAAGCTGCTT	4206	TTAG	A A A
	AGGTAA	TAA TTGCTT		
	TCCAATT	ATT GACGAA		
	_____	C C G		
GAM278 NEDD4	TGAATTTGCTTCACATGTCTTATGAA	4216	TTGCA_	TTCAA II
	GTTTC	TCTTATGAA		
	CGAAG	AGAATACTT		
	CTTAA	TGTAC GI		
GAM278 NET1	CAGTCTTTTCCATCTTATGA	4209	TTGCAG	TCA A
	TTTCT	ATCTTATGA		
	AAAGG	TAGAATACT		
	AGAA_	_____ G		
GAM278 PEX3	AGATGCCAAATAAATTGATT	4207	AGAG	CI
	GTAAATAAATTG			
	CGGTTTATTTAAC			
	TA_	TA		
GAM278 PEX3	AGATGCCAAATAAATTGATT	4207	TTAGAG	C A
	GTAAATAAATTG	TT		
	CGGTTTATTTAAC	AA		
	TA_	T A		
GAM278 PPP1R3A	TTGCAGATTCAAAAGTCAATCTTAT	4231	T T_	GAAI
	TTGCAG	TTC TCAATCTTAT		
	AACGTC	AAG AGTTAGAATA		
	T TTTC	IIIA		
GAM278 PRKRA	TGCAGTTTCTT-TCTCTGATG	4219	TT	CAA T A
	GCAGTTTCTT	TCT ATG		
	CGTCAAAGAA	AGA TAC		
	_____	AG_ C A		
GAM278 PTGES	TTGCAGTTTC--CAAACCT-TGAA	4233	TC	ATGAA
	TTGCAGTTTCT	AATCTT		

		AACGTCAAAGG TTGGAA		
		T_ CTTII		
GAM278 SDPR	CAGTTTCTTCTTCAATCTT	4210 TTGCAG	ATGA	
	TTTCTTCAATCTT			
	GAAGAAGTTAGAA			
	AAA_ CCTI			
GAM278 SERPINB6	TGCAGTTTCCTCAGATATT	4217 TT	ATCTTATGA	
	GCAGTTTCTTCA			
	CGTCAAAGGAGT			
	_ CTATAAGII			
GAM278 SHANK2	AGAGGTAGCAAAATAAATTACTT	4205 GA T	I	
	GGT AAATAAATTGCT			
	TCG TTTATTTAATGA			
	CA T I			
GAM278 SHANK2	AGAGGTAGCAAAATAAATTACTT	4205 TTAGA T	AAI	
	GGT AAATAAATTGCTT			
	TCG TTTATTTAATGAA			
	TCCA_ T CTI			
GAM278 TCF2	TTAGTGATAAAATAAATTGTTT	4226 A T	CTTAA	
	TTAG GGT AAATAAATTG			
	AATC CTA TTTATTTAAC			
	A T AAII			
GAM278 TCF2	TTAGTGATAAAATAAATTGTTT	4226 A T	CTI	
	TAG GGT AAATAAATTG			
	ATC CTA TTTATTTAAC			
	A T AAI			
GAM278 UBE2H	TTAGTAATAAAAAAATTGCTT	4225 AG T T	AA	
	TTAG GT AAA AAATTGCTT			
	AATC TA TTT TTTAACGAA			
	AT T T II			
GAM278 UBE2H	TTAGTAATAAAAAAATTGCTT	4225 AG T T	I	
	TAG GT AAA AAATTGCT			
	ATC TA TTT TTTAACGA			
	AT T T I			
GAM279 ADCY8	GCAGCCGGAG--GAGGGGT	4241 TCA TGI		
	GCAGCCGGAG GAG			
	CGTCGGCCTC CTC			
	_ CCC			
GAM279 ADCY8	GCAGCCGGAG--GAGGGGT	4241 TAGC	TCA T	
	AGCCGGAG GAG GGT			

	TCGGCCTC CTC CCA	
	_____ C	
GAM279 ADCY8	GCAGCCGGATGCAG-GTGGAGG 4242_ GT A TGI	
	CAGCCGGA CAG GTGG	
	GTCGGCCT GTC CACC	
	C AC _ TCI	
GAM279 ADCY8	GCAGCCGGATGCAG-GTGGAGG 4242 TAGC GT A T	
	AGCCGGA CAG GTGG GG	
	TCGGCCT GTC CACC CC	
	_____ AC _ T	
GAM279 ARSF	TAACAGAAGG-GCCAGGAGTGGTGG 4244 CC A _ I	
	TAGCAG GG GTCAG AGTGGTGG	
	ATTGTC CC CGGTC TCACCACC	
	TT _ C I	
GAM279 ARSF	TAACAGAAGG-GCCAGGAGTGGTGG 4244 CC A _ I	
	AGCAG GG GTCAG AGTGGTG	
	TTGTC CC CGGTC TCACCAC	
	TT _ C I	
GAM279 BMP4	CAGCCGGAG-CAGCAGCGG 4237 T _ II	
	CAGCCGGAG CAG AGTG	
	GTCGGCCTC GTC TCGC	
	_ G CI	
GAM279 BMP4	CAGCCGGAG-CAGCAGCGG 4237 TAGCAG T _	
	CCGGAG CAG AGTGGT	
	GGCCTC GTC TCGCCG	
	_____ _ G	
GAM279 DMRT1	GCAGCCGGAGGCGCAGCTGG 4240 T__ AGTGII	
	GCAGCCGGAG CAG	
	CGTCGGCCTC GTC	
	CGC GACCII	
GAM279 DMRT1	GCAGCCGGAGGCGCAGCTGG 4240 TAGC T__ AG TG	
	AGCCGGAG CAG TGG	
	TCGGCCTC GTC ACC	
	_____ CGC G_ TC	
GAM279 GNG2	CAGCTAGAATCAGAGTGGTGG 4238 CG I	
	AGC GAGTCAGAGTGGTG	
	TCG CTTAGTCTCACCAC	
	AT I	
GAM279 GNG2	CAGCTAGAATCAGAGTGGTGG 4238 TAGCAGCC	
	GGAGTCAGAGTGGTGG	

TCTTAGTCTCACCACC

GA_____

GAM279 LZTR1 AGACGACGGCCGAGTGGTGG 4236 ____ C AGTCA I
G CGG GAGTGGTGG
| ||| |||||
C GCC CTCACCAC
CTG T GG____ I

GAM279 LZTR1 AGACGACGGCCGAGTGGTGG 4236 TAGCAGC AGTCA
CGG GAGTGGTGG
||| |||||
GCC CTCACCAC
CT_____ GG____

GAM279 NPY2R GCAGCCGGAGCAGTCAGAGCGGCTGG 4239 AGC ____ GI
CGGAGT CAGAGTGGT
||||| |||||
GCCTCG GTCTCGCCG
____ TCA AI

GAM279 NPY2R GCAGCCGGAGCAGTCAGAGCGGCTGG 4239 TAGC ____ _ II
AGCCGGAGT CAGAGTGG TGG
||||| ||||| |||
TCGGCCTCG GTCTCGCC ACC
____ TCA G CG

GAM279 SLC1A2 GCGGGAGCAGAGAGTGGTGG 4243 C C_ II
GC GGAGT AGAGTGGTGG
|| |||| |||||
CG CCTCG TCTCACCAC
C TC CI

GAM279 SLC1A2 GCGGGAGCAGAGAGTGGTGG 4243 T CCGGAGTC
AGCAG AGAGTGGTGG
|||| |||||
TCGTC TCTCACCAC

GAM280 BCL2L2 GCAGCTCCTCTTGGCTAAAGGTC 4250 CAGG ____ I
CCTC GGCTAAAGGT
||| |||||
GGAG CCGATTCCA
GA__ AA I

GAM280 BCL2L2 GCAGCTCCTCTTGGCTAAAGGTC 4250 T AGG ____ GI
GGC CCTC GGCTAAAGGTCT
||| ||| |||||
TCG GGAG CCGATTCCAGG
_ A__ AA GI

GAM280 COMT GCAGGCCTCGGC-CGAGGTGTG 4253 _ AA CTI
CAGGCCTCGGCT AGGT
||||||| |||
GTCCGGAGCCGG TCCA
C C_ CAI

GAM280 COMT GCAGGCCTCGGC-CGAGGTGTG 4253 TGGC AA CTG
AGGCCTCGGCT AGGT
||||||| |||

		TCCGGAGCCGG TCCA		
		_____ C_ CAC		
GAM280 CXorf6	GGCAGGCCT-GGCCAGAAGGT	4255	C _ I	
	GCAGGCCT GGCTA AAGG			
	CGTCCGGA CCGGT TTCC			
	_____ C I			
GAM280 CXorf6	GGCAGGCCT-GGCCAGAAGGT	4255 TG	C _ CT	
	GCAGGCCT GGCTA AAGGT			
	CGTCCGGA CCGGT TTCCA			
	_____ C CI			
GAM280 CYP1A1	GCAGGCCTCCTGGCTCAAG	4251	___ AA	
	GCAGGCCTC GGCT			
	CGTCCGGAG CCGA			
	GA GTTC			
GAM280 CYP1A1	GCAGGCCTCCTGGCTCAAG	4251 TGGC	___ A GTCT	
	AGGCCTC GGCT AAG			
	TCCGGAG CCGA TTC			
	_____ GA G GT			
GAM280 EPHB2	AGGCC-CAGC-AAAGGTCTG	4248 _ T T I		
	GGCC CGGC AAAGGTCT			
	CCGG GTCG TTTCCAGA			
	T _ _ I			
GAM280 GNPI	GGCAGGCCTGTGCAAGAAGGACT	4256 G	CG TA_ TCI	
	CAGGCCT GC AAGG			
	GTCCGGA CG TTCC			
	_____ CA TTC TGI			
GAM280 GNPI	GGCAGGCCTGTGCAAGAAGGACT	4256 TG	CG TA_ T GI	
	GCAGGCCT GC AAGG CT			
	CGTCCGGA CG TTCC GA			
	_____ CA TTC T GI			
GAM280 ITPKB	GCAGGCCTCCGC---AGGT	4252	G TAA	
	GCAGGCCTC GC AGG			
	CGTCCGGAG CG TCC			
	G _____			
GAM280 ITPKB	GCAGGCCTCCGC---AGGT	4252 TGGC	G TAA	
	AGGCCTC GC AGGT			
	TCCGGAG CG TCCA			
	_____ G _____			
GAM280 NAGA	GGCAGGCCTGGGAT-GAGGT	4257 _	C CTAA I	
	GCAGGCCT GG AGG			

	CGTCCGGA CC TCC		
	C C TAC_ I		
GAM280 NAGA	GGCAGGCCTGGGAT-GAGGT	4257 TG	C CTAA CT
	GCAGGCCT GG AGGT		
	CGTCCGGA CC TCCA		
	_ C TAC_ TI		
GAM280 NPTX1	GGCAGGAGGGAGCTAAAGGTC	4258 CCTC	I
	GCAGG GGCTAAAGGT		
	CGTCC TCGATTTC		
	TCCC I		
GAM280 NPTX1	GGCAGGAGGGAGCTAAAGGTC	4258 TG CCTC	TG
	GCAGG GGCTAAAGGTC		
	CGTCC TCGATTTCAG		
	_ TCCC TI		
GAM280 RERE	CAGGCCTCGGTCCAAGCCTCTG	4249 A _ AA	I
	GGCCTCGG CTA GGTCT		
	CCGGAGCC GGT TCGGA		
	_ A _ G		
GAM280 RERE	CAGGCCTCGGTCCAAGCCTCTG	4249 TGGCAG _ AA	G
	GCCTCGG CTA GGTCT		
	CGGAGCC GGT TCGGA		
	_ _ A _ G		
GAM280 RNPEPL1	TGGCAGGCCTGGCCCCACAG	4260 C AA_	GTCT
	TGGCAGGCCT GGCT AG		
	ACCGTCCGGA CCGG TC		
	_ GTG G		
GAM280 RNPEPL1	TGGCAGGCCTGGCCCCACAG	4260 C AA	
	TGGCAGGCCT GGCT		
	ACCGTCCGGA CCGG		
	_ GTGTC		
GAM280 SLC2A3	AGGGTTTGGCTAAAGGGTCTG	4247 GGCCTC _	I
	GGCTAAAGG TCT		
	CCGATTTC AGA		
	CCAAA_ C I		
GAM280 SLC7A5	GGCAGGGGT-GAATAAAGGTCT	4259 _ CCTC GC	I
	GCAGG G TAAAGGTC		
	CGTCC C ATTTCCAG		
	C CCA_ TT I		
GAM280 SLC7A5	GGCAGGGGT-GAATAAAGGTCT	4259 TG CCTC GC	G
	GCAGG G TAAAGGTCT		

	CGTCC C ATTTCCAGA			
	__ CCA_ TT A			
GAM280 ZNF278	GCAGGGCTCAG--AAAGGTCTG 4254	C	CT	I
	GCAGG CTCGG AAAGGTC			
	CGTCC GAGTC TTTCCAG			
	C __ A			
GAM280 ZNF278	GCAGGGCTCAG--AAAGGTCTG 4254	TGGC	C	CT
	AGG CTCGG AAAGGTCT			
	TCC GAGTC TTTCCAGA			
	__ C __			
GAM281 CD79B	TCACTGAGGCCAGGGAGCCT 4270			TGGCG
	TCACTGAGG AGGGGGCCT			
	AGTGACTCC TCCCTCGGA			
	GG IGG			
GAM281 CD79B	TCACTGAGGCCAGGGAGCCT 4270			
	TCACTGAGG AGGGGGCC			
	AGTGACTCC TCCCTCGG			
	GG A			
GAM281 CYP46	CACAGAGGAGGGGCCCCTGCCGG 4265	T	G	G I
	AC GAGGAGGGG CCTTG CG			
	TG CTCCTCCCC GGGAC GC			
	T G G I			
GAM281 CYP46	CACAGAGGAGGGGCCCCTGCCGG 4265	TC T	G	G I
	AC GAGGAGGGG CCTTG CGG			
	TG CTCCTCCCC GGGAC GCC			
	__ T G G G			
GAM281 DDX11	CTGACTGAGGCTGCCTTGGCGG 4266	TC	AGGGG	
	ACTGAGG GCCTTGGCGG			
	TGACTCC CGGAACCGCC			
	__ GA__			
GAM281 DDX11	CTGACTGAGGCTGCCTTGGCGG 4266	TGAG	GG	I
	GAGG GCCTTGGCG			
	CTCC CGGAACCGC			
	CTGA GA I			
GAM281 EPHB6	TGAGGAGGGGGC--TGGTGG 4275		CT	CI
	TGAGGAGGGGGC TGG			
	ACTCCTCCCCCG ACC			
	__ AC			
GAM281 GALE	TGAGGTAGGGGAGGCCTTGGC 4274			
	TGAGG AGGGG GCCTTGG			

		ACTCC TCCCC CGGAACC			
		A TC GII			
GAM281 GALE		TGAGGTAGGGGAGGCCTTGGC	4274	TCACTG A	GG
		AGG GGGGGCCTTGGC			
		TCC CCTCCGGAACCG			
		CA_____ AA			
GAM281 ITGA11		CACAGAGCCTGAGGGAGGCCTTGGCG	4264	A__ AG	I
		CTGAGG GGGGCCTTGGC			
		GACTCC CTCCGGAACCG			
		TCG _____ I			
GAM281 ITGA11		CACAGAGCCTGAGGGAGGCCTTGGCG	4264	TCA_____ AG	GII
		CTGAGG GGGGCCTTGGCG			
		GACTCC CTCCGGAACCGC			
		TGTCTCG _____ AII			
GAM281 KIFC3		CTAAGGAGGGGGC--TGGC	4268	CT I	
		CTGAGGAGGGGGC TGG			
		GATTCCTCCCCCG ACC			
		_____ G			
GAM281 KIFC3		CTAAGGAGGGGGC--TGGC	4268	TCACTG	CT
		AGGAGGGGGC TGGC			
		TCCTCCCCCG ACCG			

GAM281 MAPRE3		CTGGGGCAGGGGGCCTTGG	4267	A _	II
		CTG GG AGGGGGCCTTG			
		GAC CC TCCCCCGAAC			
		C G CI			
GAM281 MAPRE3		CTGGGGCAGGGGGCCTTGG	4267	TCACTGA _	CG
		GG AGGGGGCCTTGG			
		CC TCCCCCGAAC			
		C_____ G CA			
GAM281 OAS3		TCAGGGAGGAGGGGGCATT	4272	CT	CTII
		TCA GAGGAGGGGGC			
		AGT CTCCTCCCCCG			
		CC TAAI			
GAM281 OAS3		TCAGGGAGGAGGGGGCATT	4272	CT	CTTGGCG
		TCA GAGGAGGGGGC			
		AGT CTCCTCCCCCG			
		CC TAAIIG			
GAM281 PLA2G2D		TCACTCAGGGAGAGGGGCCTTGG	4271	G _ _	CGGI
		TCACT AGG AG GGGGCCTTGG			

	AGTGA TCC TC CCCC	GGAACC	
	G C T	III	G
GAM281 PLA2G2D	TCACTCAGGGAGAGGGGCCTTGG	4271	CA G _ _ I
	CT AGG AG GGGGCCTTGG		
	II III II IIIIIII		
	GA TCC TC CCCC	GGAAC	
	_ G C T	I	
GAM281 PRODH	TCACAGAGGTGGGGGCCTTGG	4273	T A CGG
	TCAC GAGG GGGGGCCTTGG		
	IIII IIII IIIIIIIII		
	AGTG CTCC CCCC	GGAACC	
	T A	III	
GAM281 PRODH	TCACAGAGGTGGGGGCCTTGG	4273	T A I
	CAC GAGG GGGGGCCTTGG		
	III IIII IIIIIIIII		
	GTG CTCC CCCC	GGAAC	
	T A	I	
GAM281 RAD23A	ACTGGGGAGGGGGCCTTGG	4263	TCAC A _G
	TG GGAGGGGGCCTTGG C		
	II IIIIIIIIIII I		
	AC CCTCCCCCGGAACC	G	
	_ C	C I	
GAM281 RAD23A	ACTGGGGAGGGGGCCTTGG	4263	A II
	ACTG GGAGGGGGCCTTGG		
	IIII IIIIIIIII		
	TGAC CCTCCCCCGGAAC		
	C	C I	
GAM281 SOST	CTGAGG--GGGGCCTTGCCGG	4269	_ AG G I
	TGAGG GGGGCCTTG CG		
	IIII IIIIIII II		
	ACTCC CCCC	GGAAC GC	
	G _	G I	
GAM281 SOST	CTGAGG--GGGGCCTTGCCGG	4269	TCACTGA A G
	GG GGGGGCCTTG CG		
	II IIIIIII II		
	TC CCCC	GGAAC GC	
	_ _	G	
GAM282 ARHA	TGCCACCCATGAGAACTGGTG	4289	G _ AG TTI
	CCACCCA GA ACTG		
	IIIIII II III		
	GGTGGGT CT TGAC		
	_ A CT	CAI	
GAM282 ARHA	TGCCACCCATGAGAACTGGTG	4289	TCACTGCC _ AG T
	ACCCA GA ACTG TG		
	IIII II III II		
	TGGGT CT TGAC AC		
	_ A CT	C	
GAM282 CCBL1	CTCCCACCCAGAACATTCTGT	4282	G GA_ III
	CT CCACCCAGAA CTG		
	II IIIIIII III		

	GA GGTGGGTCTT GAC		
	G GTAA AII		
GAM282 CCBL1	CTCCCACCCAGAACATTCTGT	4282 TCACTG	GA__ TG
	CCACCCAGAA CTGT		
	GGTGGGTCTT GACA		
	_____ GTAA CA		
GAM282 CPE	CACTGGGGGCCACCCAGAGGA	4279 ____	AGIII
	CACT GCCACCCAGA		
	GTGA CGGTGGGTCT		
	CCC CCTII		
GAM282 CPE	CACTGGGGGCCACCCAGAGGA	4279 TCACT_	A CTGTT
	GCCACCCAGA GA		
	CGGTGGGTCT CT		
	TGACCC C CIIIG		
GAM282 FMR2	TCACTGCCATCCACATGTCT	4286 C	GAAGACTGTT
	TCACTGCCA CCA		
	AGTGACGGT GGT		
	A GTACAGAIII		
GAM282 FMR2	TCACTGCCATCCACATGTCT	4286 C	GAAGACI
	CACTGCCA CCA		
	GTGACGGT GGT		
	A GTACAGI		
GAM282 HOXD3	TCACTGCCACCTCCAATGTCTGCTG	4284 CA_ AGA	II
	TCACTGCCACC GA CTGTTG		
	AGTGACGGTGG TT GACGAC		
	AGG ACA II		
GAM282 HOXD3	TCACTGCCACCTCCAATGTCTGCTG	4284 C CA_ AGA	I
	ACTGCCACC GA CTGTT		
	TGACGGTGG TT GACGA		
	_ AGG ACA I		
GAM282 KRT19	TCCCT-CTACCCAGAAGAC	4285 A GCC	TGT
	TC CT ACCCAGAAGAC		
	AG GG TGGGTCTTCTG		
	_ AGA III		
GAM282 KRT19	TCCCT-CTACCCAGAAGAC	4285 A GCC	I
	TC CT ACCCAGAAGA		
	AG GG TGGGTCTTCT		
	_ AGA G		
GAM282 MAGEA9	CACTGCCACTGAGAACACTGATTG	4281 A CC G TTI	
	CTGCCAC AGAA ACTG		

	GACGGTG TCTT TGAC		
	— AC G TAA		
GAM282 MAGEA9	CACTGCCACTGAGAACACTGATTG 4281 TC	CC G _ I	
	ACTGCCAC AGAA ACTG TTG		
	TGACGGTG TCTT TGAC AAC		
	— AC G T G		
GAM282 MBNL	TCAGCTGC-AGTGAAAAGACTGTTG 4283 _ CACCC	I	
	TCA CTGC AGAAGACTGTTG		
	AGT GACG TTTTCTGACAAC		
	C TCAC_ I		
GAM282 MBNL	TCAGCTGC-AGTGAAAAGACTGTTG 4283 CA_ CACCC	I	
	CTGC AGAAGACTGTT		
	GACG TTTTCTGACAA		
	GTC TCAC_ I		
GAM282 MECP2	TGCCACCCAACAGAAGATTGT 4288 _ C		
	TGCCACCCA GAAGA TG		
	ACGGTGGGT CTTCT AC		
	TGT A A		
GAM282 MECP2	TGCCACCCAACAGAAGATTGT 4288 TCACT ACC C G		
	GCC CAGAAGA TGTT		
	TGG GTCTTCT ACAG		
	— GTT A A		
GAM282 PPP2R2C	CACTGCCACCTCTGCAG-CTGT 4280 CAGA_ A I		
	ACTGCCACC AG CTG		
	TGACGGTGG TC GAC		
	AGACG _ I		
GAM282 PPP2R2C	CACTGCCACCTCTGCAG-CTGT 4280 TC CAGA_ A G		
	ACTGCCACC AG CTGTT		
	TGACGGTGG TC GACAG		
	— AGACG _ I		
GAM282 STMN1	TCACTGCCACCAACAGCACTGT 4287 CAGA _ TG		
	TCACTGCCACC AG ACTGT		
	AGTGACGGTGG TC TGACA		
	TTG_ G		
GAM282 STMN1	TCACTGCCACCAACAGCACTGT 4287 CAGA _ I		
	CACTGCCACC AG ACTG		
	GTGACGGTGG TC TGAC		
	TTG_ G I		
GAM282 TM7SF3	ACTTGCACC-AGA-GACTGTTG 4278 C_ CAC A I		
	TGC CCAGA GACTGTT		

	ACG GGTCT CTGACAA		
	TGA T__ _ I		
GAM282 TM7SF3	ACTTGCACC-AGA-GACTGTTG 4278 TCAC CAC A		
	TGC CCAGA GACTGTT		
	ACG GGTCT CTGACAA		
	A__ T__ _		
GAM283 CDK10	GGCGGCCGCGC-TTGTTGCGG 4297 TG A AG C		
	GCGGCC TG TTGTTGCGG		
	CGCCGG GC AACACGCC		
	_ _ G_ A		
GAM283 FBXL7	GGCGGCCAC---TTGTTGCGG 4294 TG GAG		
	GCGGCCAT TTGTTGCGG		
	CGCCGGTG AACACGCC		
	_ _		
GAM283 IFRD2	TGGTGGAGACCAGTTGTTGC 4299 __ C TGA GGC		
	TGG GGCCA GTTGTGTC		
	ACC CTGGT CAACAACG		
	ACC T __		
GAM283 LASS1	GCGGCCATGAGGCGTTGCG 4292 TGGC T C		
	GGCCATGAG TGTTGCGG		
	CCGGTACTC GCAACGCT		
	_ C C		
GAM283 MUCDHL	GGCGGCCAT-AGTGCTTGTTG 4295 TG G TG C C		
	GCGGCCAT AGT TTG GG		
	CGCCGGTA TCA AAC CC		
	_ _ CG A T		
GAM283 PDAP1	GGCCATGAGGGGCTGTTGCAGCG 4293 T__ C CATGA T I		
	GG GGC GTTGT GCGGCG		
	CC CCG CAACG CGCCGC		
	TACT _ A__ T G		
GAM283 SMARCD2	TGGCGGCCA-GAGCCGCTTGC 4298 T _ GGC		
	TGGCGGCCA GAGTTGTT GC		
	ACCGCCGGT CTCGGCGA CG		
	_ A		
GAM283 SOLH	TGGCGGCCAGGAGGTCTGGCCAGGCG 4300 T TT GC GII		
	TGGCGGCCA GAG GTT GGC		
	ACCGCCGGT CTC CAG CCG		
	C _ A_ GTC		
GAM283 TBX6	GGCGGCCATTTGGTGTGGGGG 4296 TG GAG T C CG		
	GCGGCCAT TTG TG GG		

	CGCCGGTA AAC AC CC	
	___ ___ C A CC	
GAM284 ARG2	GCTCGCCATCCTGGGAGGCCTG 4306 TG _ A AAGG	
	GCTG CC TGGGAGGCCTG	
	CGGT GG ACCCTCCGGAC	
	AG A _ CA	
GAM284 B3GNT3	TGGCAGACACTG-AGGCCTGAAG 4314 TGC GG G	
	TGGC CAT GAGGCCTGAAG	
	ACCG GTG CTCCGGA CTTC	
	TCT A_ I	
GAM284 BMP1	CTGCCATGGGGAAGGGCTGA 4304 TGGCTG _ C AG	
	CCATGGG AGG CTGA	
	GGTACCC TCC GACT	
	___ CT C CT	
GAM284 BTG4	CTGCCATGGAAGCCC--AAGG 4305 TGGCTG G G	
	CCATGG AGGCCT AAG	
	GGTACC TTCGGG TTC	
	___ - -	
GAM284 ELMO1	GCAGCCATGGGAAGTGACCTGAAG 4308 TGGCT _ GI	
	GCCATGGGA GGCCTGAAG	
	CGGTACCCT CTGGACTTC	
	T___ TCA GT	
GAM284 GCN5L2	GCTGCACGCTTGGGGGTGCCTGAAGG 4307 TG _ CAT AG II	
	GC TGC GGG GCCTGAAGG	
	CG GCG CCC CGGACTTCC	
	A_ T AAC CA AG	
GAM284 HAP1	GGCTGCCATGTGGCCCAGGCCTG 4310 TG _ _ AAGGI	
	GCTGCCATG GG AGGCCTG	
	CGACGGTAC CC TCCGGAC	
	_ A GGG C IG	
GAM284 IGFBP6	CCATGGGGCGGGGCCTGAAGG 4303 T TGCCATG A	
	GGC GG GGCCTGAAGG	
	CCG CC CCGGACTTCC	
	- - -	
GAM284 LENG4	TGGAAGCCATGGGACGGCC 4311 CT _ TGAAG	
	TGG GCCATGGGA GGCC	
	ACC CGGTACCCT CCGG	
	TT G IG	
GAM284 LIF	TGTCTTCCTTCCCAGGCCTGAAGG 4317 G G ATGGG I	
	TG CT CC AGGCCTGAAGG	

	AC GA GG TCCGGA	TTCC		
	A A AAGGG	I		
GAM284 MASP1	TGCCTGCCATGGGTGAGCCT	4312 G	A_	GAAG
	TG CTGCCATGGG GGCCT			
	II IIIIIIIII IIIII			
	AC GACGGTACCC TCGGA			
	G AC IIIG			
GAM284 MUC4	GCAGCCCTTGGAGGCCTGA	4309 TGGCT	ATG	AG
	GCC GGAGGCCTGA			
	III IIIIIIIII			
	CGG CCTCCGGA	CT		
	T_ GAA CA			
GAM284 SLC7A8	TGGCTCTGATCTCAGGCCTGAAGG	4316	GCCATGGG	I
	TGGCT AGGCCTGAAGG			
	IIII IIIIIIIII			
	ACCGA TCCGGA	TTCC		
	GACTAGAG	I		
GAM284 SOX15	TGGCTATCATGGGAGGACTGCAGG	4315	C	C A I
	TGGCTG CATGGGAGG CTG AGG			
	IIII IIIIIII III III			
	ACCGAT GTACCCTCC GAC TCC			
	A T G I			
GAM284 STIM1	TGGATCCC-TGG-AGGCCTGA	4313	CTG ATG	AG
	TGG CC GGAGGCCTGA			
	III II IIIIIIIII			
	ACC GG CCTCCGGA	CT		
	TA_ GA_ II			
GAM285 CNP	TACCTAGTT-ATGGTGTGAAGG	4324	CCA _	CI
	TACCTAGTT GGT TGAGGG			
	IIIIII III IIIII			
	ATGGATCAA CCA ACTTCC			
	TA_ C II			
GAM285 CNP	TACCTAGTT-ATGGTGTGAAGG	4324	CCA _	I
	ACCTAGTT GGT TGAGG			
	IIIIII III IIIII			
	TGGATCAA CCA ACTTC			
	TA_ C I			
GAM285 DRD3	TAGATCACAGGGTTGAGGGC	4327	T _ _	III
	TAG TC CAGG TTGAGGG			
	III II III IIIII			
	ATC AG GTCC AACTCCC			
	T T C GII			
GAM285 HOXC11	ACCTAACACCAGGTTGAAGG	4321	TT	I
	CCTAG CCAGGTTGAGG			
	IIII IIIIIIIII			
	GGATT GGTCCAACTTC			
	GT I			
GAM285 HOXC11	ACCTAACACCAGGTTGAAGG	4321	TA TT	C
	CCTAG CCAGGTTGAGGG			
	IIII IIIIIIIII			

	GGATT GGTCCA	ACTTCC	
	___ GT	A	
GAM285 KCNK6	ACCTAGTTCCA-GTTCCGGG	4322 _	GTTGA I
	CCTAGTTCCAG	GG	
	GGATCAAGGTC	CC	
	T AAGG_ I		
GAM285 KCNK6	ACCTAGTTCCA-GTTCCGGG	4322 TA	GTTGA C
	CCTAGTTCCAG	GGG	
	GGATCAAGGTC	CCC	
	___ AAGG_ T		
GAM285 MYO5A	TACCTAGTT---GGTTAAGG	4325	CCA G
	TACCTAGTT GGTTGAGG		
	ATGGATCAA CCAATTCC		
	___ I		
GAM285 MYO5A	TACCTAGTT---GGTTAAGG	4325 _	CCA
	ACCTAGTT GGTTGAG		
	TGGATCAA CCAATTC		
	A ___		
GAM285 PIP5K1A	CTTGTTCCAGGTCTTCTGAGG	4323 CTA	___ IIIC
	GTTCCAGGT TGAG		
	CAAGGTCCA ACTC		
	GAA GAAG C		
GAM285 SIGLEC11	ACCTGG---CAGGTTGAGG	4320 A TTC	
	ACCT G CAGGTTGAG		
	TGGA C GTCCAACTC		
	C ___		
GAM285 SIGLEC11	ACCTGG---CAGGTTGAGG	4320 TA A TTC	
	CCT G CAGGTTGAGG		
	GGA C GTCCAACTCC		
	___ C ___		
GAM285 SIGLEC9	TAGCTCATCACGTTGAGGGC	4326 _ G	
	TAGTTC CA GTTGAGGG		
	ATCGAG GT CAACTCCC		
	TA G G		
GAM285 SIGLEC9	TAGCTCATCACGTTGAGGGC	4326 TACCTAGTTC G	
	CA GTTGAGGGC		
	GT CAACTCCCG		
	AGTA_____ G		
GAM286 AAT1	CCTCCTGGAATCCTGATGC	4331 G _	AG
	CC CC GGAATCCTGA		

	GG GG CCTTAGGACT			
	A A ACGI			
GAM286 AAT1	CCTCCTGGAATCCTGATGC	4331	TGCCG _	A CCA
	CC GGAATCCTGA GC			
	GG CCTTAGGACT CG			
	A _ A A AAI			
GAM286 ARSA	GCCGCC----TCCTGAAGCTCCA	4335	GGAA CI	
	GCCGCC TCCTGAAGC			
	CGGCGG AGGACTTCG			
	AG			
GAM286 ARSA	GCCGCC----TCCTGAAGCTCCA	4335	TG GGAA _	
	CCGCC TCCTGAAGC CCA			
	GGCGG AGGACTTCG GGT			
	A			
GAM286 ATRX	TGCAGCTCACAATCCCATGAAGCCCA	4341	C _ G _	All
	TGC GC CG AATCCT GAAGCCCA			
	ACG CG GT TTAGGG CTTCGGGT			
	T A G TA			
GAM286 ATRX	TGCAGCTCACAATCCCATGAAGCCCA	4341	GCC _ G _	I
	GC CG AATCCT GAAGCCC			
	CG GT TTAGGG CTTCGGG			
	A G TA I			
GAM286 CASP2	CCGTGCATCCTGAAGATCAA	4330	GA_ CC II	
	CCG ATCCTGAAG CA			
	GGC TAGGACTTC GT			
	ACG TA TI			
GAM286 CASP2	CCGTGCATCCTGAAGATCAA	4330	TGCCGCCGGA CC	
	ATCCTGAAG CA			
	TAGGACTTC GT			
	G _ TA			
GAM286 CDKN2B	GCCGCCGGGGACTTACTGAAGCCCA	4333	CC ATC_ I	
	CCG GGA CTGAAGCCC			
	GGC CCT GACTTCGGG			
	C_ GAAT I			
GAM286 CDKN2B	GCCGCCGGGGACTTACTGAAGCCCA	4333	TG AATC_ All	
	CCGCCG CTGAAGCCCA			
	GGCGGCC GACTTCGGGT			
	CCTGAAT GII			
GAM286 CHIC2	TGCCGCCGG-CTCC-GAGGCC	4342	AA T A CA	
	TGCCGCCGG TCC GA GCC			

	ACGGCGGCC AGG CT CGG			
	G_ _ C II			
GAM286 CHIC2	TGCCGCCGG-CTCC-GAGGCC	4342 _	AA T A I	
	GCCGCCGG TCC GA GC			
	CGGCGGCC AGG CT CG			
	A G_ _ C I			
GAM286 EBAF	TGCCCCCAG---CCTGAAGCCC	4343 G AAT	A	
	TGCC CCGG CCTGAAGCCC			
	ACGG GGTC GGA CTTCGGG			
	G _ _ I			
GAM286 EBAF	TGCCCCCAG---CCTGAAGCCC	4343 _ G AAT		
	GCC CCGG CCTGAAGCC			
	CGG GGTC GGA CTTCGG			
	A G _ _			
GAM286 LANCL1	GCCTCCCGCGTCCTGAAGCCC	4339 _ CGGAA	I	
	CCGC TCCTGAAGCC			
	GGCG AGGA CTTCGG			
	GGAG C_ _ I			
GAM286 LANCL1	GCCTCCCGCGTCCTGAAGCCC	4339 TG_ CGGAA	AA	
	CCGC TCCTGAAGCCC			
	GGCG AGGA CTTCGGG			
	GGAG C_ _ AI			
GAM286 PAX7	GCGGCCGGAATC--GAGGCC	4338 C CTGAAGI		
	GC GCCGGAATC			
	CG CGGCCTTAG			
	C CTCCGGI			
GAM286 PAX7	GCGGCCGGAATC--GAGGCC	4338 TGCC CT A C		
	GCCGGAATC GA GCC			
	CGGCCTTAG CT CGG			
	GC_ _ C C			
GAM286 PTPRE	GCCGTGGGT-TCCTGAAGCC	4337 CC GAA_ I		
	GCCG TCCTGAAGC			
	CGGC AGGA CTTCG			
	_ ACCCA I			
GAM286 PTPRE	GCCGTGGGT-TCCTGAAGCC	4337 TG CC AA CA		
	CCG GG TCCTGAAGCC			
	GGC CC AGGA CTTCGG			
	_ A_ CA CI			
GAM286 ROCK2	GCC-CCGGGAGGCTGAAGCCCA	4340 _ G AATC I		
	CC CCGG CTGAAGCCC			

	GG GGCC GACTTCGGG			
	C _ CTCC I			
GAM286 ROCK2	GCC-CCGGGAGGCTGAAGCCCA	4340	TG G AATC	A
	CC CCGG CTGAAGCCCA			
	GG GGCC GACTTCGGGT			
	_ _ CTCC C			
GAM286 RPS6KA2	GCCAGCGGGCACCTCCTGAAGCCC	4332	CC C AA_	I
	GC GG TCCTGAAGCC			
	CG CC AGGACTTCGG			
	_ C GTGG I			
GAM286 RPS6KA2	GCCAGCGGGCACCTCCTGAAGCCC	4332	TG _ C AA_	AAI
	CC GC GG TCCTGAAGCCC			
	GG CG CC AGGACTTCGGG			
	_ T C GTGG AII			
GAM286 SMARCA3	GCC-CCGCAGCCCTGAAGCC	4336	_ C AA	I
	CCGC GG TCCTGAAGC			
	GGCG TC GGGACTTCG			
	CGG _ _ I			
GAM286 SMARCA3	GCC-CCGCAGCCCTGAAGCC	4336	TG C AA	CA
	CCGC GG TCCTGAAGCC			
	GGCG TC GGGACTTCGG			
	GG _ _ CI			
GAM286 TNFSF10	GCAGCCGG--TCACTGAAGCCC	4334	CC_ AA _	I
	GCCGG TC CTGAAGCC			
	CGGCC AG GACTTCGG			
	CGT _ T I			
GAM286 TNFSF10	GCAGCCGG--TCACTGAAGCCC	4334	TGCC AA _	A
	GCCGG TC CTGAAGCCC			
	CGGCC AG GACTTCGGG			
	GT_ _ T A			
GAM287 CRAT	GGGAACCAAGGAGCTGAGCCCTG	4348	T_ G _ GTI	
	AT AAGGAGCTG GCC			
	TG TTCCTCGAC CGG			
	CT G T III			
GAM287 CRAT	GGGAACCAAGGAGCTGAGCCCTG	4348	TCGGGT G _ G I	
	AT AAGGAGCTG GCC TG			
	TG TTCCTCGAC CGG AC			
	CT_ G T G C			
GAM287 ISG20	TCAGGGCTGACGGAGCTGGC	4352	TA A CGT	
	TCGGG TGA GGAGCTGGC			

	AGTCC ACT CCTCGACCG				
	CG G III				
GAM287 ISG20	TCAGGGCTGACGGAGCTGGC	4352	C_ A A I		
	GGGT TGA GGAGCTGG				
	CCCG ACT CCTCGACC				
	GT _ G I				
GAM287 MBD3	CGGGCATGGGGAGGAGCTGGCC	4346	____ TAT A I		
	GGG GA GGAGCTGGC				
	CCC CT CCTCGACCG				
	CGTA _ _ I				
GAM287 MBD3	CGGGCATGGGGAGGAGCTGGCC	4346	TC A__ GTG		
	GGGTATG AGGAGCTGGCC				
	CCCGTAC TCCTCGACCGG				
	_ CCC AII				
GAM287 NAGA	GGGCAT--AGAACCTGGCCGTG	4350	GA G I		
	GGGTAT AGGA CTGGCCG				
	CCCGTA TCTT GACCGGC				
	_ G A				
GAM287 NAGA	GGGCAT--AGAACCTGGCCGTG	4350	TCGG GA G		
	GTAT AGGA CTGGCCGT				
	CGTA TCTT GACCGGCA				
	_ _ G				
GAM287 PCDH1	GGGCATTTGGGAGCTGGCCG	4349	GAA I		
	GGTAT GGAGCTGGCC				
	CCGTA CCTCGACCGG				
	AAC I				
GAM287 PCDH1	GGGCATTTGGGAGCTGGCCG	4349	TCGG GAA T		
	GTAT GGAGCTGGCCG				
	CGTA CCTCGACCGGC				
	_ AAC C				
GAM287 PCDHGB7	CGGGTCTC--GGAGCTGGC	4347	ATGAA I		
	CGGGT GGAGCTGG				
	GCCCA CCTCGACC				
	GAG_ G				
GAM287 PCDHGB7	CGGGTCTC--GGAGCTGGC	4347	TC ATGAA CG		
	GGGT GGAGCTGGC				
	CCCA CCTCGACCG				
	_ GAG_ TI				
GAM287 TLL2	GGTATGAAGAAGCATAGCCG	4351	_ II		
	GGTATGAAGGAGC TGGCC				

	CCATACTTCTTCG ATCGG			
	T C I			
GAM287 TLL2	GGTATGAAGAAGCATAGCCG 4351 TCGGGT	_	T	
	ATGAAGGAGC TGGCCG			
	TACTTCTTCG ATCGGC			
	_____ T C			
GAM288 BCAT1	GGTAAGGTAAGTTACTACTACCA 4362 TGGC	_	C_	AI
	AAGG AAGT CTACTACCAG			
	TTCC TTCA GATGATGGTT			
	CA_ A AT II			
GAM288 BUB3	GGAAAGGTCCAAGTCCTACT--CAGA 4361 TGGC	___		AC I
	AAGG AAGTCCTACT CAGA			
	TTCC TTCAGGATGA GTCT			
	CT_ AGG _ C			
GAM288 EIF2B5	GCAAGGAAG--CTGCCACC 4358 TGGC		CCTA	A
	AAGGAAGT CTACC			
	TTCTTCG GGTGG			
	_____ AC_ C			
GAM288 NOTCH2	CAAGGAAGTAACCATAGTACCA 4355 TGGCAA	___ _	C	GA
	GGAAGT CC TA TACCA			
	CCTTCA GG AT ATGGT			
	_____ TT T C GA			
GAM288 OVOL1	TGGGTAGGAAGTCCTGCTGCCAG 4367 CA		A A	AI
	TGG AGGAAGTCCT CT CCAG			
	ACC TCCTTCAGGA GA GGTC			
	CA C C II			
GAM288 PAEP	GGCAGGAGGAAGTCCCACT 4360 TG	___		ACCAG
	GCA AGGAAGTCCTACT			
	CGT TCCTTCAGGGTGA			
	_ CC CIIIA			
GAM288 PPP1R12B	TGGCAAGGAACT-CTATTGCCAGA 4368		G C CTA	I
	TGGCAAGGAA TC TA CCAGA			
	ACCGTTCCTT AG AT GGTCT			
	G _ AAC I			
GAM288 RAD52	GCAAGGAAGTCTTTCT-CCAG 4359 TGGC		CTA	A
	AAGGAAGTC CT CCAG			
	TTCTTCAG GA GGTC			
	_____ AAA _			
GAM288 RBBP9	GCATATGAAGTCCTAATAC 4357 TGGCAAG		C	CAG
	GAAGTCCTA TAC			

	CTTCAGGAT ATG		
	TATA___ T AAI		
GAM288 RNMT	TGTCAAGGAAGAGTCCTACTA 4365 G	___	CCAGA
	TG CAAGGA AGTCCTACTA		
	AC GTTCCT TCAGGATGAT		
	A TC IIIAG		
GAM288 RRM2	TGGCAAA-AGGTGATACTACCAG 4366	AA CC	A
	TGGCAAGG GT TACTACCAG		
	ACCGTTTT CA ATGATGGTC		
	C_ CT I		
GAM288 SULT2B1	TGGCAAGGAACTTCCTCCT--CAGA 4364	G_ A AC	I
	TGGCAAGGAA TCCT CT CAGA		
	ACCGTTCCTT AGGA GG GTCT		
	GA _ A_ I		
GAM288 TEM5	GGCAAGGAAGTGCT-CTTCC 4363 TG	C A A AG	
	GCAAGGAAGT CT CT CC		
	CGTTCCTTCA GA GA GG		
	___ C _ A AI		
GAM288 TNFRSF17	CAAGGAAGT--TTCTACCA 4356 TGGCAA	CCTA	
	GGAAGT CTACCA		
	CCTTCA GATGGT		
	___ AA_		
GAM289 CTBP1	CAGCGCTGCCCCCTCCCGC 4372 TGTCAG	CG A	
	CGCTGCTCTC CCGC		
	GCGACGGGGG GGCG		
	___ AG G		
GAM289 EGFL4	TGCCGGCGCTGCTC-CTGCCGC 4377 A	CC AG	
	TGTC GCGCTGCTCT GCCGC		
	ACGG CGCGACGAGG CGGCG		
	C A_ II		
GAM289 KPNB1	CAGCGCTGCTGTTGGCGGC 4373 TGTCAG	CTCC C A	
	CGCTGCT GC GC		
	GCGACGA CG CG		
	___ CAAC C A		
GAM289 NEDD4L	TGCCTGCAGCTGCTCTCTGCC 4374 A _	C GCAG	
	TGTC GC GCTGCTCTC GCC		
	ACGG CG CGACGAGAG CGG		
	A T A III G		
GAM289 PER2	TGGCAGTGGCTGCTCTCGGCC 4375 T C_	C GCAG	
	TG CAG GCTGCTCTC GCC		

	AC GTC CGACGAGAG CGG		
	C AC C III G		
GAM289 PVR	CAGCGCTGC-CTCCCCCTGCA 4371	TGTCAG T G _	
	CGCTGC CTCC CC GCA		
	II		
	GCGACG GAGG GG CGT		
	_____ _ G A		
GAM289 RELA	TGCCAGC-CTGCTCTCCCCC 4376	G G GCA	
	TGTCAGC CTGCTCTCC CC		
	II		
	ACGGTCG GACGAGAGG GG		
	_ G III		
GAM290 ARHGAP6	CGCTCAGACAGCACTGGGGA 4386	C _ AGGT	
	CGCTCAGACA CA TGGGGA		
	II		
	GCGAGTCTGT GT ACCCCT		
	C G III G		
GAM290 ARHGAP6	CGCTCAGACAGCACTGGGGA 4386	C _ II	
	CGCTCAGACA CA TGGGG		
	II		
	GCGAGTCTGT GT ACCCC		
	C G TI		
GAM290 ARHGEF12	CTCA-ATACCACTGGGGAAGG 4391	AC _ I	
	TCAG ACCA TGGGGAAG		
	AGTT TGGT ACCCCTTC		
	A_ C I		
GAM290 ARHGEF12	CTCA-ATACCACTGGGGAAGG 4391	CGCTCAGAC _	
	ACCA TGGGGAAGGT		
	TGGT ACCCCTTCCG		
	GTTA_____ C		
GAM290 C18orf2	AGTCTCCATGGG-AAGGTG 4382	AGACA G I	
	CCATGGG AAGGT		
	GGTACCC TTCCA		
	TCAGA _ C		
GAM290 COLQ	CAGACACCA-GGTGATGGT 4385	T G A I	
	CAGACACCA GG GA GG		
	II II II		
	GTCTGTGGT CC CT CC		
	_ A A A		
GAM290 COLQ	CAGACACCA-GGTGATGGT 4385	CGCTCAGA T G A	
	CACCA GG GA GG		
	II II II		
	GTGGT CC CT CC		
	_____ _ A A		
GAM290 CST	CTCAGACACCA-GGCG-TGGTG 4395	T GGAAGGI	
	CTCAGACACCA GG		
	II		

	GAGTCTGTGGT CC		
	_ GCACCAC		
GAM290 CST	CTCAGACACCA-GGCG-TGGTG	4395 CGCT	T GGAA
	CAGACACCA GG GGT		
	GTCTGTGGT CC CCA		
	_ GCA_		
GAM290 HBQ1	CTCAAACAC---GGGGAAGGT	4394 _	CAT
	TCAGACAC GGGGAAGG		
	AGTTTGTG CCCCTTCC		
	G _		
GAM290 HBQ1	CTCAAACAC---GGGGAAGGT	4394 CGCT	CAT
	CAGACAC GGGGAAGG		
	GTTTGTG CCCCTTCC		
	_ _		
GAM290 IER5	CTCTTAAACCCTGGGGAAGG	4393 CG C	A A T
	CT AGAC CC TGGGGAAGG		
	GA TTTG GG ACCCCTTCC		
	_ A _ _ T		
GAM290 IER5	CTCTTAAACCCTGGGGAAGG	4393 TC_	A A I
	AGAC CC TGGGGAAG		
	TTTG GG ACCCCTTC		
	AGAA _ _ I		
GAM290 ILK	AGACACCATGTGGCAAGTG	4381	_ G GTII
	AGACACCATG GG AAG		
	TCTGTGGTAC CC TTC		
	A G ACII		
GAM290 KIF5C	CGCTCCGAGCCC---GGGAAGGTG	4389	A CA ATG
	CGCTC GA CC GGGAAGGTG		
	GCGAG CT GG CCCTTCCAC		
	G CG _		
GAM290 KIF5C	CGCTCCGAGCCC---GGGAAGGTG	4389 _	A CA ATG
	GCTC GA CC GGGAAGGT		
	CGAG CT GG CCCTTCCA		
	G G CG _		
GAM290 MMP15	CGCTCAGGG-CCATGGGGAAG	4387	ACA GT
	CGCTCAG CCATGGGGAAG		
	GCGAGTC GGTACCCCTTC		
	CC_ II		
GAM290 MMP15	CGCTCAGGG-CCATGGGGAAG	4387 _	ACA I
	GCTCAG CCATGGGGAA		

	CGAGTC GGTACCCCTT		
	G CC_ I		
GAM290 NEK6	GCTCAGACA--AT-TGGAAGGT 4397	CCATGG I	
	GCTCAGACA GGAAG		
	CGAGTCTGT CCTTC		
	TAA_ C		
GAM290 NEK6	GCTCAGACA--AT-TGGAAGGT 4397 CG	CCATGG	
	CTCAGACA GGAAGGT		
	GAGTCTGT CCTTCCA		
	_ TAA_		
GAM290 PCDHGA1	TCAGT-ACCATGGGGATGGTG 4399 _ AC	A I	
	CAG ACCATGGGGA GGT		
	GTC TGGTACCCCT CCA		
	A A_ A I		
GAM290 PCDHGA1	TCAGT-ACCATGGGGATGGTG 4399 CGCTCAGAC	A	
	ACCATGGGGA GGT		
	TGGTACCCCT CCA		
	CA_____ A		
GAM290 PCDHGA10	TCAGT-ACCATGGGGATGGTG 4399 _ AC	A I	
	CAG ACCATGGGGA GGT		
	GTC TGGTACCCCT CCA		
	A A_ A I		
GAM290 PCDHGA10	TCAGT-ACCATGGGGATGGTG 4399 CGCTCAGAC	A	
	ACCATGGGGA GGT		
	TGGTACCCCT CCA		
	CA_____ A		
GAM290 PCDHGA11	TCAGT-ACCATGGGGATGGTG 4399 _ AC	A I	
	CAG ACCATGGGGA GGT		
	GTC TGGTACCCCT CCA		
	A A_ A I		
GAM290 PCDHGA11	TCAGT-ACCATGGGGATGGTG 4399 CGCTCAGAC	A	
	ACCATGGGGA GGT		
	TGGTACCCCT CCA		
	CA_____ A		
GAM290 PCDHGA12	TCAGT-ACCATGGGGATGGTG 4399 _ AC	A I	
	CAG ACCATGGGGA GGT		
	GTC TGGTACCCCT CCA		
	A A_ A I		
GAM290 PCDHGA12	TCAGT-ACCATGGGGATGGTG 4399 CGCTCAGAC	A	
	ACCATGGGGA GGT		

			TGGTACCCCT CCA		
			CA_____A		
GAM290	PCDHGA2	TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290	PCDHGA2	TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			
		TGGTACCCCT CCA			
		CA_____A			
GAM290	PCDHGA3	TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290	PCDHGA3	TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			
		TGGTACCCCT CCA			
		CA_____A			
GAM290	PCDHGA4	TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290	PCDHGA4	TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			
		TGGTACCCCT CCA			
		CA_____A			
GAM290	PCDHGA5	TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290	PCDHGA5	TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			
		TGGTACCCCT CCA			
		CA_____A			
GAM290	PCDHGA6	TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290	PCDHGA6	TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			

			TGGTACCCCT CCA		
			CA_____A		
GAM290	PCDHGA7	TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290	PCDHGA7	TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			
		TGGTACCCCT CCA			
		CA_____A			
GAM290	PCDHGA8	TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290	PCDHGA8	TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			
		TGGTACCCCT CCA			
		CA_____A			
GAM290	PCDHGA9	TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290	PCDHGA9	TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			
		TGGTACCCCT CCA			
		CA_____A			
GAM290	PCDHGB1	TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290	PCDHGB1	TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			
		TGGTACCCCT CCA			
		CA_____A			
GAM290	PCDHGB2	TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290	PCDHGB2	TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			

			TGGTACCCCT CCA		
			CA_____A		
GAM290	PCDHGB3	TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290	PCDHGB3	TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			
		TGGTACCCCT CCA			
		CA_____A			
GAM290	PCDHGB4	TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290	PCDHGB4	TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			
		TGGTACCCCT CCA			
		CA_____A			
GAM290	PCDHGB5	TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290	PCDHGB5	TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			
		TGGTACCCCT CCA			
		CA_____A			
GAM290	PCDHGB6	TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290	PCDHGB6	TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			
		TGGTACCCCT CCA			
		CA_____A			
GAM290	PCDHGB7	TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290	PCDHGB7	TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			

		TGGTACCCCT CCA			
		CA_____ A			
GAM290 PCDHGC3		TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290 PCDHGC3		TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			
		TGGTACCCCT CCA			
		CA_____ A			
GAM290 PCDHGC4		TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290 PCDHGC4		TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			
		TGGTACCCCT CCA			
		CA_____ A			
GAM290 PCDHGC5		TCAGT-ACCATGGGGATGGTG	4399 _ AC	A I	
		CAG ACCATGGGGA GGT			
		GTC TGGTACCCCT CCA			
		A A_ A I			
GAM290 PCDHGC5		TCAGT-ACCATGGGGATGGTG	4399 CGCTCAGAC	A	
		ACCATGGGGA GGT			
		TGGTACCCCT CCA			
		CA_____ A			
GAM290 PRDM2		CAGAGCTCACCATGGGCTGCAGGTG	4383 AGA	GA__ I	
		CACCATGGG AGGT			
		GTGGTACCC TCCA			
		A_ GACG I			
GAM290 PRDM2		CAGAGCTCACCATGGGCTGCAGGTG	4383 C AGAC	GA__ II	
		GCTC ACCATGGG AGGTG			
		CGAG TGGTACCC TCCAC			
		_ _ _ GACG TG			
GAM290 PRDM2		CTCAGACACCTTAGGCAAGG	4392 A G I		
		TCAGACACC TGGG AAG			
		AGTCTGTGG ATCC TTC			
		A G I			
GAM290 PRDM2		CTCAGACACCTTAGGCAAGG	4392 CGCT	A G T	
		CAGACACC TGGG AAGG			

	GTCTGTGG ATCC TTCC		
	_____ A G T		
GAM290 PXN	CAGACACCATCAGTGAAGG 4384	G _ II	
	CAGACACCAT GG GAAG		
	II		
	GTCTGTGGTA TC CTTC		
	G A CI		
GAM290 PXN	CAGACACCATCAGTGAAGG 4384	CGCTCAGA G _	
	CACCAT GG GAAGGT		
	II		
	GTGGTA TC CTTCCG		
	_____ G A		
GAM290 RAI14	AGACACCATGGCTGAAAGT 4380	G_ II	
	AGACACCATGG GAAGG		
	TCTGTGGTACC CTTTC		
	GA AI		
GAM290 RARB	CTCAAACAGCTCGCATGGGGAA 4390	C_____ IIIT	
	CTCAGACA CATGGGGA		
	GAGTTTGT GTACCCCT		
	CGAGC TIII		
GAM290 SLA	TCAGACACCA--GGGAGGG 4398	T AAGI	
	TCAGACACCA GGGG		
	AGTCTGTGGT CCCT		
	_ CCCI		
GAM290 SLA	TCAGACACCA--GGGAGGG 4398	CGCTCA T AA	
	GACACCA GGGG GG		
	II		
	CTGTGGT CCCT CC		
	_____ _ CC		
GAM290 SPG3A	CGCTCAGACTC--TGAGGATGTTG 4388	ACCA AG G	
	CGCTCAGAC TGGGGA GT		
	II		
	GCGAGTCTG ACTCCT CA		
	AG_ A_ A		
GAM290 SPG3A	CGCTCAGACTC--TGAGGATGTTG 4388	ACCA AGGI	
	CGCTCAGAC TGGGGA		
	GCGAGTCTG ACTCCT		
	AG_ ACAA		
GAM290 ZNF24	GCTCAGACA--A-GGGGAAG 4396	CCAT I	
	GCTCAGACA GGGGA		
	CGAGTCTGT CCCCT		
	T_ T		
GAM290 ZNF24	GCTCAGACA--A-GGGGAAG 4396	CG CCAT	
	CTCAGACA GGGGAAGG		

	GAGTCTGT CCCCTTCT			
	___ T___			
GAM291 ANXA9	TCTGGCCAGGGTACAGGAGG	4425	A	C I
	CTG CCAGGGTACGG AG			
	GAC GGTCCCATGTC TC			
	C C I			
GAM291 ANXA9	TCTGGCCAGGGTACAGGAGG	4425	AGTC A	C C
	TG CCAGGGTACGG AGG			
	AC GGTCCCATGTC TCC			
	___ C C C			
GAM291 AQP6	TGACCAGGGCTTGCTCCAGGC	4426	ACGG_	
	TGACCAGGGT CAGG			
	ACTGGTCCCG GTCC			
	AACGAG G			
GAM291 ARHGDIA	AGGCGGACCAGGGT--GGGAGG	4405	AGTCT	AC C C
	GACCAGGGT GG AGG			
	CTGGTCCCA CC TCC			
	TCCGC _ C I			
GAM291 ARHGDIA	GACCAGGGT--GGGAGGGGC	4419	AC C CI	
	GACCAGGGT GG AGG			
	CTGGTCCCA CC TCC			
	_ C CC			
GAM291 ATP11A	TGAGCAGGGTACGGC-GGTGC	4427	_ C	A CGI
	GA CAGGGTACGGC GG			
	CT GTCCCATGCCG CC			
	A C _ ACI			
GAM291 BACE	TCTG-CCAGGGTACCACAGG	4423	_ A	G I
	CTG CCAGGGTAC GCAG			
	GAC GGTCCCATG TGTC			
	A _ G I			
GAM291 BACE	TCTG-CCAGGGTACCACAGG	4423	AGTC A	G C
	TG CCAGGGTAC GCAGG			
	AC GGTCCCATG TGTCC			
	___ _ G C			
GAM291 BIRC7	TCTGACCAGGTTTGCAGCAG	4422	GTA_	
	TCTGACCAGG CGGCA			
	AGACTGGTCC GTCGT			
	AAAC CI			
GAM291 BIRC7	TCTGACCAGGTTTGCAGCAG	4422	AGTC	GTA_ C
	TGACCAGG CGGCAGG			

	ACTGGTCC GTCGTCT	
	____ AAAC T	
GAM291 GNAZ	GTTTCACCA---TA-GGCAGGCGC 4421 TCTG_ GGGTAC	
	ACCA GGCAGGCG	
	TGGT CCGTCCGC	
	CAAAG AT____	
GAM291 HRASLS	ACCCGGG-A-GGCAGGCGC 4402 A TAC I	
	ACC GGG GGCAGGCG	
	TGG CCC CCGTCCGC	
	G T__ G	
GAM291 MAPT	CTGAGGCCGCGCGGGCGGCAGGCGC 4409 TGACCA__ TA I	
	GGG CGGCAGGCG	
	CCC GCCGTCCGC	
	TCCGGCCG __ I	
GAM291 MEN1	TGCCCAGCGGAGGGCAGGCGC 4428 GA _ TAC I	
	CCAG GG GGCAGGCG	
	GGTC CC CCGTCCGC	
	CG G TC_ I	
GAM291 MUC1	GAACAGATTCAGGCAGGCGC 4418 AC GTAC I	
	CAGG GGCAGGCG	
	GTCT CCGTCCGC	
	TT AAGT I	
GAM291 MUS81	CTGACCAGGGAATTCCAGGTGC 4415 TACGG CGI	
	TGACCAGGG CAGG	
	ACTGGTCCC GTCC	
	TTAAG ACI	
GAM291 MUS81	CTGACCAGGGAATTCCAGG 4411 AGTCTG TACGG C	
	ACCAGGG CAGG	
	TGGTCCC GTCC	
	____ TTAAG A	
GAM291 NEO1	CTGACCAGGGAAGGCAGG 4412 TAC II	
	CTGACCAGGG GGCAG	
	GACTGGTCCC CCGTC	
	CTT CI	
GAM291 NEO1	AGGCTGACCAGGGGAAGGCAGG 4406 T TAC CG	
	AG CTGACCAGGG GGCAGG	
	TC GACTGGTCCC CCGTCC	
	C CTT II	
GAM291 NR1I2	AGGCTGACCAGGAGT-GGGGAGG 4404 T _ AC C CG	
	AG CTGACCAGG GT GG AGG	

	TC GACTGGTCC CA CC TCC		
	C T CC _ II		
GAM291 OPHN1	CTGACCAGGG-CCCGCTGGC	4413 AGTCTG	ACG A
	ACCAGGGT GC GGC		
	II		
	TGGTCCCG CG CCG		
	_____ GG_ A		
GAM291 OPHN1	CTGACCAGGG-CCCGCTGGC	4413 C	AC___ AGI
	TGACCAGGGT GGC		
	ACTGGTCCCG CCG		
	_ GCGA III		
GAM291 OPTN	CTGACCAGGGAACCTGCCGGCG	4410 T	T G_ A I
	GACCAGGG AC GC GGC		
	II II		
	CTGGTCCC TG CG CCG		
	_ T GA G I		
GAM291 PES1	TCTGACCAGGCACCAGCAGG	4424	GTA I
	CTGACCAGG CGGCAG		
	GA CTGGTCC GTCGTC		
	GTG I		
GAM291 PES1	TCTGACCAGGCACCAGCAGG	4424 AGTC	GTA _
	TGACCAGG CGGCAGG C		
	I		
	ACTGGTCC GTCGTCC G		
	_____ GTG C		
GAM291 PIGR	CCAGGCGTGCTGGCAGGCGC	4408	_ AC_ III
	CCAGG GT GGCAGGCG		
	II		
	GGTCC CA CCGTCCGC		
	G CGA GII		
GAM291 PLGL	AGTCTGACCTAGGT-CTGCGGG	4407	A ACG A CG
	AGTCTGACC GGGT GC GG		
	II II		
	TCAGACTGG TCCA CG CC		
	A GA_ C II		
GAM291 PRKCABP	GAGCAGGG-A-GGCAGGCGC	4420 AC_	TAC I
	CAGGG GGCAGGCG		
	GTCCC CCGTCCGC		
	CTC T_ I		
GAM291 SLC21A2	GACCAGGGTTAGTTGCAGG	4417	ACG_ III
	GACCAGGGT GCAG		
	CTGGTCCCA CGTC		
	ATCAA CII		
GAM291 SLC8A2	GACCAGGGTCCAAGAGCAGGTGC	4416 ACC	AC___ CGI
	AGGGT GGCAGG		

	TCCCA TCGTCC		
	___ GGTTC ACI		
GAM291 SSX3	AGCCTGACCAGGACGCATGGCA	4403	TACG _
	AGTCTGACCAGGG GCA GGCG		
	TCGGA CTGGTCCT CGT CCGT		
	G___ A		
GAM291 USP11	CTGACCAGGTAATGCCAAGC	4414	GTACG AGGI
	TGACCAGG GC		
	ACTGGTCC CG		
	ATTA_ GTTC		
GAM291 USP11	CTGACCAGGTAATGCCAAGC	4414	AGTCTG GTACG _
	ACCAGG GC AGGC		
	TGGTCC CG TTCG		
	___ ATTA_ G		
GAM292 ABCC3	CACCTG-CTTCAGGAAGCTGGG	4436 _	T CGI
	ACTTG CTTCAGGAAGCT		
	TGGAC GAAGTCCTTCGA		
	G _ CCI		
GAM292 ACCN2	TCACTTGTCTCTCATTAAGATAGG	4442	_ GG CTCGI
	ACTTGTCT TCA AAG		
	TGAACAGA AGT TTC		
	G AA TATII		
GAM292 APM1	CACTT-TCTCTGAGGAAGCTC	4433	G C_ I
	ACTT TCTT AGGAAGCT		
	TGAA AGAG TCCTTCGA		
	_ AC I		
GAM292 AQP1	CTTGGTCCCCAGGAAGCTCTGA	4438	TT GI
	GTCTTCAGGAAGCTC		
	CAGGGGTCCTTCGAG		
	C_ AC		
GAM292 ASL	CTCGTCGTCCGGAAGCTTCGG	4439	TT T A _ I
	GTC TC GGAAGCT CG		
	CAG AG CCTTCGA GC		
	G_ C G A I		
GAM292 CABC1	TGGCTGCAGGAAGCTGGGA	4446	T T C II
	TG CT CAGGAAGCT GG		
	AC GA GTCCTTCGA CC		
	C C C TI		
GAM292 CDR1	TGTCTTCCA ACTAAGCTCGGA	4444	AGG_ III
	TGTCTTC AAGCTCGG		

	ACAGAAG	TTCGAGCC		
	GTTGA	TII		
GAM292 DAAM2	CACTTGTCTTGCAGTGGGAGCTC	4434 ACT	_ GA_	I
	TGTCTT CAG AGCT			
	ACAGAA GTC TCGA			
	_ C ACCC I			
GAM292 GBP1	TTGTCTTCACTAAGAAGCTAGG	4447	_	CGIII
	TTGTCTTCA GGAAGCT			
	AACAGAAGT TCTTCGA			
	GAT TCCII			
GAM292 IRF2	TTGTCTTCA--AATCTGGGA	4448 _	GAAG C I	
	TGTCTTCAG CT GG			
	ACAGAAGTT GA CC			
	A TA_ C I			
GAM292 NFRKB	CACT-GTCTTCAGGAAACTGGG	4437 C		CI
	TTGTCTTCAGGAAGCT			
	GACAGAAGTCCTTTGA			
	T CI			
GAM292 NUCB1	ACTGGTCTTCAGG-GGCTC	4432 T	AA I	
	ACT GTCTTCAGG GCT			
	TGA CAGAAGTCC CGA			
	C C_ G			
GAM292 PHEMX	TGTCCTCAGGAAGCTCCGGA	4445	_ II	
	TGTCTTCAGGAAGCTC GG			
	ACAGGAGTCCTTCGAG CC			
	G TI			
GAM292 RAB27A	TCACATGTCCTCTTCAGGAAG	4441 T	_	III
	TCAC TGTCT TCAGGAA			
	AGTG ACAGG AGTCCTT			
	T AGA CII			
GAM292 SCAP1	CACTTGTCTTACTGGTAGCT	4435	CA_ A II	
	CACTTGTCTT GG AGC			
	GTGAACAGAA CC TCG			
	TGA A AI			
GAM292 SELPLG	TCACTTGTCACTAGATGGAAGCTC	4440 CAC	TTCA_	I
	TTGTC GGAAGCT			
	AACAG CCTTCGA			
	_ TGATCTA I			
GAM292 SLC4A4	TCA-TTGTCTTCAGGTTCAAGTTC	4443 AC		AAGCTI
	TTGTCTTCAGG			

	AACAGAAGTCC			
	— AAGTTC			
GAM292 USP14	ACATGTCTTCAGCCAAGCTC	4431	T G_ II	
	AC TGTCTTCAG AAGCT			
	II IIIIIII IIIII			
	TG ACAGAAGTC TTCGA			
	T GG GI			
GAM293 CYP26A1	GGGGTGCGGGGCTAGGAGCTGC	4453	CCTCC I	
	GGGTGTG AGGAGCTG			
	IIIIII IIIIIII			
	CCCACGC TCCTCGAC			
	CCCGA I			
GAM293 LPL	GGGCGCGTCCCTCTGGAGGAGCTGC	4451	GGG G C_ I	
	GTGT CCTC AGGAGCTG			
	IIII III IIIIIII			
	CGCA GGAG TCCTCGAC			
	G_ G ACC I			
GAM293 LPL	GGGCGCGTCCCTCTGGAGGAGCTGC	4451	TG G G C_ II	
	GG GTGT CCTC AGGAGCTGC			
	II IIII IIIIIII			
	CC CGCA GGAG TCCTCGACG			
	_ G G ACC TI			
GAM293 MAGEA2	GGAGTGCGGGCAGGAGCTG	4455	T CTC II	
	GG GTGC CAGGAGCT			
	II IIII IIIIIII			
	CC CACG GTCCTCGA			
	T CCC CI			
GAM293 NCF4	GGGAGT-CC-CCAGGAGCTGC	4454	T G T I	
	GGG GT CC CCAGGAGCT			
	III II IIIIIII			
	CCC CA GG GGTCTCGA			
	T _ _ C			
GAM293 NCF4	GGGAGT-CC-CCAGGAGCTGC	4454	TGGGGGTGTGC	
	CTCCAGGAGCTG			
	IIIIIIIIII			
	GGGGTCCTCGAC			
	TCA_____			
GAM293 NDN	GGGCCTCTGCGTCCAGGAGCT	4452	GG G_ C I	
	GGT TGC TCCAGGAGC			
	III III IIIIIII			
	CCG ACG AGGTCCTCG			
	_ GAG C I			
GAM293 NDN	GGGCCTCTGCGTCCAGGAGCT	4452	TGGG G_ C GC	
	GGT TGC TCCAGGAGCT			
	III III IIIIIII			
	CCG ACG AGGTCCTCGA			
	_ GAG C GI			
GAM293 TJP1	TGGGGGTGTCCTTCCCTG-GCTGC	4457	G _ AGGA I	
	TGGGGGTGT CCT CC GCTGC			
	IIIIII III II IIIII			

	ACCCCCACA GGA GG CGACG	
	_ A GAC_ I	
GAM293 TJP1	TGGGGGTGTCCTTCCCTG-GCTGC 4457 _ G _ AGGA I	
	GGGGGTGT CCT CC GCTG	
	CCCCCACA GGA GG CGAC	
	A _ A GAC_ I	
GAM293 TMC1	TGGGGGTGT-CCTGTCAGAAG 4456 G C_ CTG	
	TGGGGGTGT CCT CAGGAG	
	ACCCCCACA GGA GTCTTC	
	_ CA	
GAM293 TMC1	TGGGGGTGT-CCTGTCAGAAG 4456 G C_ I	
	GGGGGTGT CCT CAGGA	
	CCCCCACA GGA GTCTT	
	_ CA I	
GAM294 NXF1	GCTTCTGA-GGCATGACTAC 4460 A _ C II	
	GC TC GA GGCATGACTA	
	CG AG CT CCGTACTGAT	
	A A _ GI	
GAM294 NXF1	GCTTCTGA-GGCATGACTAC 4460 TGGCATC C TG	
	GA GGCATGACTAC	
	CT CCGTACTGATG	
	AAGA__ _ CT	
GAM294 SPON1	TGGCATCCAC---AAGACTACTGG 4461 G CAT	
	TGGCATC ACGG GACTACTGG	
	ACCGTAG TGTT CTGATGACC	
	G _	
GAM294 SPON1	TGGCATCCAC---AAGACTACTGG 4461 _ G CAT	
	GGCATC ACGG GACTACTG	
	CCGTAG TGTT CTGATGAC	
	A G _	
GAM295 CTH	TATAACCAAGTCGAA---GCCGGGT 4472 TAA G AGA	
	AA CGGTCGA AGCCGGGT	
	TT GTCAGCT TCGGCCCA	
	ATA G _	
GAM295 MAP3K5	TACAAGGGGTGGG-GAAGCCGGGT 4471 TAA C CGAA I	
	AAG GGT GAAGCCGGGT	
	TTC CCA CTTCGGCCCA	
	ATG C CCC_ I	
GAM295 PITX2	GCGGTCGAACAGGAGCCGGG 4467 TAAAAG TCGA A	
	CGG AG AGCCGGG	

	GCT TC TCGGCC	
	_____ TG_ C	
GAM295 STUB1	AAGCGGTCGGGGTGGCCAGG 4466 TAAAAG AAGAA	
	CGGTTCG GCCGGG	
	GCCAGC CGGTCC	
	_____ CCCAC	
GAM295 SUOX	TAAATG-GGT-GAAGAAGCC 4468 TAAAAGC C GG	
	GGT GAAGAAGCC	
	CCA CTTCTTCGG	
	ATTTAC_ _ II	
GAM295 SWAP70	TAAAAGCAG-C--A-AAGCCGGGT 4469 CGAA	
	TAAAAGCGGT GAAGCCGGG	
	ATTTTCGTTCG TTTCGGCCC	

GAM295 TAF6	AAGCAGGTCGAAGATCCCCGG 4465 TAAAAGC AG_	
	GGTCGAAGA CCGGGT	
	CCAGCTTCT GGCCCG	
	GT_____ AGG	
GAM295 TNFAIP2	TAAAAGCGGTAGAGCAGGCCGGGT 4470 C A AA_ I	
	TAAAAGCGGT GA G GCCGGGT	
	ATTTTCGCCA CT C CGGCCCA	
	T _ GTC I	
GAM295 ZFH1B	AAAAGCA-T-GAAGAAGCCG 4464 TA GTC G	
	AAAGCG GAAGAAGCCG	
	TTTCGT CTTCTTCGGC	
	_ A_ G	
GAM296 DLG5	CAGAGGGGACAGGGGCTGGGCACCGGCA4478 TCAGA_ CGA _	
	GAC GGCT GCACCGGCA	
	CTG CCGA CGTGGCCGT	
	TCTCCC TCC CC TII	
GAM296 EXTL1	CAGACGGCCGAGGCTGAGCCG 4477 TC GA_ CA GCA	
	AGA CCGAGGCTG CCG	
	TCT GGCTCCGAC GGC	
	_ GCC TC GII	
GAM296 GJB1	CAGCAGGCAGAGGCCTGTGCACCGGCA4476 TCAGAGACC _	
	GAGGCT GCACCGGCA	
	CTCCGG CGTGGCCGT	
	TCGTCCGT_ ACA CII	
GAM296 GLUD1	CACAGAGCAAGGCTGCACAGCCA 4483 T AC C AI	
	CAGAG CGAGGCTGCAC GGC	

	GTCTC GTTCCGACGTG TCG			
	T _ _ _ GT			
GAM296 HS2ST1	CAGAGACCGTATGGGCTGCA	4480 TC	A _ _	CCGGC
	AGAGACCG GGCTGCA			
	TCTCTGGC CCGACGT			
	_ ATAC TIIIA			
GAM296 MAN2A2	TCAGATACCGTCGGGGCTGCACC	4484	G A _ _	GGCAI
	TCAGA ACCG GGCTGCACC			
	AGTCT TGGC CCGACGTGG			
	A AGCC IIIAC			
GAM296 MYOM2	CAGAGACCGCCACATGCTGCAC	4479 TC	AG _ _	CGGCA
	AGAGACCG GCTGCAC			
	TCTCTGGC CGACGTG			
	_ GGTGTA TIIIA			
GAM296 NTSR1	CAGGGATAGGGGCTGCACCG	4481 TC	A CCGA	C
	AG GA GGCTGCACCGG			
	TC CT CCGACGTGGCT			
	_ C ATCC I			
GAM296 NTSR1	TCAGAGACC-AGGCACCATCG	4487	G TGC GC	
	TCAGAGACC AGGC ACCG			
	AGTCTCTGG TCCG TGGT			
	_ _ AG			
GAM296 PRKAB1	TCACAGACCGAGGCGCTGCA	4485	G _ CCGGC	
	TCA AGACCGAGGC TGCA			
	AGT TCTGGCTCCG ACGT			
	G CG IIIAC			
GAM296 SEPX1	TCAGAGACC-A-GCTGCACC	4486	GA GG	
	TCAGAGACC GGCTGCACC			
	AGTCTCTGG TCGACGTGG			
	_ II			
GAM296 TCOF1	CAGAGACCGA-GCGGCACGGG	4482 TC	G T C C	
	AGAGACCGAG C GCAC GG			
	TCTCTGGCTC G CGTG CC			
	_ _ C C T			
GAM296 XRCC2	AGAGGCAGAGGCTGCAGCGG	4475 TCAGAGACC	C _	
	GAGGCTGCA CGG C			
	CTCCGACGT GCC G			
	TCCGT _ C C			
GAM297 BMPR1A	GCATATTTTCATAAGTCCGG	4504 _	C II	
	GCA ATTTTCATAA TCTG			

	CGT TAAAAGTATT AGGC			
	A C CI			
GAM297 BMPR1A	GCATATTTTCATAAGTCCGG	4504	AGCA	C TGA
	ATTTTCATAA TCTGG			
	TAAAAGTATT AGGCC			
	GTA_ C TII			
GAM297 C7orf2	ATTTTCATA--TCAGGTGAA	4498	_ AC T I	
	TTTTCATA TC GGTGA			
	AAAAGTAT AG CCACT			
	T _ T I			
GAM297 CDH10	AGCATCACTTT--TAACTCTGG	4491	_ CA TGA	
	AGCA ATTTT TAACTCTGG			
	TCGT TGAAA ATTGAGACC			
	AG _ III			
GAM297 CDH10	AGCATCACTTT--TAACTCTGG	4491	_ CA I	
	GCA ATTTT TAACTCTG			
	CGT TGAAA ATTGAGAC			
	AG _ I			
GAM297 FBXW1B	TTCATAACTCAGCTGTGAA	4506	TG_ III	
	TTCATAACTC GTGA			
	AAGTATTGAG CACT			
	TCGA TII			
GAM297 FGG	CAATTTTAAATAACTCTG	4502	C_ III	
	CAATTTT ATAACTCT			
	GTAAAA TATTGAGA			
	ATT CII			
GAM297 FGG	CAATTTTAAATAACTCTG	4502	AGCAA TC GA	
	TTT ATAACTCTGGT			
	AAA TATTGAGACTA			
	TAA_ TT II			
GAM297 GATA6	ATTTTAAAACTCTGGTGAA	4500	_ CAT I	
	TTTT AACTCTGGTGA			
	AAAA TTGAGACCACT			
	A TT_ I			
GAM297 GATA6	ATTTTAAAACTCTGGTGAA	4500	AGCAATTTTCAT	
	AACTCTGGTGA			
	TTGAGACCACT			
	AATT_____			
GAM297 IL4R	AGCAATTTTTCATGTCCTCTGTTG	4493	_ AA_ G AAI	
	AGCAATTTT CAT CTCTG TG			

	TCGTTAAAA GTA GAGAC AC		
	A CAG A III		
GAM297 IL4R	AGCAATTTTTCATGTCCTCTGTTG 4493 CAA	AA_	GI
	TTTTTCAT CTCTG		
	AAAAGTA GAGAC		
	TA_ CAG AI		
GAM297 LLT1	AGCATATTTTCATATAC-CTGTTG 4492 _	_ T	G AAI
	AGCA ATTTTCATA AC CTG TG		
	TCGT TAAAAGTAT TG GAC AC		
	A A _ A III		
GAM297 LLT1	AGCATATTTTCATATAC-CTGTTG 4492 CA	_ T	GI
	ATTTTCATA AC CTG		
	TAAAAGTAT TG GAC		
	TA A _ AI		
GAM297 MADH4	AGCAATTTTGAT-CCTTTGG 4495	CATAA C	TGA
	AGCAATTTT CT TGG		
	TCGTTAAAA GA ACC		
	CTAG_ A III		
GAM297 MBNL	AGCAATTTTGTAGAA-CTGCTGAA 4497	CAT _	TGAA
	AGCAATTTT AACT CTGG		
	TCGTTAAAA TTGA GACT		
	ATC C TIII		
GAM297 MBNL	AGCAATTTTGTAGAA-CTGCTGAA 4497	CAT _	TGI
	AGCAATTTT AACT CTGG		
	TCGTTAAAA TTGA GACT		
	ATC C TII		
GAM297 MBNL	AGCAATTTTGCTCAGTCTG 4494	CATAAC	GTGA
	AGCAATTTT TCTG		
	TCGTTAAAA AGAC		
	CGAGTC IIIA		
GAM297 MS4A6A	ATTTTCATA--TCCAGTGAA 4499_	AC TG	I
	TTTTTCATA TC GTGA		
	AAAAGTAT AG CACT		
	T _ GT I		
GAM297 NBS1	TTTCCAT---TCTGGTGAA 4507	AAC	
	TTTTTCAT TCTGGTGA		
	AAAGGTA AGACCACT		
	—		
GAM297 NFIA	GCATATTTTCATATATCTGG 4505 _	AC	II
	GCA ATTTTCATA TCTG		

	CGT TAAAAGTAT AGAC			
	A AT CI			
GAM297 NFIA	GCATATTTTCATATATCTGG	4505 AGCA	AC	TGA
	ATTTTCATA TCTGG			
	TAAAAGTAT AGACC			
	GTA_ AT CII			
GAM297 PPP1R12B	CAATTTTCAACAAACAGGTG	4503 AGCA	TAACTCT	A
	ATTTTCA GGTG			
	TAAAAGT CCAC			
	____ TGTTTGT C			
GAM297 SLC10A2	CAATTTTCACTTTAACTCT	4501	____	III
	CAATTTTCAT AACTC			
	GTAAAAAGTG TTGAG			
	AAA AII			
GAM297 SLC10A2	CAATTTTCACTTTAACTCT	4501 AGCA	____	GGTGA
	ATTTTCAT AACTCT			
	TAAAAGTG TTGAGA			
	____ AAA AIII			
GAM297 VDAC1	AGCTATTT-CATA-CTCTGGTG	4496 AAT	A	A
	AGC TTTCATA CTCTGGTG			
	TCG AAAGTAT GAGACCAC			
	AT_ _ I			
GAM297 VDAC1	AGCTATTT-CATA-CTCTGGTG	4496 _ AAT	A	I
	GC TTTCATA CTCTGGT			
	CG AAAGTAT GAGACCA			
	T AT_ _ I			
GAM297 ZNF192	AATTTCTCAATTCCAACCTCTGGTGAA	4490 AG_	TCA	II
	CAATTT TAACTCTGGTGAA			
	GTTAAG GTTGAGACCACTT			
	AAGA _ AT			
GAM297 ZNF192	AATTTCTCAATTCCAACCTCTGGTGAA	4490 ATT_	A	I
	TTC TAACTCTGGTGAA			
	AAG GTTGAGACCACT			
	AGTT _ I			
GAM298 ASH1	TGAGTTATACCTGGGTATA	4518 TATGA	_	ACTA
	TTATAC TGGGTATA			
	AATATG ACCCATAT			
	TC_ G CCII			
GAM298 C4orf1	ATG-TTATAGTCAATATAACTAT	4511 TA A	CTG	
	TG TTATA GGTATAACTAT			

	AC AATAT TTATATTGATA	
	___ CAG	
GAM298 FBXL2	TGATTATACTACAGATAACT 4520 TATG _ T A	
	ATTATACTG GG ATAACT	
	TAATATGAT TC TATTGA	
	___ G _ A	
GAM298 FMR2	TATGTTCTTTTCTGGGTATAA 4513 TATGATTATA_ CTAT	
	CTGGGTATAA	
	GACCCATATT	
	ATACAAGAAAA IIIT	
GAM298 IREB2	TGAGTATACTGGGACTATCT 4519 TATGAT TATA	
	TATACTGGG ACTA	
	ATATGACCC TGAT	
	TC___	
GAM298 MAP3K7IP2	ATTATACTGAGGTATTATTA 4512 TATGATTA _ AACTA	
	TACTG GGTAT	
	ATGAC CCATA	
	___ T ATAAT	
GAM298 PRKAR2B	TATGATTATCAGTCTGAATAAGTA 4514 A___ TAACTATI	
	TATGATTAT CTGGGTA	
	ATACTAATA GACTTAT	
	GTCA TCATIIIT	
GAM298 RB1CC1	TATGATTATTCTAGAGTCATAA 4515 A _ ATAACATAT	
	TATGATTAT CTGG GT	
	ATACTAATA GATC CA	
	A T GTATTIII	
GAM298 SCN3A	ATGGTTA---GGGTATAAC 4510 TATGATTATACT	
	GGGTATAAC	
	CCCATATTG	
	ACCAAT___	
GAM298 TSG	TATGATTATACT-TGTTTAA 4516 GG ATAACATA	
	TATGATTATACT GT	
	ATACTAATATGA CA	
	A_ AATTIII	
GAM298 USP6	TATGATTAT--T-GGTA-AACT 4517 ACTG T	
	TATGATTAT GGTA AACT	
	ATACTAATA CCAT TTGA	
	A___	
GAM299 ACTN4	TTGCATAGATACA-GAGTGGAGGAAT 4536 TCCA _ T A I	
	AGA ACA GA TGGAGGAA	

	TCT TGT CT ACCTCCTT	
	CGTA A _ C I	
GAM299 ACTN4	TTGCATAGATACA-GAGTGGAGGAAT 4536 TTCCA_ _ T A II	
	AGA ACA GA TGGAGGAAT	
	TCT TGT CT ACCTCCTTA	
	AACGTA A _ C II	
GAM299 ALPPL2	TTCCCAGAA---GAATGGAGG 4543 A CAT A	
	TTCC AGAA GAATGGAGG	
	AAGG TCTT CTTACCTCC	
	G _ _ I	
GAM299 ALPPL2	TTCCCAGAA---GAATGGAGG 4543 _ A CAT	
	TCC AGAA GAATGGAG	
	AGG TCTT CTTACCTC	
	A G _	
GAM299 ATP10C	TTCCAAGAACA-GA--GGAGG 4541 T AT A	
	TTCCAAGAACA GA GGAGG	
	AAGGTTCTTGT CT CCTCC	
	_ _ I	
GAM299 ATP10C	TTCCAAGAACA-GA--GGAGG 4541 _ T AT	
	TCCAAGAACA GA GGAG	
	AGGTTCTTGT CT CCTC	
	A _ _	
GAM299 ATRX	AAGAACATGATGATGAGAGAAA 4523 _ _ III	
	AAGAACATGA ATG GAGGA	
	TTCTTGTA CT TAC CTCTT	
	AC T TII	
GAM299 BSG	AGAATCCTGAATGGAGAAA 4525 CA_ II	
	AGAA TGAATGGAGGA	
	TCTT ACTTACCTCTT	
	AGG TI	
GAM299 BSG	AGAATCCTGAATGGAGAAA 4525 TTCCAAGAACA	
	TGAATGGAGGAA	
	ACTTACCTCTTT	
	GG_____	
GAM299 DEDD	TTTCAAGC-CATGGAATGGAGGAA 4540 TC AA _ I	
	CAAG CATG AATGGAGGA	
	GTTC GTAC TTACCTCCT	
	AA G_ C I	
GAM299 DEDD	TTTCAAGC-CATGGAATGGAGGAA 4540 TTC AA _ TI	
	CAAG CATG AATGGAGGAA	

	GTTC GTAC TTACCTCCTT		
	AAA G_ C II		
GAM299 DSC1	TTCCAAGAACCTTAGAAGTTGGAG 4539	AT__ __	GAATI
	TTCCAAGAAC GAA TGGAG		
	III		
	AAGGTTCTTG CTT ACCTC		
	GAAT CA IIITA		
GAM299 ESRRG	CAGGAACCT--ATGGAGGAAT 4530 AA_ ATGA I		
	GAAC ATGGAGGAA		
	CTTG TACCTCCTT		
	GTC GA_ I		
GAM299 ESRRG	CAGGAACCT--ATGGAGGAAT 4530 TTCCAA ATGA		
	GAAC ATGGAGGAA		
	CTTG TACCTCCTT		
	_____ GA_		
GAM299 FZD8	TCCCCGCACATCAATGGAGGAA 4535_ AAGA G I		
	CC ACAT AATGGAGGA		
	GG TGTA TTACCTCCT		
	G GCG_ G I		
GAM299 FZD8	TCCCCGCACATCAATGGAGGAA 4535 TT AAGA G T		
	CC ACAT AATGGAGGAA		
	GG TGTA TTACCTCCTT		
	G_ GCG_ G T		
GAM299 HNF3B	CAACAACAGCAATGGAGGA 4528 G TG II		
	CAA AACA AATGGAGG		
	GTT TTGT TTACCTCC		
	G CG TI		
GAM299 HNF3B	CAACAACAGCAATGGAGGA 4528 TTCCAAG TG A		
	AACA AATGGAGGA		
	TTGT TTACCTCCT		
	G_____ CG C		
GAM299 ITGAV	AAGTACATGAATGGAGGAA 4524 A II		
	AAG ACATGAATGGAGGA		
	TTC TGTACTTACCTCCT		
	A TI		
GAM299 ITGAV	AAGTACATGAATGGAGGAA 4524 TTCCAAGA		
	ACATGAATGGAGGAA		
	TGTACTTACCTCCTT		

GAM299 LILRB4	TTCCAAGAACAAGA---GAGG 4542 T AT AI		
	TTCCAAGAACA GA GG		

	AAGGTTCTTGT CT CC		
	T CT II		
GAM299 LILRB4	TTCCAAGAACAAGA---GAGG 4542	TGAAT A	
	TTCCAAGAACA GGAGG		
	AAGGTTCTTGT TCTCC		
	TC___ I		
GAM299 MEN1	CAATAACAGGAAAAATGGAGGA 4527	G T___ III	
	CAA AACA GAATGGAGG		
	GTT TTGT TTTACCTCC		
	A CCTT TII		
GAM299 MEN1	CAATAACAGGAAAAATGGAGGA 4527	TTCCAAG T___ AT	
	AACA GAATGGAGGA		
	TTGT TTTACCTCCT		
	A_____ CCTT AT		
GAM299 OXR1	CAAGAACATGATTTGAAAAAT 4529	ATG I	
	AAGAACATGA GAGGAA		
	TTCTTGTA CT TTTT		
	AAA I		
GAM299 OXR1	CAAGAACATGATTTGAAAAAT 4529	TTCCAA ATG	
	GAACATGA GAGGAAT		
	CTTGTA CT TTTTA		
	_____ AAA		
GAM299 RPA1	CAAAATACATGAATGCAGGAAT 4526	AAGA G I	
	ACATGAATG AGGAA		
	TGTACTTAC TCCTT		
	TTTA G I		
GAM299 RPA1	CAAAATACATGAATGCAGGAAT 4526	TTCCAAGA G	
	ACATGAATG AGGAAT		
	TGTACTTAC TCCTTA		
	TTA_____ G		
GAM299 SLC19A2	CCAAGAACATTCATATGATGAAT 4531	C GA _ G I	
	AAGAACAT ATG GA GAA		
	TTCTTGTA TAT CT CTT		
	_ AG A A I		
GAM299 SLC19A2	CCAAGAACATTCATATGATGAAT 4531	TTCC GA _ G I	
	AAGAACAT ATG GA GAAT		
	TTCTTGTA TAT CT CTTA		
	_____ AG A A A		
GAM299 SPON1	TCCAAGAAC---AAGGGAGCAA 4534	TGAAT GI	
	TCCAAGAACA GGAG		

	AGGTTCTTGT	CCTC	
	TC__	GT	
GAM299 SPON1	TCCAAGAAC--AAGGGAGCAA	4534 TT	TGAAT G
	CCAAGAACA	GGAG AA	
	GGTTCTTGT	CCTC TT	
	__	TC__ G	
GAM299 TRPS1	CCAAGAACATGTTTGTGAG	4532	AA GAI
	CCAAGAACATG	TG	
	GGTTCTTGTAC	AC	
	AA	ACTC	
GAM299 TRPS1	CCAAGAACATGTTTGTGAG	4532 TTCC	AA _ GAA
	AAGAACATG	TG GAG	
	TTCTTGTAC	AC CTC	
	__	AA A ATI	
GAM299 TRPS1	TTTCAAGAGAACACATGAATG	4537 TTC	__ GAGGAAT
	CAAGA	ACATGAATG	
	GTTCT	TGTACTTAC	
	AAA	CTTG IIITAAG	
GAM299 TRPS1	TTTCAAGAGAACACATGAATG	4537 TTC	__ IIIC
	CAAGA	ACATGAAT	
	GTTCT	TGTACTTA	
	AAA	CTTG CIII	
GAM299 TRPS1	TTCCAAGAATAGTGATATG	4538	CA_ _ GAGGAA
	TTCCAAGAA	TGA ATG	
	AAGGTTCTT	ACT TAC	
	ATC	A IIITAA	
GAM299 TRPS1	TTCCAAGAATAGTGATATG	4538	CA_ ATIII
	TTCCAAGAA	TGA	
	AAGGTTCTT	ACT	
	ATC	ATACI	
GAM299 VPS26	CCATGCATATGAATGGATGA	4533 CCAAGAAC	GI
	ATGAATGGA		
	TACTTACCT		
	TACGTA__	AC	
GAM299 VPS26	CCATGCATATGAATGGATGA	4533 TTCCAAGAAC	G A
	ATGAATGGA	GA	
	TACTTACCT	CT	
	TACGTA__	A G	
GAM300 BACE	TGGGTGGGGAGGGTCCTGAG	4555 TC	TACTTAC T
	TGGG	GGTCCTGAG	

	ACCC CCAGGACTC		
	CC CTC_____ C		
GAM300 GOLGA4	TCTGGGTACAATTAATGTTTCTGA 4548	TTACG__ C_ GTCI	
	TCTGGGTAC GT CTGA		
	II		
	AGACCCATG CA GACT		
	TTAATTA AA IIIC		
GAM300 GPR30	TCTGGGTACCTGCCGTCCAGA 4549	ACG T GTC	
	TCTGGGTACTT GTCC GA		
	II		
	AGACCCATGGA CAGG CT		
	CGG T III		
GAM300 IFNW1	TCTGGGTAC-TAAAGTCATAAGT 4552	TAC C C	
	TCTGGGTACT GGTC TGAGT		
	AGACCCATGA TCAG ATTCA		
	TT_ T I		
GAM300 JAM3	TCTGGGTACAGACTGTCCT-AGTC 4553	TT G G I	
	TCTGGGTAC AC GTCCT AGTC		
	II		
	AGACCCATG TG CAGGA TCAG		
	TC A _ I		
GAM300 KIF3B	TCAGGATGCT-ACGGTCCTGAG 4550	T A T TC	
	TC GGGT CT ACGGTCCTGAG		
	II II		
	AG CCTA GA TGCCAGGACTC		
	T C _ II		
GAM300 MAT1A	GGGTATGTCACAGGCTCCTGAGTC 4546	TCTGGGTAC _ _ I	
	TTAC GG TCCTGAGTC		
	II		
	AGTG CC AGGACTCAG		
	ATAC_____ T G T		
GAM300 MEOX2	GGATAATCCCGGTCCTGAG 4547	TCTGGGTACTTA	
	CGGTCCTGAGT		
	GCCAGGACTCG		
	ATTAGG_____		
GAM300 SORCS2	TGGGCACTG--GGTCCTGAG 4554	TCTG TAC	
	GGTACT GGTCTGAG		
	CCGTGA CCAGGACTC		
	_____ C_		
GAM300 SP110	TCTGGGT--TTG-GGTCCTGAG 4551	ACTTAC T	
	TCTGGGT GGTCCTGAG		
	AGACCCA CCAGGACTC		
	AAC_____ I		
GAM301 ANXA4	GACATTAATAATAATATGG 4567	TG C _ AA	
	ACATTAATAAAT TATGGG		

		TGTAATTGAT TTA ATACCT	
		___ A TT II	
GAM301 CDH5	CAATTACTACAATTATAGAAA	4564 ATTA	I
	ACTACAATTATGGGA		
	TGATGTTAATATCTT		
	TTAA	I	
GAM301 CDH5	CAATTACTACAATTATAGAAA	4564 TGACATTA	
	ACTACAATTATGGGAA		
	TGATGTTAATATCTTT		
	AA_____		
GAM301 CHD2	GACTTTGACTCTTCAATTATGGG	4566 _____ ATTA A	AAI
	TGAC CT CAATTATGGG		
	ACTG GA GTTAATACCC		
	TGAA A_____ A	GII	
GAM301 CHD2	GACTTTGACTCTTCAATTATGGG	4566 ACATTAA A	I
	CT CAATTATGG		
	GA GTTAATACC		
	AAACTGA A	I	
GAM301 DCX	ATTAACTACAAAATGTTNTGGGA	4561 TG	C _ G AA
	ACATTA ACTA AA TTAT GG		
	TGTAATTGAT TT AATG CC		
	___ T C A AI		
GAM301 ENC1	TGACATTAATCCACAATTA	4571 _	TGGGA
	TGACATTAA CTACAATTA		
	ACTGTAATT GGTGTTAAT		
	A IIIAA		
GAM301 ENC1	TGACATTAATCCACAATTA	4571 _	II
	TGACATTAA CTACAATT		
	ACTGTAATT GGTGTAA		
	A TI		
GAM301 FOXO1A	TGGCTTTA--TACAATTATAGCAA	4577 ACATTAAC	GI
	TACAATTATGG		
	ATGTTAATATC		
	ACCGAAAT	GI	
GAM301 FOXO1A	TGGCTTTA--TACAATTATAGCAA	4577 TGACATTAAC	G
	TACAATTATGG AA		
	ATGTTAATATC TT		
	ACCGAAAT_____ G		
GAM301 IRTA1	TGACATTAAC-ATAATTAT	4574 TAC	GGG
	TGACATTAAC AATTAT		

	ACTGTAATTG TTAATA			
	TA_ III			
GAM301 IRTA1	TGACATTAAC-ATAATTAT	4574	TAC	I
	TGACATTAAC AATTA			
	ACTGTAATTG TTAAT			
	TA_ A			
GAM301 LEP	GACAAGAACTACAATT-TGG	4568	G TT	ATI
	ACA AACTACAATT			
	TGT TTGATGTAA			
	_ TC ACC			
GAM301 LEP	GACAAGAACTACAATT-TGG	4568	TG TT	A GA
	ACA AACTACAATT TGG			
	TGT TTGATGTAA ACC			
	_ TC _ GI			
GAM301 LPIN2	ATCAACTACAATGTAATTGGA	4562	TA__	III
	ATTAACTACAAT TGGG			
	TAGTTGATGTAA ACCT			
	CATTA III			
GAM301 PCDHA9	ACAT--ACTACAATTCAGGAAA	4560	ATTA	A I
	ACTACAATT TGGGA			
	TGATGTAA GTCCT			
	TGTA _ I			
GAM301 PCDHA9	ACAT--ACTACAATTCAGGAAA	4560	TGACATTA	A
	ACTACAATT TGGGA			
	TGATGTAA GTCCT			
	TA_____ _			
GAM301 PPP3CA	ACATGTAACACTACAACTTAT	4558	_	TTAIII
	ACAT TAACTACAA			
	TGTA ATTGATGTT			
	C TGAATA			
GAM301 PTPRH	ATTTAATA-AATTATGGGA	4563	TGACATTA	ACTAC
	AATTATGGG			
	TTAATACCC			
	TTAT_____			
GAM301 SEL1L	TGACATTAAGAAC--TTATG	4575	CT AA	GG
	TGACATTAA AC TTATG			
	ACTGTAATT TG AATAC			
	CT _ II			
GAM301 SEL1L	TGACATTAAGAAC--TTATG	4575	CT AATT	AI
	TGACATTAA AC			

		ACTGTAATT TG		
		CT AATACI		
GAM301 SGK	ACAATACATACAATTATCAGGAA	4559 TGACATTA _ _ I		
	AC TACAATTAT GGGAA			
	TG ATGTTAATA TCCTT			
	TTA____ T G A			
GAM301 SGK	ACAATACATACAATTATCAGGAA	4559 CATTA _ _ I		
	AC TACAATTAT GGGA			
	TG ATGTTAATA TCCT			
	TTA__ T G I			
GAM301 SUFU	TGACATTAAAACTAATAT	4573 CT AATTAl		
	TGACATTAA AC			
	ACTGTAATT TG			
	TT ATTATAI			
GAM301 SUFU	TGACATTAAAACTAATAT	4573 CT AATTATGGGA		
	TGACATTAA AC			
	ACTGTAATT TG			
	TT ATTATAIIIA			
GAM301 TCF3	TGACACGTA-TACAATTAT	4572 TAAC GGG		
	TGACAT TACAATTAT			
	ACTGTG ATGTTAATA			
	CAT_ III			
GAM301 TCF3	TGACACGTA-TACAATTAT	4572 TAAC I		
	TGACAT TACAATTA			
	ACTGTG ATGTTAAT			
	CAT_ A			
GAM301 TFRC	CATGAAGAA-AATTATGGGAA	4565 ATTAAC TAC I		
	AATTATGGGA			
	TTAATACCCT			
	GTACTTCTT I			
GAM301 TFRC	CATGAAGAA-AATTATGGGAA	4565 TGACATTAAC TAC		
	AATTATGGGA			
	TTAATACCCT			
	CTTCTT_____			
GAM301 TRIM	GAAATTTATTTC AATTATGGG	4569 ACATTAAC TAC I		
	CAATTATGG			
	GTTAATACC			
	TTTAAATAAA I			
GAM301 TRIM	GAAATTTATTTC AATTATGGG	4569 TGACATTAAC TAC AA		
	CAATTATGGG			

		GTTAATACCC		
		TTTAAATAAA__ GI		
GAM301 TRIP15	TGACAGTATGCCACTATAATTATGGG 4570	TTA__ C	AAII	
	TGACA ACTA AATTATGGG			
	ACTGT TGAT TTAATACCC			
	CATACGG A IIIA			
GAM301 TRIP15	TGACAGTATGCCACTATAATTATGGG 4570	GACATTA C I		
	ACTA AATTATGG			
	TGAT TTAATACC			
	CATACGG A I			
GAM301 TUFT1	TGACATTAACAAGCCTAATGGGAA 4576	TACAATT I		
	TGACATTAAC ATGGGAA			
	ACTGTAATTG TACCCTT			
	TTCGGAT I			
GAM301 TUFT1	TGACATTAACAAGCCTAATGGGAA 4576	TACAATT I		
	GACATTAAC ATGGGA			
	CTGTAATTG TACCCT			
	TTCGGAT I			
GAM302 ATP5A1	ACAATGACAA-AACTGAACTGG 4580	TGACC _ C C		
	ATG CAG AACTGAACTGG			
	TAC GTT TTGACTTGACC			
	T__ T _ A			
GAM302 AVPR1A	TGTCCATGCAGCTCCT--ACTCGGC 4590	TGA AA AAC I		
	CCATGCAGC CTG TGGC			
	GGTACGTCG GAT GCCG			
	ACA AG GA_ I			
GAM302 EPHB6	TGACCATGCCGGCACCCTGATCT 4587	A_ A_ A GGCI		
	TGACCATGC GCA CTGA CT			
	ACTGGTACG CGT GACT GA			
	GC GG A IIIC			
GAM302 FUT3	TGGCC-TGAAGCAACTGAAGATCTGG 4589	A A C _ CII		
	TG CC TG AGCAACTGAA CTGG			
	AC GG AC TCGTTGACTT GACC			
	C _ T CTA III			
GAM302 GALNT1	TGACCCAAG-AGCAACTGAA 4586	ATGC CTGG		
	TGACC AGCAACTGAA			
	ACTGG TCGTTGACTT			
	GTTC IIIC			
GAM302 ITGA4	ACAACGCAACACACCTGAACTGG 4581	TGACC A_ CI		
	ATGCAGCA CTGAACTGG			

	TGCGTTGT GACTTGACC	
	T_____ GTG CA	
GAM302 KCNA7	CATGACCCAACTGAACTGGC 4583 TGACCATGCAG	
	CAACTGAACTGG	
	GTTGACTTGACC	
	TGG_____	
GAM302 LPTM5	TGACCACAGAGCAACTGAA 4588 C CTGG	
	TGACCATG AGCAACTGAA	
	ACTGGTGT TCGTTGACTT	
	C IIC	
GAM302 MAD2L2	CCATGCAGC-ACTGCCCTAGGC 4584 TGACCA A AA _	
	TGCAGCA CTG CT GGC	
	ACGTCGT GAC GA CCG	
	_____ _ GG T	
GAM302 NR1I2	CCCTACAG--ACTGAACTGG 4585 TGACCA CA	
	TGCAG ACTGAACTG	
	ATGTC TGACTTGAC	
	_____ _	
GAM302 PBP	CATGCAACA-CTGAACTGG 4582 TGACCATG A	
	CAGCA CTGAACTG	
	GTTGT GACTTGAC	
	_____ _	
GAM302 SLC6A5	TGACACAGGCAACAGACTGAACTGG 25 _ T _ CII	
	TGAC CA GCAGCA ACTGAACTGG	
	ACTG GT CGTTGT TGACTTGACC	
	T C C III	
GAM303 ALDH3B1	CGCAGGCC--GCAGGAGCAGC 4599 TGACGCC AGGG	
	GGCT AGGAGCAG	
	CCGG TCCTCGTC	
	T_____ CG_____	
GAM303 ALDH3B1	GACCCAGG--AGGGAGGAGGCAG 4605 TG G CT _ C	
	AC CCGG AGGGAGGAG CAG	
	TG GGTC TCCCTCCTC GTC	
	_____ C_ C C	
GAM303 ARHGAP6	CGGCGGC--GGCAGGAGCAGC 4600 TGACGC TA G	
	CGGC GG AGGAGCAG	
	GCCG CC TCCTCGTC	
	_____ _ G	
GAM303 CAPON	GCCGGCTA-GGAGG-GCGGC 4609 TGACGCCG GA A_	
	GCTAGG GG GCA	

	CGATCC CC CGT	
	_____ TC GC	
GAM303 DAZL	CCGGCTCCAGGAGGAGCAG 4594 TGACGCCGG G	
	CTAGG AGGAGCAG	
	GGTCC TCCTCGTC	
	A_____ _	
GAM303 EN2	CGCCG-CTGGGTGACAGGAGCAGC 4598 TGA C CTA G I	
	CGC GG GG AGGAGCAGC	
	GCG CC CT TCCTCGTCG	
	___ A CA_ G G	
GAM303 FLT1	CGCCGCTGCCGGGGAGGAGC 4595 TGA CG TA AG	
	CGC GC GGGAGGAGC	
	GCG CG CCCTCCTCG	
	___ A_ GC GC	
GAM303 FXVD6	ACGGGGGC-AGGGAGGAGCAG 4593 TGACGCC T	
	GGC AGGGAGGAGCAG	
	CCG TCCCTCCTCGTC	
	CCC_____ _	
GAM303 HMGA2	GACGCCGGC--GGGGCGAGC 4606 TG TA AG A	
	ACGCCGGC GGG GAGC	
	TGCGGCCG CCC CTCG	
	___ C_ G_ C	
GAM303 IHPK1	TGA-GCC--CT-GGGAGGAGCAGC 4616 C GG A	
	TGA GCC CT GGGAGGAGCAG	
	ACT CGG GA CCCTCCTCGTC	
	___ _ _	
GAM303 IL2RB	GAGGACGG-TAGGGAGGATTGCAG 4604 TGACGC C ___ CI	
	CGG TAGGGAGGA GCAG	
	GCC ATCCCTCCT CGTC	
	TCCT___ _ AA TI	
GAM303 IMMP2L	CGCCGGCTCGGCGGGGAGGAGC 4597 TGAC _ TA AGC	
	GC CGGC GGGAGGAGC	
	CG GCCG CCCTCCTCG	
	GC___ A C_ CCC	
GAM303 KCNMB4	TGCCTCGGGC--GGGAGGAGCCGC 4617 TGAC ___ TA A	
	GCC GGC GGGAGGAGC GC	
	CGG CCG CCCTCCTCG CG	
	A___ AGC ___ G	
GAM303 LASS2	TGACTTGCGGGTAGGGAGGA 4610 GC___ C GCAGC	
	TGAC CGG TAGGGAGGA	

	ACTG GCC ATCCCTCCT		
	AACC C IIICG		
GAM303 LENG4	GACGCCGGC--GGCATGAAGCAGC 4603 TG TA GA_		
	ACGCCGGC GG GGAGCAGC		
	II		
	TGCGGCCG CC CTTCGTCG		
	__ __ GTA		
GAM303 MBD3	GACAGCGGGCATGGGGAGGAGC 4601 TGAC C TA_ AGC		
	GC GGC GGGAGGAGC		
	II III		
	CG CCG CCCTCCTCG		
	TGT_ C TAC AII		
GAM303 PAX2	GCAGGCCAGG-AGGAGCAG 4607 TGACGCCG G		
	GCTAGG AGGAGCA		
	CGGTCC TCCTCGT		
	_____ -		
GAM303 PPFA3	TGACGCCGGGCAGCGCGTGGAGCAG 4611 C GGA_ CII		
	TGACGCCGG TAG GGAGCAG		
	III		
	ACTGCGGCC GTC CCTCGTC		
	C GCGCA III		
GAM303 PPT2	GCCAGATACGGAGGAGCAGC 4608 TGACGCCGGC G		
	TA GGAGGAGCAG		
	II		
	AT CCTCCTCGTC		
	CT_____ G		
GAM303 PYCR1	TGACGCCGGCCGCGCAGGA 4613 AGGG GCAG		
	TGACGCCGGCT AGGA		
	III		
	ACTGCGGCCGG TCCT		
	CGCG IIIC		
GAM303 RIMS1	CGGCGGCAGGAGGAGGAGCAGC 4596 TGACGC TA_		
	CGGC GGGAGGAGCAGC		
	III		
	GCCG TCCTCCTCGTCG		
	_____ TCC		
GAM303 SLC17A7	TGAGGCAGGACAGAGAGGAGCAG 4615 C C C CI		
	TGA GC GG TAGGGAGGAGCAG		
	III II II		
	ACT CG CC GTCTCTCCTCGTC		
	C T T II		
GAM303 SLC9A1	TGAGGCAG---AGGGAGGAGC 4614 TGACGCC T_ A		
	GGC AGGGAGGAGC		
	III		
	CCG TCCCTCCTCG		
	ACT_____ TC I		
GAM303 SLC9A1	GAAGCCTGGATCTAGGGAGGGGCAG 4602 TGAC _ _ A CII		
	GCC GG CTAGGGAGG GCAG		
	III II III		

	CGG CC GATCCCTCC CGTC	
	TT__ A TA C CII	
GAM303 WWP2	TGGCGCCTGCTAGGGAGGCAGGCAG 4612 A G A__ CII	
	TG CGCC GCTAGGGAGG GCAG	
	II IIII IIIIIIIII IIII	
	AC GCGG CGATCCCTCC CGTC	
	C A GTC III	
GAM304 ATP11A	GAC-TGGGTGTGAATCATGC-AGCAG 4623 ACG _ _ T I	
	TGGGTGTGA TC GC AGCA	
	IIIIIIII II II IIII	
	ACCCACACT AG CG TCGT	
	G__ T TA _ I	
GAM304 ATP11A	GAC-TGGGTGTGAATCATGC-AGCAG 4623 TG G _ _ T I	
	AC TGGGTGTGA TC GC AGCAG	
	II IIIIIIIII II II IIII	
	TG ACCCACACT AG CG TCGTC	
	_ _ T TA _ C	
GAM304 GARP	CGTGGGTGTGATCCCAACCAG 4621 G AI	
	GTGGGTGTGATC CTAGC	
	IIIIIIIIII IIII	
	CACCCACACTAG GGTTG	
	_ GT	
GAM304 GARP	CGTGGGTGTGATCCCAACCAG 4621 TGACGT G AG	
	GGGTGTGATC CTAGC	
	IIIIIIIIII IIII	
	CCCACACTAG GGTTG	
	_ _ GT	
GAM304 POLR2C	ACCTGGGAATTTGAAGCGCTAGCAG 4620 CGT TG__ T_ I	
	GGG TGA CGCTAGCA	
	III III IIIIIII	
	CCC ACT GCGATCGT	
	_ TTAA TC I	
GAM304 POLR2C	ACCTGGGAATTTGAAGCGCTAGCAG 4620 TGACG TG__ T_ II	
	TGGG TGA CGCTAGCAG	
	III III IIIIIII	
	ACCC ACT GCGATCGTC	
	G__ TTAA TC CG	
GAM304 PTBP1	GTGGGTGTG-TGGCT-GCAG 4624 ATC A I	
	GTGGGTGTG GCT GC	
	IIIIIIII III II	
	CACCCACAC CGA CG	
	AC_ _ T	
GAM304 SSRP1	TGA-GTGGGTGTGCGGAT-GCTCAGCAG4625 C ATC__ _ II	
	TGA GTGGGTGTG GCT AGCAG	
	III IIIIIII III IIII	
	ACT CACCCACAC CGA TCGTC	
	_ GCCTA G II	
GAM304 SSRP1	TGA-GTGGGTGTGCGGAT-GCTCAGCAG4625 GAC ATC__ _ I	
	GTGGGTGTG GCT AGCA	
	IIIIIIII III IIII	

		CACCCACAC CGA TCGT		
		___ GCCTA G I		
GAM304 THY1	GACGTGGGTAGATAATCGCATGCAG 4622 AC	___ TA I		
	GTGGGT GTGATCGC GCA			
	CACCCA TATTAGCG CGT			
	___ TC TA I			
GAM304 THY1	GACGTGGGTAGATAATCGCATGCAG 4622 TG	___ TA II		
	ACGTGGGT GTGATCGC GCAG			
	TGCACCCA TATTAGCG CGTC			
	___ TC TA GI			
GAM304 WHSC1	TGACGTGGGCGTGGTGTCTGCT 4626	A___ AGCAG		
	TGACGTGGGTGTG TCGCT			
	ACTGCACCCGCAC AGCGA			
	CAC IIIGA			
GAM304 WHSC1	TGACGTGGGCGTGGTGTCTGCT 4626	A___ III		
	TGACGTGGGTGTG TCGC			
	ACTGCACCCGCAC AGCG			
	CAC AII			
GAM305 ABCC5	TGATGACAGCAGTGACCACGC 4643 ___ GA	___ AGATGC		
	TGA AGCAGTGACC CGC			
	ACT TCGTCACTGG GCG			
	ACT G_ T IIICGT			
GAM305 ABCC5	TGATGACAGCAGTGACCACGC 4643 ___ GA	___ III		
	TGA AGCAGTGACC CG			
	ACT TCGTCACTGG GC			
	ACT G_ T GII			
GAM305 APCS	AGAAGCAGTGACCAG--GATG 4635	CGCAGAI		
	AGAAGCAGTGACC			
	TCTTCGTCACTGG			
	TCCTACI			
GAM305 APCS	AGAAGCAGTGACCAG--GATG 4635 TGAG	CGCA		
	AAGCAGTGACC GATG			
	TTCGTCACTGG CTAC			
	___ TC___			
GAM305 CARS	TGGAATCCCGGACCCGCAGCTGC 4646 A	GCAGT ATI		
	GAA GACCCGCAG			
	CTT CTGGGCGTC			
	C AGGGC GAI			
GAM305 CCKAR	GAAGC-GT--CTCGCAGATGC 4637 AAGC	ACC		
	AGTG CGCAGATG			

	TCGC GCGTCTAC		
	CT__ AGA		
GAM305 CCKAR	GAAGC-GT--CTCGCAGATGC	4637	TGAGAAGCA ACC
	GTG CGCAGAT		
	CGC GCGTCTA		
	_____ AGA		
GAM305 EIF2B1	AAGCAGTGAACCATGCAGA	4630	_ C_
	AAGCAGTGA CC GCAG		
	TTCGTCACT GG CGTC		
	T TA T		
GAM305 GAMT	TGGGCAGCAGTGACCCTCA	4645	AGA G GATG
	TG AGCAGTGACCC CA		
	AC TCGTCACTGGG GT		
	CCG A C		
GAM305 GAMT	TGGGCAGCAGTGACCCTCA	4645	AGA GC
	TG AGCAGTGACCC		
	AC TCGTCACTGGG		
	CCG AGTI		
GAM305 GNAI2	GAGAAGCAGGGGCCCCCTCCAGACGC	4640	TG TGA_ G_
	AGAAGCAG CCC CAGATGC		
	TCTTCGTC GGG GTCTGCG		
	___ CCCG AG TI		
GAM305 GNAI2	GAGAAGCAGGGGCCCCCTCCAGACGC	4640	AG TGA_ G_ I
	AAGCAG CCC CAGATG		
	TTCGTC GGG GTCTGC		
	___ CCCG AG I		
GAM305 KRTHA5	GAGAAGCAGCTCCTTACCC-CAGAT	4638	AGA G___ G I
	AGCAGT ACCC CAGA		
	TCGTCTG TGGG GTCT		
	___ AGGAA _ I		
GAM305 KRTHA5	GAGAAGCAGCTCCTTACCC-CAGAT	4638	TG G___ G GCI
	AGAAGCAGT ACCC CAGAT		
	TCTTCGTCG TGGG GTCTA		
	___ AGGAA _ A		
GAM305 MAPK8IP1	AGAAGC----CCCGCAGATG	4634	_ AGTGA
	GAAGC CCCGCAGA		
	CTTCG GGGCGTCT		
	T _____		
GAM305 MAPK8IP1	AGAAGC----CCCGCAGATG	4634	TGAG AGTGA
	AAGC CCCGCAGA		

TTCG GGGCGTCT

GAM305 MYO1E	AAGCAGTGACACTCCGTAGTTG 4629	___ C ATIII
	AAGCAGTGAC CCG AG	
	TTCGTCACTG GGC TC	
	TGA A AACII	
GAM305 NRG2	AGCAGAGCCACGCAGATGC 4636	TGA _ II
	AGCAG CC CGCAGATG	
	TCGTC GG GCGTCTAC	
	TC_ T GI	
GAM305 RBM3	AGAATGAAGGAAGCCGCAGATG 4633	___ CAGT C I
	GAAG GA CCGCAGAT	
	CTTC TT GCGTCTA	
	TTA C___ C I	
GAM305 RBM3	AGAATGAAGGAAGCCGCAGATG 4633	TGA CAGT C C
	GAAG GA CCGCAGATG	
	CTTC TT GCGTCTAC	
	TTA C___ C C	
GAM305 RERE	TGAGAAGCAGCCCCACACAGCATGC 4644	GA _ _ II
	TGAGAAGCAGT CC CGCAG ATGC	
	ACTCTTCGTCG GG GTGTC TACG	
	GG T G II	
GAM305 RERE	TGAGAAGCAGCCCCACACAGCATGC 4644	GA GA _ _ I
	GAAGCAGT CC CGCAG ATG	
	CTTCGTCG GG GTGTC TAC	
	GG T G I	
GAM305 RU2	AATCAG-GACCCGCAG-TGC 4632	AAG T ATI
	CAG GACCCGCAG	
	GTC CTGGGCGTC	
	TTA _ ACG	
GAM305 SLC25A1	GAGAAGCAGGGGGCTGCAG 4641	TGACCC II
	GAGAAGCAG GCA	
	CTCTTCGTC CGT	
	CCCCGA CI	
GAM305 SLC25A1	GAGAAGCAGGGGGCTGCAG 4641	TG TGACCC ATG
	AGAAGCAG GCAG	
	TCTTCGTC CGTC	
	CCCCGA GII	
GAM305 ST3GALVI	AAG-AGTGACCCGCCGAGGC 4631	A C A TI
	AG AGTGACCCGC GA	

	TC TCACTGGGCG CT		
	— — G CC		
GAM305 ST3GALVI	AAG-AGTGACCCGCCGAGGC	4631	TGAGAAGCA A T
	GTGACCCGC GA G		
	CACTGGGCG CT C		
	— — — — — G C		
GAM305 TACC1	GAGAAGCAGCCAAATGCAGAT	4642	GACCC I
	AGAAGCAGT GCAGA		
	TCTTCGTCG CGTCT		
	GTTTA I		
GAM305 TACC1	GAGAAGCAGCCAAATGCAGAT	4642 TG	GACCC GC
	AGAAGCAGT GCAGAT		
	TCTTCGTCG CGTCTA		
	— GTTTA GI		
GAM305 TREM2	GAGAAGCAGTGTTCAGGCAGA	4639 A	ACCC_ I
	GAAGCAGTG GCAG		
	CTTCGTCAC CGTC		
	— AAGTC I		
GAM305 TREM2	GAGAAGCAGTGTTCAGGCAGA	4639 TG	ACCC_ TGC
	AGAAGCAGTG GCAGA		
	TCTTCGTCAC CGTCT		
	— AAGTC CII		
GAM306 CYBB	AAAGGCTATA--TTCGCACAG	2739 TCAA	AGACT G
	AGGT TTCGCACAG		
	TCCG AAGCGTGTC		
	— — — — — ATAT_ G		
GAM306 MECP2	TCAAAGGTAGGATTTCTCCAGG	2743	AC GCA TI
	TCAAAGGTAG TTTC CAGG		
	AGTTTCCATC AAAG GTCC		
	CT GAG II		
GAM306 TCEA1	AAATGTAGACTTT-GCAACAG	2740 TCAAAG	C _ G
	GTAGACTTT GCA CAG		
	CATCTGAAA CGT GTC		
	TA_ _ _ T A		
GAM306 TEM8	TCAAAGGTATACATTTGGAAC	2742	G TTTCGCACAGGT
	TCAAAGGTA AC		
	AGTTTCCAT TG		
	A TAAACCTTGIII		
GAM306 TRIM14	CAAAGGTAGACTCAAGTCTCGCAGAG	2741 TC	_____ C GTII
	AAAGGTAGACTT TCGCA AG		

	TTTCCATCTGAG AGCGT TC		
	___ TTCAG C AIII		
GAM307 ADRA2A	TGGAAGGGGAATTAGCCAGG 4665	___	CGIII
	TGGAAGGGG TGGCC		
	ACCTTCCCC ATCGG		
	TTA TCCII		
GAM307 CSPG2	ACATAGGAAGCGTGGTGGCCCGG 4656	CCTT G__	I
	GGAAG GGTGGCCCG		
	CCTTC CCACCGGGC		
	AT__ GCA I		
GAM307 CSPG2	ACATAGGAAGCGTGGTGGCCCGG 4656	TGACCTT G__	TI
	GGAAG GGTGGCCCGG		
	CCTTC CCACCGGGCC		
	TAT___ GCA CC		
GAM307 DGKG	CTTGGTTGCGCGGTGGCCCGG 4661	AAGG__	III
	CTTGG GGTGGCCCG		
	GAACC CCACCGGGC		
	AACGCG CII		
GAM307 EGFL4	TGACCTTGCGAAGGGGCGGC 4662	___	CCGGT
	TGACCTTGG AAGGGGTGGC		
	ACTGGAACC TTCCCCGCCG		
	GC IIITG		
GAM307 EGFL4	TGACCTTGCGAAGGGGCGGC 4662	___	III
	TGACCTTGG AAGGGGTGG		
	ACTGGAACC TTCCCCGCC		
	GC GII		
GAM307 FLNB	TGAACT-GGAAGGGGCTG--CCGGT 4663	C T	G C
	TGA CT GGAAGGGGT GCC GGT		
	ACT GA CCTTCCCCG CGG CCA		
	T _ A _		
GAM307 FLNB	TGAACT-GGAAGGGGCTG--CCGGT 4663	_ C T	G C I
	GA CT GGAAGGGGT GCC GG		
	CT GA CCTTCCCCG CGG CC		
	A T _ A _ I		
GAM307 HOXD4	ACCTAGCACAGGGGTGGCC 4655	TGGA_	II
	ACCT AGGGGTGGC		
	TGGA TCCCCACCG		
	TCGTG GI		
GAM307 HOXD4	ACCTAGCACAGGGGTGGCC 4655	TGACCTTGGA	CGG
	AGGGGTGGCC		

		TCCCCACCGG			
		GATCGTG__ TT			
GAM307 INHBC		CCATGGAAGGGGGTAGCCAGGT	4657 CT	_ C	I
		TGGAAGGGG TGGCC GG			
		ACCTTCCCC ATCGG CC			
		T_ C T I			
GAM307 INHBC		CCATGGAAGGGGGTAGCCAGGT	4657 TGACCT	_ C	
		TGGAAGGGG TGGCC GGT			
		ACCTTCCCC ATCGG CCA			
		_____ C T			
GAM307 MAGEA12		CCTTGGAAGGTGCACTGGCCC	4658	GG__	
		CCTTGGAAGG TGGCC			
		GGAACCTTCC ACCGG			
		ACGTG GII			
GAM307 MAGEA12		CCTTGGAAGGTGCACTGGCCC	4658 TGACCT	GG__	T
		TGGAAGG TGGCCCGG			
		ACCTTCC ACCGGGTC			
		_____ ACGTG T			
GAM307 MPP2		TGAC-TGGGGAGGGGTGGC	4664 CTT A	CCG	
		TGAC GG AGGGGTGGC			
		ACTG CC TCCCCACCG			
		AC_ C			
GAM307 MPP2		TGAC-TGGGGAGGGGTGGC	4664 CTT A	I	
		TGAC GG AGGGGTGG			
		ACTG CC TCCCCACC			
		AC_ C G			
GAM307 RAP1GA1		ACCTTCAGAGGGGGTGGCCCCG	4654 CC TG A	I	
		T GA GGGGTGGCCCG			
		A CT CCCCACCGGGC			
		GA GT C I			
GAM307 SACM2L		TGGAAGGGGTACCCAGGT	4666	G	II
		TGGAAGGGGTG CCCGG			
		ACCTTCCCCAT GGGTC			
		G CA			
GAM307 SLC22A12		CCCTGGAAGGGG-GGCTGGGT	4660 _	T CC	I
		CTTGGAAGGGG GGC GG			
		GGACCTTCCCC CCG CC			
		G _ A_ C			
GAM307 SLC22A12		CCCTGGAAGGGG-GGCTGGGT	4660 TGACCT	T CC	
		TGGAAGGGG GGC GG			

	ACCTTCCCC CCG CC		
	_____ _ AC		
GAM307 WNT3A	CCGTGGAAGGGGCCTTGCCCTGGT	4659 CTT	G__ _ I
	GGAAGGGGT GCCC GG		
	CCTTCCCCG CGGG CC		
	_____ GAA A I		
GAM307 WNT3A	CCGTGGAAGGGGCCTTGCCCTGGT	4659 TGACCT	G__ _ I
	TGGAAGGGGT GCCC GGT		
	ACCTTCCCCG CGGG CCA		
	_____ GAA A G		
GAM308 ADCY8	AGCGGTGG-G-AGCTTAGTG	4672 TA TC AGC	
	GC TGG AGCTTAGTGT		
	CG ACC TCGAATCACG		
	___ CC C__		
GAM308 ATF5	GCTCTGGAGGATGCTCAG-GTG	4675 TAGC	CA_ T T
	TCTGGAG GCTTAG GTG		
	AGACCTC CGAGTC CAC		
	_____ CTA _ C		
GAM308 CYP4A11	AGCTCTGGAAGTGCAGATTA	4669 TA	___ C GTGTG
	GCTCTGGA GCAG TTA		
	CGAGACCT CGTC AAT		
	_____ TCA T AIIIT		
GAM308 DAAM2	AGCTCTGGAACAACGTATTTGTGT	4671 TA	TTAG_ I
	GCTCTGGAGCAGC TGTGT		
	CGAGACCTTGTG ACACA		
	_____ CATAA G		
GAM308 GCK	AGCTGTGG-G--GCTTAGTGT	4673 TA C AGCA	
	GCT TGG GCTTAGTGT		
	CGA ACC CGAATCACA		
	___ C C__		
GAM308 JUN	TAGCTCTGG-GCAG-TTAG	4677	A C TGT
	TAGCTCTGG GCAG TTAG		
	ATCGAGACC CGTC AATC		
	_____ _ III		
GAM308 LANGERIN	GCTCTGGAGTAACTTTGATGTG	4676 TAGC	C A_ T
	TCTGGAG AGCTT GTGTG		
	AGACCTC TTGAA TACAC		
	_____ A AC T		
GAM308 MASP1	TCTGGAGCAGC-AGGTGTG	4679 TAGCTCTG	TTA
	GAGCAGC GTGT		

	CTCGTCG CACA		
	_____ TC_		
GAM308 NDRG2	TAGCTCTGGGGGAGGTGAG	4678	AGCAGCTTAGTGTG
	TAGCTCTGG		
	ATCGAGACC		
	CCCTCCACTCIIIT		
GAM308 SALL2	AGCTCTGGAGCCTACAGCTT	4670 TA	_____ AGTGTG
	GCTCTGGAGC AGCTT		
	CGAGACCTCG TCGAA		
	_____ GATG CIIITG		
GAM308 SEPN1	GCTCTGGAGAAGGCTGTGGTGT	4674 TAGC	CA_ TA_ GT
	TCTGGAG GCT GTGT		
	AGACCTC CGA CACA		
	_____ TTC CAC AA		
GAM309 ARNT2	TGCAGGGTTTCAACCACCTG	4694	C G CAC
	TGCAGGGTTTC AGCT ACC		
	ACGTCCCAAAG TTGG TGG		
	_____ _ _ ACI		
GAM309 BCRP2	TGCCAGGTTTCCA---GACCCACA	4700 A	GCT
	TGC GGGTTTCCA GACCCACA		
	ACG TCCAAAGGT CTGGGTGT		
	G _____		
GAM309 DDX11	GCAGAAGATCCCAGCTGA-CCACA	4689 TG	T_ _ CAI
	CAGGG TTCCAGCTGACC CA		
	GTCTT AGGGTCGACTGG GT		
	_____ CT T CII		
GAM309 EGFL3	CAGGCAGCTTCCAGCTGATCCCA	4683 T GG	_ CAI
	GCA GTTTCCAGCTGA CCA		
	CGT CGAAGGTCGACT GGGT		
	C _____ A CCI		
GAM309 EPS8	TGCAGACTTTCCAGCTGACTCA	4697 G	C CA
	TGCAGG TTTCCAGCTGAC CA		
	ACGTCT AAAGGTCGACTG GT		
	G A II		
GAM309 FMN2	TGCA---TTACGAGCTGACCCA	4696	GGGTTTCC C
	TGCA AGCTGACCCA		
	ACGT TCGACTGGGT		
	AATGC_____ I		
GAM309 GNAO1	GCAGGGTTTGCAG-TGGCC	4690 TG	C C A CA
	CAGGGTTT CAG TG CC		

	GTCCCAA GTC AC GG	
	___ C _ C AI	
GAM309 INMT	GCAGTGGTATGTTCCAGCTGACTCCA 4688 TG _ _ _ CAII	
	CAG GGT TTCCAGCTGAC CCA	
	GTC CCA AAGGTCGACTG GGT	
	___ A TAC A T	
GAM309 MAPT	AGGGTGGCACA-CTGACCCACA 4682 TGCAG TTCCA	
	GGT GCTGACCCACA	
	CCG TGA CTGGGTGT	
	CA___ TG___	
GAM309 NHP2L1	CAGAGAGTACATCTGACCCACA 4687 TGC TTC G	
	AGGGT CA CTGACCCACA	
	TCTCA GT GACTGGGTGT	
	C___ T___ A	
GAM309 PIM1	GCAGGGTT----CTGACCCAC 4691 TG TCCAG	
	CAGGGTT CTGACCCA	
	GTCCCAA GACTGGGT	
	___ _	
GAM309 PPAT	CAGGGTT---ATCTGACCCAC 4686 TGCA TCCAG	
	GGGTT CTGACCCA	
	CCCAA GACTGGGT	
	___ TA___	
GAM309 PVT1	TGCAGGGTT--CAGGCCTGACGCA 4695 CCAG C CA	
	TGCAGGGTTT CTGAC CA	
	ACGTCCCAAG GACTG GT	
	TCCG C	
GAM309 PYCS	TGCAGCTTGGGTTCCAGCTG 4693 ___ T ACCCAC	
	TGCAG GG TTCCAGCTG	
	ACGTC CC AAGGTCGAC	
	GAA C ACA	
GAM309 RAMP3	CAGCCTTTCCAGCTGTCTTCCAC 4685 TGCAGGG A___ AI	
	TTTCCAGCTG CCCAC	
	AAAGGTCGAC GGGTG	
	CGG___ AGAA GT	
GAM309 RPL10	TGCAGGGTTT---GCTGCCTCA 4698 CCA A _ C	
	TGCAGGGTTT GCTG CC CA	
	ACGTCCCAAA CGAC GG GT	
	___ _ A I	
GAM309 SIX2	TGCAGC--TCCA-CTGACCCACA 4699 GG G	
	TGCA GTTCCA CTGACCCACA	

ACGT CGAGGGT GACTGGGTGT

GAM309 SLC14A1 CAGGGTTTCACCATGCTG-CCCA 4684 TGCA _ _ A CA
GGGTTT CCA GCTG CCCA
||||| ||| ||| |||
CCCAAA GGT CGAC GGGT
_ _ GT A _ CC
GAM309 SLC7A8 GGGTCTCTCCAGCTGACCC 4692 TGCAGGG AC
TTTCCAGCTGACCC
|||||||
AGAGGTCGACTGGG
G _ _ GA
GAM310 BAALC CTAATAGGA-TAGTAAGGA 4708 C _ II
CTAATAGGA TAG AAGG
||||||| ||| |||
GATTATCCT ATC TTCC
_ A TI
GAM310 DNC11 TAATAGGACTATGCCAGGAG 4718 GA_ III
TAATAGGACTA AGGA
||||||| |||
ATTATCCTGAT TCCT
ACGG CII
GAM310 EIF2AK3 GCTACAAATAGGACTATAA 4711 A T GAI
GC AC AATAGGACTA
|| || |||||
CG TG TTATCCTGAT
A T ATTI
GAM310 GJB5 AATAGGACTCAGCAAGCAG 4705 _ _ GAI
AATAGGACT AG AAG
||||||| |||
TTATCCTGA TC TTC
G G GTCII
GAM310 HLF GCAACTTATAAAGGACTAGA 4710 AAT_ III
GCAACT AGGACTAG
||||| |||||
CGTTGA TCCTGATC
ATATT TII
GAM310 HSPA9B TACTAGGCTAACTAGAAGGA 4717 TAA _ III
TAGG ACTAGAAGG
||| |||||
ATCC TGATCTTCC
ATG GAT TII
GAM310 ISLR CTAGAAGAGATTAGAAGGAG 4707 AT _ C II
CTA AG GA TAGAAGGA
||| ||| |||||
GAT TC CT ATCTTCCT
CT T A CI
GAM310 ITM2B GGCAACTAACA-ACTACAA 4715 AG GI
GGCAACTAAT GACTA
||||||| |||||

	CCGTTGATTG TTGAT			
	___ GT			
GAM310 MIPOL1	GGCATC--ACAAGA-TAGAAGGAG	4716	ACTA C I	
	GGCA ATAGGA TAGAAGG			
	CCGT TGTTCT ATCTTCC			
	AG___ _ T			
GAM310 MTMR2	GCAAGTATGTTAAGACTAGAAG	4709	CAACTAA I	
	TAGGACTAGAA			
	ATTCTGATCTT			
	TCATACA I			
GAM310 OA1	GGCAACTA--AGG-CTAGA	4714	AT A	
	GGCAACTA AGG CTAG			
	CCGTTGAT TCC GATC			
	___ _			
GAM310 OGT	GGCTACAGAATAGGACT-GAGGGAG	4713	A T_ A A I	
	GC AC AATAGGACT GA GGA			
	CG TG TTATCCTGA CT CCT			
	A TC _ C I			
GAM310 SLC21A3	AAGTATTAG---TAGAAGGAG	4704	ACTAA_ GAC	
	TAG TAGAAGGA			
	ATC ATCTTCCT			
	TTCATA ___			
GAM310 TPT	AATTTATAGGACTAGAATGA	4703	ACTA GGI	
	ATAGGACTAGAA			
	TATCCTGATCTT			
	TAAA ACI			
GAM310 VAPB	CAACTAGTA---CTAGAAGGA	4706	AACTAA G	
	TAG ACTAGAAGG			
	ATC TGATCTTCC			
	GTTG_ A			
GAM310 XRCC5	GGCAGAGTAATGTGGTAACTAGAAGG	4712	_____ C AT ACTAGI	
	GG AACTA AGG			
	CC TTGAT TCC			
	TTACA A CT GAT			
GAM311 ADRBK1	CAGAGCCCAGGGTGGCACAGC	4728	A TG T_ I	
	GAGCT G TGGCACAG			
	CTCGG C ACCGTGTC			
	_ GT CC I			
GAM311 ADRBK1	CAGAGCCCAGGGTGGCACAGC	4728	TC TG T_ CGG	
	AGAGCT G TGGCACAGC			

	TCTCGG C ACCGTGTCG	
	___ GT CC AII	
GAM311 APS	AGAGCTTGGCGTGTCCCACCCGG 4723 G	_ GCA G I
	AGCTTGGT TG CA CCG	
	II II III	
	TCGAACCG AC GT GGC	
	_ C AGG G I	
GAM311 APS	AGAGCTTGGCGTGTCCCACCCGG 4723 TCAG	_ GCA G I
	AGCTTGGT TG CA CCGG	
	II II III	
	TCGAACCG AC GT GGCC	
	___ C AGG G C	
GAM311 CACNB1	CAGTCCTTG-TTGGCACACTCGG 4733 AG	_ G GC I
	AG CTT GTTGGCACA CG	
	II III II	
	TC GGA CAACCGTGT GC	
	G_ A A GA I	
GAM311 CACNB1	CAGTCCTTG-TTGGCACACTCGG 4733 TCAG	_ G GC
	AG CTT GTTGGCACA CGG	
	II III III	
	TC GGA CAACCGTGT GCC	
	___ A A GA	
GAM311 CAPNS1	AGTGCTAGGCTTGGCACAG 4721 AGA T	_ II
	GCT GGTT GGCACA	
	III	
	CGA CCGA CCGTGT	
	TCA T A CI	
GAM311 CAPNS1	AGTGCTAGGCTTGGCACAG 4721 TCAGA T	_ CCG
	GCT GGTT GGCACAG	
	III	
	CGA CCGA CCGTGTC	
	A___ T A CAI	
GAM311 COL17A1	GAGCT--GATGGCACAGCC 4734 T T	I
	GAGCT GGT GGCACAGC	
	III	
	CTCGA CTA CCGTGTCTG	
	_ _ G	
GAM311 COL17A1	GAGCT--GATGGCACAGCC 4734 TCAGAGCT T	
	TGGT GGCACAGCC	
	ACTA CCGTGTCTGG	
	G_____ _	
GAM311 ETV3	AGAGCTTGGTAGTTTCACAG 4725 TGG_	III
	AGAGCTTGGT CACA	
	III	
	TCTCGAACCA GTGT	
	TCAAA CII	
GAM311 ETV3	AGAGCTTGGTAGTTTCACAG 4725 TCAG TGG_	CCG
	AGCTTGGT CACAG	

	TCGAACCA GTGTC	
	_____ TCAA TTI	
GAM311 EXTL2	AGAGCT-GGTTGGCAGGGCC 4726 _ T CA I	
	GAGCT GGTTGGCA GC	
	CTCGA CCAACCGT CG	
	T _ CC I	
GAM311 EXTL2	AGAGCT-GGTTGGCAGGGCC 4726 TCAG T CA	
	AGCT GGTTGGCA GCCG	
	TCGA CCAACCGT CGGT	
	_____ CC	
GAM311 FAT	AGACGTTGGGAAATGGCACAGCCG 4724 GAGC T____ I	
	TTGG TGGCACAGCC	
	AACC ACCGTGTCGG	
	C____ CTTT I	
GAM311 FAT	AGACGTTGGGAAATGGCACAGCCG 4724 TCAGA _ T____ I	
	GC TTGG TGGCACAGCCGG	
	TG AACC ACCGTGTCGGCT	
	_____ C CTTT A	
GAM311 FCN3	CAGAGGT-GGTTGGCAAAG 4729 CT CAI	
	CAGAG TGGTTGGCA	
	GTCTC ACCAACCGT	
	C_ TTC	
GAM311 FCN3	CAGAGGT-GGTTGGCAAAG 4729 TC CT C CC	
	AGAG TGGTTGGCA AG	
	TCTC ACCAACCGT TC	
	_ C_ T CI	
GAM311 IL2RB	CAGAGCTTGG-TGCCAAACCC 4730 _ T G CAGCI	
	AGAGCTTGGT G CA	
	TCTCGAACCA C GT	
	G _ G TTGGI	
GAM311 IL2RB	CAGAGCTTGG-TGCCAAACCC 4730 TC T G C G	
	AGAGCTTGGT G CA AGCC	
	TCTCGAACCA C GT TTGG	
	_____ G _ G	
GAM311 KCNAB2	GAGCTTGGTAGGCATGGCC 4735 T CA II	
	GAGCTTGGT GGCA GC	
	CTCGAACCA CCGT CG	
	T AC GI	
GAM311 KCNAB2	GAGCTTGGTAGGCATGGCC 4735 TCAGAG T CA G	
	CTTGGT GGCA GCC	

	GAACCA CCGT CGG	
	_____ T AC G	
GAM311 MASP1	AGTGCTGGGATTGGCACAG 4722 AGA T _ II	
	GCT GG TTGGCACACA	
	CGA CC AACCGTGT	
	TCA C T CI	
GAM311 MASP1	AGTGCTGGGATTGGCACAG 4722 TCAGA T _ CCG	
	GCT GG TTGGCACAG	
	CGA CC AACCGTGTC	
	A_____ C T TCI	
GAM311 MVK	CAGAGCTTGGCTGGCATCGCC 4731 CA I	
	AGAGCTTGGTTGGCA GC	
	TCTCGAACCGACCGT CG	
	AG I	
GAM311 MVK	CAGAGCTTGGCTGGCATCGCC 4731 TC CA G	
	AGAGCTTGGTTGGCA GCCG	
	TCTCGAACCGACCGT CGGT	
	_____ AG I	
GAM311 OGDH	TCTGACCTGCTTTGGCACAGC 4737 CA G G_ I	
	GA CTTG TTGGCACAG	
	CT GGAC AACCGTGTC	
	GA _ GA I	
GAM311 OGDH	TCTGACCTGCTTTGGCACAGC 4737 TCA G G_ CCG	
	GA CTTG TTGGCACAGC	
	CT GGAC AACCGTGTCG	
	AGA _ GA III	
GAM311 PMX1	CAGGGCTATTGTTGGCACACA 4727 A TG_ II	
	CAG GCT GTTGGCAC	
	GTC CGA CAACCGTG	
	C TAA TI	
GAM311 PMX1	CAGGGCTATTGTTGGCACACA 4727 TC A TG_ GCCG	
	AG GCT GTTGGCACACA	
	TC CGA CAACCGTGT	
	_____ C TAA AIII	
GAM311 RNF14	TCAGAGCTT--TGGGCACA 4736 GGTT GCC	
	TCAGAGCTT GGCACA	
	AGTCTCGAA CCGTGT	
	AC_____ III	
GAM311 RNF14	TCAGAGCTT--TGGGCACA 4736 GGTT I	
	TCAGAGCTT GGCAC	

	AGTCTCGAA CCGTG		
	AC__ T		
GAM311 SUV39H1	CAGAGCTTGGT---CCCAGCC 4732	__ ACAI	
	CAGAGCTTGGTT GGC		
	GTCTCGAACCAG TCG		
	GG GIII		
GAM311 SUV39H1	CAGAGCTTGGT---CCCAGCC 4732 TC	GGCA	
	AGAGCTTGGTT CAGCC		
	TCTCGAACCAG GTCGG		
	__ G__		
GAM312 ABCA2	CTCCCTGGCCCAGCTCTGG 4754 GCC	II	
	CTCC GCCCAGCTCTG		
	GAGG CGGGTCGAGAC		
	GAC CI		
GAM312 ABCA2	CTCCCTGGCCCAGCTCTGG 4754 GAGCT GCC	T	
	CC GCCCAGCTCTGG		
	GG CGGGTCGAGACC		
	__ AC_ C		
GAM312 ABCA2	AGCTCCGCCCACAGCCC-GCTCT 4743 GA	__ A GGTG	
	GCTCCGCC GCCC GCTCT		
	CGAGGCGG CGGG CGAGA		
	__ GTGT _ GIII		
GAM312 ABCA2	AGCTCCGCCCACAGCCC-GCTCT 4743	__ A III	
	AGCTCCGCC GCCC GCTC		
	TCGAGGCGG CGGG CGAG		
	GTGT _ AII		
GAM312 ABCA2	GAG-TCCCTGGCCCAGCTCTGG 4761 CT GCC	TG	
	GAG CC GCCCAGCTCTGG		
	CTC GG CGGGTCGAGACC		
	AG AC_ II		
GAM312 ABCA2	GAG-TCCCTGGCCCAGCTCTGG 4761 _ CT GCC	I	
	AG CC GCCCAGCTCTG		
	TC GG CGGGTCGAGAC		
	C AG AC_ I		
GAM312 ACADVL	GAGCTCTGAC--CCAGCTCTGG 4763 CGCC	T	
	GAGCTC GCCCAGCTCTGG		
	CTCGAG TGGGTCGAGACC		
	AC_ I		
GAM312 ACADVL	GAGCTCTGAC--CCAGCTCTGG 4763 CGCC	I	
	GAGCTC GCCCAGCTCT		

	CTCGAG TGGGTCGAGA		
	AC__ C		
GAM312 ADA	CTCCGCCGCC--GCTC-GGTG 4755	CA T I	
	CTCCGCCGCC GCTC GG		
	GAGGCGGCGG CGAG CC		
	__ _ A		
GAM312 ADA	CTCCGCCGCC--GCTC-GGTG 4755 GAGCTC	CA T	
	CGCCGCC GCTC GG		
	GCGGCGG CGAG CC		
	_____ _ _		
GAM312 ALDH1B1	TCCGGCCCTCCCAGCTCTG 4770 _ G_ III		
	TCCG CC CCCAGCTCT		
	AGGC GG GGGTCGAGA		
	C GA CII		
GAM312 ALDH1B1	TCCGGCCCTCCCAGCTCTG 4770 GAGCTCC G_ GT		
	GCC CCCAGCTCTG		
	CGG GGGTCGAGAC		
	_____ GA AG		
GAM312 APOL1	CTCAGCCGCCCAGTTAGCTGG 4752 C CT_ III		
	CTC GCCGCCCAG CTG		
	GAG CGGCGGGTC GAC		
	T AATC CII		
GAM312 APOL1	CTCAGCCGCCCAGTTAGCTGG 4752 GAGCTCC CT_ TG		
	GCCGCCCAG CTGG		
	CGGCGGGTC GACC		
	T_____ AATC TT		
GAM312 ARL2	AGCTCCTCCCCGCCCAGCCCT 4744 G_ III		
	AGCTCC CCGCCCAGCTC		
	TCGAGG GGCGGGTCGGG		
	AGG AII		
GAM312 ARL2	AGCTCCTCCCCGCCCAGCCCT 4744 GAG_ G GGTG		
	CTCC CCGCCCAGCTCT		
	GAGG GGCGGGTCGGGA		
	CGAG _ GIII		
GAM312 CDR2	GCGCCGCCGCCCAGACTCCGCTG 4767 GAGCT _ G I		
	CCGCCGCCCAG CTCTG TG		
	GGCGGCGGGTC GAGGC AC		
	C_____ T G G		
GAM312 CDR2	GCGCCGCCGCCCAGACTCCGCTG 4767 T _ GTI		
	CCGCCGCCCAG CTCTG		

	GGCGGCGGGTC GAGGC			
	C T GII			
GAM312 CEP2	GAGCTCCGCCACCAGCAGC 4759	___	TCTGGT	
	GAGCTCCGCCGCC CAGC			
	CTCGAGGCGGTGG GTCG			
	TC IIIGTG			
GAM312 CEP2	GAGCTCCGCCACCAGCAGC 4759	___	III	
	GAGCTCCGCCGCC CAG			
	CTCGAGGCGGTGG GTC			
	TC GII			
GAM312 CNTNAP2	GCTTCGCCTGTGCCCAGCTCT 4766	C ___	III	
	GCT CGCC GCCCAGCTC			
	CGA GCGG CGGGTCGAG			
	A ACA AII			
GAM312 CNTNAP2	GCTTCGCCTGTGCCCAGCTCT 4766	GAGCTC ___	GGTG	
	CGCC GCCCAGCTCT			
	GCGG CGGGTCGAGA			
	AA___ ACA GTII			
GAM312 ESRRA	AGCTCCGC--CCCAGCCCT 4747	GC I		
	AGCTCCGCC CCAGCTC			
	TCGAGGCGG GGTCGGG			
	___ A			
GAM312 ESRRA	AGCTCCGC--CCCAGCCCT 4747	GA GC GG		
	GCTCCGCC CCAGCTCT			
	CGAGGCGG GGTCGGGA			
	___ ___ AI			
GAM312 GAB2	GCTTGGTCGCCCAGCT-TGGT 4769	CTCCGC_ C I		
	CGCCCAGCT TGG			
	GCGGGTCGA ACC			
	CGAACCA _ I			
GAM312 GAB2	GCTTGGTCGCCCAGCT-TGGT 4769	GAGCTCCGC C		
	CGCCCAGCT TGGT			
	GCGGGTCGA ACCA			
	AACCA___ _			
GAM312 GNA11	CTCCAGCCGCCAGCCACGTG 4750	GAGCTCC TG		
	GCCGCCAGCTC GTG			
	CGGCGGGTCGGG CAC			
	GT___ TG			
GAM312 GNA11	CTCCAGCCGCCAGCCACGTG 4750	T _ _ GTI		
	CC GCCGCCAGCTC TG			

	GG CGGCGGGTCGGG GC			
	_ T T AII			
GAM312 IKBKG	GAGCT--GCCACCCAGCTCTG 4760 CC GT			
	GAGCT GCCGCCCAGCTCTG			
	CTCGA CGGTGGGTCGAGAC			
	— II			
GAM312 IKBKG	GAGCT--GCCACCCAGCTCTG 4760 CC I			
	GAGCT GCCGCCCAGCTC			
	CTCGA CGGTGGGTCGAG			
	— A			
GAM312 KCNJ6	CTCCGCCCCGCCAGCCTCT 4751 _ CIII			
	CTCCGCC GCCCAGCT			
	GAGGCGG CGGGTCGG			
	G AGAI			
GAM312 KCNJ6	CTCCGCCCCGCCAGCCTCT 4751 GAGCTC _ _ GGT			
	CGCC GCCCAGC TCT			
	GCGG CGGGTCG AGA			
	— G G GGT			
GAM312 LENG4	CTCC-CTGCACAGCTCTGG 4753 GCC C I			
	CTCC GC CAGCTCTG			
	GAGG CG GTCGAGAC			
	GA_ T C			
GAM312 LENG4	CTCC-CTGCACAGCTCTGG 4753 GAGCTCCG _ C			
	CC GC CAGCTCTGG			
	GG CG GTCGAGACC			
	— A T			
GAM312 LENG4	GCTCCCAGCCGCCAGGGCTG 4765 _ CT III			
	GCTCC GCCGCCCAG CT			
	CGAGG CGGCGGGTC GA			
	GT CC CII			
GAM312 LENG4	GCTCCCAGCCGCCAGGGCTG 4765 GAG C CT GTG			
	CTC GCCGCCCAG CTG			
	GGG CGGCGGGTC GAC			
	A_ T CC GGI			
GAM312 LY94	GAGCTCACGCCGCCAGGCTC 4756 _ _ TGGTG			
	GAGCTC CGCCGCCAG CTC			
	CTCGAG GCGGCGGGTC GAG			
	T C IIIGT			
GAM312 LY94	GAGCTCACGCCGCCAGGCTC 4756 _ _ III			
	GAGCTC CGCCGCCAG CT			

	CTCGAG GCGGCGGGTC GA			
	T C GII			
GAM312 MAG	AGCTCAG--GTCCAGCTCTGG 4749 _ CGCCGC I			
	GCTC CCAGCTCTG			
	CGAG GGTCTGAGAC			
	T TCCA_ I			
GAM312 MAG	AGCTCAG--GTCCAGCTCTGG 4749 GA CGCCGC T			
	GCTC CCAGCTCTGG			
	CGAG GGTCTGAGACC			
	_ TCCA_ C			
GAM312 MFNG	GAGC-CC-CAGCCCAGCTCAAGTG 4764 CC T			
	GAGCTCCG GCCCAGCTC GGTG			
	CTCGGGGT CGGGTCGAG TCAC			
	_ T			
GAM312 MFNG	GAGC-CC-CAGCCCAGCTCAAGTG 4764 CC T I			
	GAGCTCCG GCCCAGCTC GG			
	CTCGGGGT CGGGTCGAG TC			
	_ T A			
GAM312 PIG8	AGCTCCGCCGCCGCCGGCTCCGG 4746 G CA_ I			
	CTCCGCCGCC GCTCTG			
	GAGGCGGCCG CGAGGC			
	_ CGC I			
GAM312 PIG8	AGCTCCGCCGCCGCCGGCTCCGG 4746 GA CA_ G			
	GCTCCGCCGCC GCTCTGGT			
	CGAGGCGGCCG CGAGGCCG			
	_ CGC I			
GAM312 PSMB2	GAGCCACCACACCAGCTCTGG 4762 _ C TG			
	GAGCT CCGC GCCCAGCTCTGG			
	CTCGG GGTG TGGGTCGAGACC			
	T _ II			
GAM312 PSMB2	GAGCCACCACACCAGCTCTGG 4762 _ C I			
	AGCT CCGC GCCCAGCTCTG			
	TCGG GGTG TGGGTCGAGAC			
	T _ I			
GAM312 PTBP1	GCGCCGCCGCC--CTCGGGT 4768 T AG TGI			
	GC CCGCCGCC CTC			
	CG GGCGGCGGG GAG			
	C _ CCC			
GAM312 PTBP1	GCGCCGCCGCC--CTCGGGT 4768 GAGCT AG T			
	CCGCCGCC CTC GGT			

	GGCGGCGGG GAG CCA	
	C_____ C	
GAM312 PTPN1	AGCTACCGCCGCCCTAGCCGCTGCTG 4740 CT	_ _ GTI
	CCGCCGCC AGCT CTG	
	GGCGGCGGG TCGG GAC	
	T_ A C GII	
GAM312 PTPN1	AGCTACCGCCGCCCTAGCCGCTGCTG 4740 GA	_ _ _ G II
	GCT CGGCCGCC AGCT CTG TG	
	CGA GGCGGCGGG TCGG GAC AC	
	_ T A C G GI	
GAM312 RABGGTA	AGCTCCGCC-CACAGCTGTG 4748 _	GCC CTI
	GCTCCGCC CAGCT	
	CGAGGCGG GTCGA	
	T GT_ CAI	
GAM312 RABGGTA	AGCTCCGCC-CACAGCTGTG 4748 GA	GCC C GT
	GCTCCGCC CAGCT TG	
	CGAGGCGG GTCGA AC	
	_ GT_ C AI	
GAM312 RFP	GAGCTCCGCACTGAGCCCAACTCT 4758	C_____ GGTGI
	GAGCTCCGC GCCCAGCTCT	
	CTCGAGGCG CGGGTTGAGA	
	TGACT IIIGT	
GAM312 RFP	GAGCTCCGCACTGAGCCCAACTCT 4758 AGCT	C_____ I
	CCGC GCCCAGCTC	
	GGCG CGGGTTGAG	
	_____ TGACT I	
GAM312 SLC9A1	GAGCCCCCAGCAGCCCCTGCTCTGGTG4757	_ C A_ III
	GAGCTCC GC GCCC GCTCTGGTG	
	CTCGGGG CG CGGG CGAGACCAC	
	GT T GA III	
GAM312 SLC9A1	GAGCCCCCAGCAGCCCCTGCTCTGGTG4757 AG	_ C A_ I
	CTCC GC GCCC GCTCTGGT	
	GGGG CG CGGG CGAGACCA	
	_____ T T GA I	
GAM312 SMARCD2	AGCTCCCCAGAGCCAGCTCTG 4745 G G C_	I
	CTCC CCG CCAGCTCT	
	GAGG GGT GGTCGAGA	
	_ _ CTC I	
GAM312 SMARCD2	AGCTCCCCAGAGCCAGCTCTG 4745 GA	G C_ TG
	GCTCC CCG CCAGCTCTGG	

	CGAGG GGT GGTCTGAGACT	
	___ _ CTC II	
GAM312 TCF20	AGCTCACACTGCC-AGCTCTGG 4741 _ C C I	
	GCTC CGC GCC AGCTCTG	
	CGAG GTG CGG TCGAGAC	
	T A _ I	
GAM312 TCF20	AGCTCACACTGCC-AGCTCTGG 4741 GA _ C C G	
	GCTC CGC GCC AGCTCTGGT	
	CGAG GTG CGG TCGAGACCG	
	___ T A _ I	
GAM312 TEM6	AGCCCAGCTCGCCCAGCTC 4742 C _ II	
	AGCTC GC CGCCCAGCT	
	TCGGG CG GCGGGTCGA	
	T A GI	
GAM312 TEM6	AGCCCAGCTCGCCCAGCTC 4742 GA C _ TGGT	
	GCTC GC CGCCCAGCTC	
	CGGG CG GCGGGTCGAG	
	___ T A CIII	
GAM313 ARCN1	GGTCTCCAGTGGCTTGTAATCT 4779 TGA GTCACC G I	
	CAG GT TGTAATCT	
	GTC CG ACATTTAGA	
	G_ AC_ A C	
GAM313 DIO1	CAAGTCACAGCCGTGTGTA 4776 TG_ GTCA AATC	
	ACAG CCGTGTGTA	
	TGTC GGCACACAT	
	CAG _ GAAI	
GAM313 E2F3	ACAGGTCACCCTGTAACAAATCT 4773 TGAC G TA_ I	
	AGGTCACC TGTG AATCT	
	TCCAGTGG ACAT TTAGA	
	___ G TGT T	
GAM313 GNA11	CAGGTCACCTTGTG-CAATCT 4777 TGACAG G A	
	GTCACC TGTGTAA TC	
	CAGTGG ACACGTT AG	
	___ A _	
GAM313 MUC4	ACAGGTCACACTG-G-AAAT 4775 TGAC CG TGTAAT	
	AGGTCAC TG	
	TCCAGTG AC	
	___ TG CTTTACC	
GAM313 PPM1D	ACAGGTCAC--TATGAAAAT 4774 TGAC CG T	
	AGGTCAC TGTG AAAT	

	TCCAGTG ATAC TTTA		
	_____ T		
GAM313 PTEN	GAAAGGT---GTGTGTAAAT 4778 TGAC CACC		
	AGGT GTGTGTAAAT		
	TCCA CACACATTTA		
	TT_____		
GAM313 YWHAZ	TGACAAATGGTCTAC-TGTGTAAAT 4780 _____ CG CTI		
	TGACA GGTC AC TGTGTAAAT		
	ACTGT CCAG TG ACACATTTA		
	TTA A _____		
GAM314 ARSB	AAAAGAGCCA-GCTGTTCCAGCCT 4784 T _ TI		
	AAAAGAGCCA GCTGT CTAGTCT		
	TTTTCTCGGT CGACA GGTCGGA		
	_ A II		
GAM314 ARSB	AAAAGAGCCA-GCTGTTCCAGCCT 4784 T _ I		
	AAAGAGCCA GCTGT CTAGTC		
	TTTCTCGGT CGACA GGTCGG		
	_ A I		
GAM314 C14orf1	AGCCATGC--TCTTGTCTT 4796 TG A I		
	AGCCATGC TCT GTCT		
	TCGGTACG AGA CAGA		
	_ A A		
GAM314 CD164	AAGAGCCATGATGT-T-GTCT 4792 AAAA C CTA		
	GAGCCATG TGT GTCT		
	CTCGGTAC ACA CAGA		
	_____ T A_		
GAM314 CD164	AAGAGCCATGATGT-T-GTCT 4792 C_ AGTI		
	AAGAGCCATG TGTCT		
	TTCTCGGTAC ACAGA		
	TACA IIIT		
GAM314 CDH12	AAAAGAGCCAAGCTGT-TAG 4785 T C TCT		
	AAAAGAGCCA GCTGT TAG		
	TTTTCTCGGT CGACA ATC		
	T _		
GAM314 CDH12	AAAAGAGCCAAGCTGT-TAG 4785 A T CTI		
	AAAGAGCCA GCTGT		
	TTTCTCGGT CGACA		
	_ T ATC		
GAM314 CLASP1	AGAGACACTATGCTGTCTGAGTTCTT 4794 A C _ CTI		
	GC ATGCTGTCT AGT		

	TG TACGACAGA TCA		
	_ A C AGI		
GAM314 CLASP1	AGAGACACTATGCTGTCTGAGTTCTT 4794 AAAAGA C	_ _ II	
	GC ATGCTGTCT AGT CTT		
	II IIIIIII III III		
	TG TACGACAGA TCA GAA		
	CTG__ A C A GT		
GAM314 CTSZ	AGAGCCATGCTGTGCAAGT 4795	CTAGII	
	AGAGCCATGCTGT		
	IIIIIIIIII		
	TCTCGGTACGACA		
	CGTTCA		
GAM314 CTSZ	AGAGCCATGCTGTGCAAGT 4795 AAAAGA	CT_ CT	
	GCCATGCTGT AGT		
	IIIIIIII III		
	CGGTACGACA TCA		
	_____ CGT CA		
GAM314 EIF2B5	AAAGAGCCAAGTCTCTCT 4787	_ G III	
	AAAGAGCCA TGCT TC		
	IIIIIIII III II		
	TTTCTCGGT ACGA AG		
	TG G AII		
GAM314 EIF2B5	AAAGAGCCAAGTCTCTCT 4787 AA	_ G AGTCT	
	AAGAGCCA TGCT TCT		
	IIIIII III III		
	TTCTCGGT ACGA AGA		
	_ TG G CIIIT		
GAM314 GHR	AAAATAGCCATGCT-TGAAGTCT 4786 G	GTCT T	
	AAAA AGCCATGCT AGTCT		
	III IIIIIII IIII		
	TTTT TCGGTACGA TCAGA		
	A ACT_ I		
GAM314 GHR	AAAATAGCCATGCT-TGAAGTCT 4786 AAAG_	GTCT I	
	AGCCATGCT AGTC		
	IIIIII III		
	TCGGTACGA TCAG		
	TTTTA ACT_ I		
GAM314 ITCH	AAAGAGCCAT--TGTCCAATTTT 4791	GC CI	
	AAAGAGCCAT TGTCTAGT		
	IIIIIIII IIIIIII		
	TTTCTCGGTA ACAGGTTA		
	_ AA		
GAM314 ITCH	AAAGAGCCAT--TGTCCAATTTT 4791 AA	GC CTT	
	AAGAGCCAT TGTCTAGT		
	IIIIII IIIIIII		
	TTTCTCGGTA ACAGGTTA		
	_ _ AAA		
GAM314 NR0B2	AAGGAGCCAAGTGTGTCTA 4788 AAA	_ III	
	GAGCCA TGCTGTCT		
	IIII IIIIIII		

	CTCGGT ACGACAGA		
	TTC TC TII		
GAM314 NR0B2	AAGGAGCCAAAGTGCTGTCTA 4788 AAAA	___	GTCT
	GAGCCA TGCTGTCTA		
	CTCGGT ACGACAGAT		
	TC__ TC AIII		
GAM314 PPP1R8	AAAGAGCCAGGGCAGTCTA 4789	T_ T II	
	AAAGAGCCA GC GTCT		
	II		
	TTTCTCGGT CG CAGA		
	CC T TI		
GAM314 PPP1R8	AAAGAGCCAGGGCAGTCTA 4789 AA	T_ T	GTCT
	AAGAGCCA GC GTCTA		
	II		
	TTCTCGGT CG CAGAT		
	___ CC T AIII		
GAM314 PRKAR2B	AAAAGTGATGCCATGCTGTGTAG 4783 AAAA	_	CTI
	GA GCCATGCTGT		
	II		
	CT CGGTACGACA		
	A__ A CAT		
GAM314 PRKAR2B	AAAAGTGATGCCATGCTGTGTAG 4783 AAAA	__ _	C TCTTI
	GA GCCATGCTGT TAG		
	II III		
	CT CGGTACGACA ATC		
	TTTTCA A C IIIT		
GAM314 PTK2B	AGGGCACATGCTGTC-AGTC 4793 A	_ T II	
	AG GC CATGCTGTC AGT		
	II II III		
	TC CG GTACGACAG TCA		
	C T _ GI		
GAM314 PTK2B	AGGGCACATGCTGTC-AGTC 4793 AAAAGA	_	T
	GC CATGCTGTC AGTCT		
	II		
	CG GTACGACAG TCAGG		
	_____ T _		
GAM314 RAB6A	AAAGAGCCAT-TTGTTTTAGTC 4790	GC C_ I	
	AAGAGCCAT TGT TAGT		
	III		
	TTCTCGGTA ACA ATCA		
	A_ AA I		
GAM314 RAB6A	AAAGAGCCAT-TTGTTTTAGTC 4790 AA	GC C_ TT	
	AAGAGCCAT TGT TAGTC		
	III		
	TTCTCGGTA ACA ATCAG		
	___ A_ AA TI		
GAM314 SHANK2	GAGCCATGC-GTCT--TCTT 4797	T	AGTCI
	GAGCCATGC GTCT		

	CTCGGTACG CAGA		
	— AGAAI		
GAM315 BTG2	AGAGGAGAGTTGTGCTTTTG 4802 TGGC TAAAT		
	AGAGT TGTGCTTTT		
	TCTCA ACACGAAAA		
	C___		
GAM315 CASP4	GCAGAACATAAATTGTGATTT 4805 TGGC GT_ C G		
	AGA TAAATTGTG TTTT		
	TCT ATTAAACAC AAAG		
	___ TGT T A		
GAM315 HS3ST2	GCAGAATTA---TGTGCTTTTG 4806 TGGC AAT		
	AGAGTTA TGTGCTTTT		
	TCTTAAT ACACGAAAA		

GAM315 MEOX2	CAGAGTTAAAATACACTTTT 4804 TGGCAG T TG		
	AGTTAAA TG CTTT		
	TCAATTT AT GAAAA		
	___ T GT		
GAM315 NCOA6	TGACATAGATAG-TTGTGCTTTT 4809 G TTAA G		
	TGGCA AG TTGTGCTTTT		
	ACTGT TC AACACGAAAA		
	A TATC_ I		
GAM315 PIK3CD	TGGCAGAGT---ATT-CGCTTCTG 4811 TAAATTG		
	TGGCAGAGT TGCTTTT		
	ACCGTCTCA GCGAAGA		
	TAA___		
GAM315 PIK3CD	GCAGAGTT-AGTTG-GCTTCTG 4807 TGGC AA T		
	AGAGTTA TTG GCTTTT		
	TCTCAAT AAC CGAAGA		
	___ C_ _		
GAM315 T	AGA-TTAAGAGTGTGCTTTT 4800 TG C TAAATT		
	G AGAGT GTGCTTTT		
	A TCTCA CACGAAAA		
	___ T ___		
GAM315 TRPC6	TGGCACA---AAATTGTGCT 4808 G GTT TT		
	TGGCA A AAATTGTGCT		
	ACCGT T TTTAACACGA		
	G ___		
GAM315 TSGA10	AGATTTATTTTGTGCTTTT 4801 TGGCAGAGTTAAA		
	TTGTGCTTTT		

		AACACGAAAA		
		AATAA_____		
GAM315 WASF3	TGG-AGAAATGAAATGTGCTTTTG	4810	C	TTAAAT I
	TGG AGAG TGTGCTTTTG			
	ACC TCTT ACACGAAAAC			
	_ TACTTT I			
GAM315 ZNF277	CAAATTTAAATTGTTCTTT	4803	TGGCAGAG	G
	TTAAATTGT CTTTT			
	AATTTAACA GAAAG			
	TA_____ A			
GAM316 AEGL1	TAGCCCAGGTTACTGTTGAGG	4816	A _ _	
	TAG CCAG TT CTGTTGAG			
	ATC GGTC AA GACAACTC			
	G C T C			
GAM316 EML1	ATATACCAGTTACTTCTGTTGA	4814	G _ _	T
	ATA ACCAGT TCTGTTG			
	TAT TGGTCA AGACAAC			
	A ATGA T			
GAM316 EPB41L2	ATAGACCAGAGCTGGTAAGG	4815	TT T I	
	TAGACCAG CTG TGAG			
	ATCTGGTC GAC ATTC			
	TC C I			
GAM316 EPB41L2	ATAGACCAGAGCTGGTAAGG	4815	TCAGATAG	TT T
	ACCAG CTG TGAG			
	TGGTC GAC ATTC			
	_____ TC C			
GAM316 HS3ST3B1	TCAGA-ATAC-AGCCCTGTTGAGG	4818	TAGAC	
	TCAGA CAGTTCTGTTGAGG			
	AGTCT GTCGGGACAACTCC			
	TAT__			
GAM316 HS3ST3B1	TCAGA-ATAC-AGCCCTGTTGAGG	4818	_ TAGAC	I
	CAGA CAGTTCTGTTGAG			
	GTCT GTCGGGACAACTC			
	A TAT__ I			
GAM316 UBL1	TCAAAAAGAGCAGTGTCTGTTG	4817	T C _	AGGI
	TCAGA AGA CAGT TCTGTTG			
	AGTTT TCT GTCA AGACAAC			
	T C CA G			
GAM316 UBL1	TCAAAAAGAGCAGTGTCTGTTG	4817	CAGAT C _	I
	AGA CAGT TCTGTT			

	TCT GTCA AGACAA		
	TTT__ C CA I		
GAM317 ACADVL	TGAGAGCAGGCACAGTGCTGG	4838	C CTCA AAT
	TGA AGCAGGCACA TGG		
	ACT TCGTCCGTGT ACC		
	C CACG		
GAM317 BCLG	TGACAGCAGTGCAAAC-AATGAAA	4829	_ C TC TI
	TGACAGCAG GCA AC ATGGAA		
	ACTGTCGTC CGT TG TACTTT		
	A T T_		
GAM317 CD2	ACAGAAAACAC-CTCATGGAA	4824	TGAC C A
	AG AGGCAC CTCATGGAA		
	TC TTTGTG GAGTACCTT		
	____ T _		
GAM317 CD83	ACAGACAGGCACACCCCTG	4821	TGACA A AA
	GCAGGCACACTC TGG		
	TGTCCGTGTGGG ACT		
	TC__ G CI		
GAM317 CDC27	TGAAAGT-GGCACACTCATGGTAT	4841	C CA AATI
	TGA AG GGCACACTCATGG		
	ACT TC CCGTGTGAGTACC		
	T A_ ATAI		
GAM317 CHS1	TGACAGCAG--AGACT-TTGGGAAT	4842	CAC CA
	TGACAGCAGG ACT TGGAAT		
	ACTGTCGTCT TGA ACCTTA		
	C_ A_		
GAM317 DRD3	TGACAGCAGACATACCCAAGCAA	4840	C TGGAATI
	TGACAGCAGGCA ACTCA		
	ACTGTCGTCTGT TGGGT		
	A TCGTTII		
GAM317 DRG2	TGACAGCAGCCACAGCCTCCAGGGA	4832	G _ AT_ ATII
	TGACAGCAG CACA CTC GGA		
	ACTGTCGTC GTGT GAG CCT		
	G CG GTC IIIT		
GAM317 ENG	TGACAGCAG---CAGTCCTGG	4836	G CAC A A
	TGACAGCAG CA TC TGG		
	ACTGTCGTC GT AG ACC		
	_ C_ G I		
GAM317 HCFC1	ACAGCAGGC-CCCTCGTGG	4823	TGAC ACA A A
	AGCAGGC CTC TGG		

	TCGTCCG GAG ACC		
	_____ GG_ C G		
GAM317 KIF1B	TGACAGCA-GCACAGACAT 4834	G CT GGA	
	TGACAGCAG CACA CAT		
	ACTGTCGTC GTGT GTA		
	_ CT		
GAM317 MASP2	TGACAGCAGCCTCAC-C-TGGA 4839	G A_ CA A	
	TGACAGCAG C CACT TGGA		
	ACTGTCGTC G GTGG ACCT		
	_ GA _ I		
GAM317 MFAP4	CAGCAGAGGGGAGCACTCATGGA 4826	TGA C CA_ AT	
	CAG AGG CACTCATGGA		
	GTC TCC GTGAGTACCT		
	___ _ CTC CT		
GAM317 PDXK	CAGCAGATGCCGGACACTCATGAAA 4825	TGACA A C TII	
	GC GG ACACTCATGGAA		
	CG CC TGTGAGTACTTT		
	GTCTA G _ CTT		
GAM317 PPARGC1	TGACA-CAGAGCACACACTCATG 4828	G _ GAAT	
	TGACA CAG GCACACTCATG		
	ACTGT GTC TGTGTGAGTAC		
	_ TCG IIIT		
GAM317 SH3BP4	TGACAGCAGG-GCACGCAGGG 4837	CA T T AA	
	TGACAGCAGG CAC CA GG		
	ACTGTCGTCC GTG GT CC		
	C_ C C II		
GAM317 TF	TGAAACCAGGGCAAACACTCATGGA 4830	TGA_ CA C ATI	
	CAG GGCA ACTCATGGA		
	GTC CCGT TGAGTACCT		
	ACTTTG _ T		
GAM317 THPO	ACAGCAGGCAGCCCTC-TGG 4822	TGAC CA_ A AA	
	AGCAGGCA CTC TGG		
	TCGTCCGT GAG ACC		
	_____ CGG _ CC		
GAM317 TIRAP	TGACAGCAGTGACA-TCAT 4835	GC C GGA	
	TGACAGCAG ACA TCAT		
	ACTGTCGTC TGT AGTA		
	AC _		
GAM317 TMPRSS3	TGA-AGCAGGCACA-TCAT 4833	C C GGA	
	TGA AGCAGGCACA TCAT		

	ACT TCGTCCGTGT AGTA		
	— — III		
GAM317 TPK1	CAG-AGGCACACTTATGGA 4827 TGACAGC C		
	AGGCACACT ATGGA		
	TCCGTGTGA TACCT		
	— A		
GAM317 ZNF22	TGACACTTGGCACCATTCTCATGGAA 4831 GCA A__ TII		
	TGACA GGCAC CTCATGGAA		
	ACTGT CCGTG GAGTACCTT		
	GAA GTAA III		
GAM318 ARNT2	GAGCCTTACTGTGGCTGCATCTG 4854 A GTA _ GI		
	AG CC ATTGTGGCTGCA CTG		
	TC GG TGACACCGACGT GAC		
	_ AA_ A AI		
GAM318 ARNT2	GAGCCTTACTGTGGCTGCATCTG 4854 A GTA CTI		
	CC ATTGTGGCTGCA		
	GG TGACACCGACGT		
	C AA_ AGA		
GAM318 CXCL16	GACCTGTGAG-GCGGCTGCACTG 4853 GTAATT I		
	ACC GTGGCTGCACT		
	TGG CGCCGACGTGA		
	ACACTC I		
GAM318 CXCL16	GACCTGTGAG-GCGGCTGCACTG 4853 AG GTAATT G		
	ACC GTGGCTGCACTG		
	TGG CGCCGACGTGAC		
	_ ACACTC G		
GAM318 DDX5	ACCATAATTACTGCTGCACTG 4845 TG I		
	CCGTAATTG GCTGCACT		
	GGTATTAAT CGACGTGA		
	GA I		
GAM318 DDX5	ACCATAATTACTGCTGCACTG 4845 AGAC TG G		
	CGTAATTG GCTGCACTG		
	GTATTAAT CGACGTGAC		
	— GA G		
GAM318 EPB42	AGATCGTTATC-TGGACTGCACTGG 4847 C A GT I		
	AGA CGT ATT GGCTGCACTGG		
	TCT GCA TAG CTGACGTGACC		
	A A AC I		
GAM318 EPB42	AGATCGTTATC-TGGACTGCACTGG 4847 GAC A GT I		
	CGT ATT GGCTGCACTG		

	GCA TAG CTGACGTGAC		
	CTA A AC I		
GAM318 EPOR	CCATAAGTCTTGAGTCTGCACTGG	4851	AGACCGTAA TGG I
	TTG CTGCACTGG		
	AAC GACGTGACC		
	ATTCAG__ TCA A		
GAM318 EPOR	CCATAAGTCTTGAGTCTGCACTGG	4851	C_ AA TGG I
	GT TTG CTGCACTG		
	CA AAC GACGTGAC		
	TT G_ TCA I		
GAM318 FN1	GACCAGAGAAGTTGTGGCTGCA	4852	TAA__ III
	GACCG TTGTGGCTGC		
	CTGGT AACACCGACG		
	CTCTTC TII		
GAM318 FN1	GACCAGAGAAGTTGTGGCTGCA	4852	AG TAA__ CTGG
	ACCG TTGTGGCTGCA		
	TGGT AACACCGACGT		
	_ CTCTTC CIII		
GAM318 FZD7	AGACCGTAA-TGT-CTGACCCTGG	4848	TG_ GCA
	AGACCGTAAT TGGCT CTGG		
	TCTGGCATTACTGG GACC		
	CAG _		
GAM318 FZD7	AGACCGTAA-TGT-CTGACCCTGG	4848	TG_ GCACTI
	AGACCGTAAT TGGCT		
	TCTGGCATTACTGG		
	CAG GACCII		
GAM318 GGPS1	AGACCTACATAACTGTGGCTGC	4846	_ ACTGG
	AGACC GTAATTGTGGCTGC		
	TCTGG TATTGACACCGACG		
	ATG IIIGG		
GAM318 GGPS1	AGACCTACATAACTGTGGCTGC	4846	_ III
	AGACC GTAATTGTGGCTG		
	TCTGG TATTGACACCGAC		
	ATG GII		
GAM318 MAP1A	AGAGC-TGATGCTGTCTGCACTGG	4850	AGACC AAT GG_ I
	GT TGT CTGCACTGG		
	CG ACG GACGTGACC		
	TCT_ ACT ACA I		
GAM318 MAP1A	AGAGC-TGATGCTGTCTGCACTGG	4850	GACC AAT GG_ I
	GT TGT CTGCACTG		

	CG ACG GACGTGAC		
	TCT_ ACT ACA I		
GAM318 NUMB	GTAACAGTGGCTGCACTGG	4857	T II
	GTAAT GTGGCTGCACTG		
	CATTG CACCGACGTGAC		
	T CI		
GAM318 PRIM2A	GTAATTGTGTCACTGCACT	4856	AGACCGTAAT G
	TGT GCTGCACTG		
	ACA TGACGTGAT		
	AC_____ G		
GAM318 PRIM2A	GTAATTGTGTCACTGCACT	4856	___ III
	GTAATTGTG GCTGCAC		
	CATTAACAC TGACGTG		
	AG AII		
GAM318 VIM	GTAATATATTGCTGCACTG	4855	_ G II
	GTAAT TGT GCTGCACT		
	CATTA ATA CGACGTGA		
	T A CI		
GAM318 VIM	GTAATATATTGCTGCACTG	4855	AGACCGTAATTGTG
	GCTGCACTG		
	CGACGTGAC		
	TATAA_____		
GAM318 WNT8B	AGACC-TAGGTGTGGCTGC	4849	GTAAT ACT
	AGACC TGTGGCTGC		
	TCTGG ACACCGACG		
	ATCC_ III		
GAM318 WNT8B	AGACC-TAGGTGTGGCTGC	4849	GTAAT I
	AGACC TGTGGCTG		
	TCTGG ACACCGAC		
	ATCC_ G		
GAM319 AHSG	GTCA-AGACTTGATATTAATGTA	4861	TG TA _ CA
	TCA GCTT ATATTAATGTA		
	AGT TGAA TATAATTACAT		
	_ TC C CI		
GAM319 CCNG1	TCATAGCTTAAATCCATTGTA	4862	TGTC T AA_ CA
	ATAGCTTA ATT TGTA		
	TATCGAAT TAG ACAT		
	_____ T GTA TG		
GAM319 E2F3	TGTTATGG--TATATTAATGTA	4872	TGTCATAGCT C
	TATATTAATGTA		

	ATATAATTACAT			
	ACAATACC_ I			
GAM319 EIF1A	TGTGCATAGCTTATAGCACTGTA	4865	_ T A CAI	
	TGT CATAGCTTATA TA TGTA			
	ACA GTATCGAATAT GT ACAT			
	C C G			
GAM319 GPM6A	CAAAGCTATTATATTAATG	4860	TGTCAT _ TAC	
	AGCT TATATTAATG			
	TCGA ATATAATTAC			
	_ TA CTT			
GAM319 GYP A	TGTAATATTTTCATATTAATG	4868	C GC TAC	
	TGT ATA TTATATTAATG			
	ACA TAT AGTATAATTAC			
	T AA			
GAM319 NFATC1	TCTTTGCACATATTAATGTTCA	4864	TGTCATA T ACA	
	GC TATATTAATGT			
	CG GTATAATTACA			
	AAA_ T AGT			
GAM319 PCDHB4	TGTCCATATCTGCAAAGTAATGTACA	4866	_ G _ TAT	
	TGTC ATA CT TA TAATGTACA			
	ACAG TAT GA GT ATTACATGT			
	G A C TTC			
GAM319 SCML2	TCATAGCTTATAAACAT-TACA	4863	TGTC TTAATG	
	ATAGCTTATA TACA			
	TATCGAATAT ATGT			
	_ TTGTA_			
GAM319 SIM2	TGTCTCTGCATAAATTAATGTA	4871	ATA T T CA	
	TGTC GC TA ATTAATGTA			
	ACAG CG AT TAATTACAT			
	AGA T T			
GAM319 SUV39H2	TGTCATAGC-AATA-TAATG	4869	TT T TA	
	TGTCATAGC ATAT AATG			
	ACAGTATCG TATA TTAC			
	T_ _			
GAM319 VCAM1	TGTCA--GCAAATATTAATGT	4870	TA TT AC	
	TGTCA GC ATATTAATGT			
	ACAGT CG TATAATTACA			
	_ TT			
GAM319 VSNL1	TGACATAGCTTATAATTAAGTTACA	4867	T _ TG	
	TG CATAGCTTATA TTAA TACA			

AC GTATCGAATAT AATT ATGT
 T T CA II
 GAM320 ABCD4 GACAACT---GAACTG-GAGGG 4913 TG GGGA C
 ACAACTGA ACTG GAG
 ||||| ||| ||
 TGTGACT TGAC CTC

 GAM320 AHR ACAGCAGATTTTTCACATTGCA 4879 CA C_ A GC
 CAGCAGATT TGCA TGCAG
 ||||| ||| ||||
 GTCGTCTAA GTGT ACGTT
 AAA A II
 GAM320 AMFR CACAG--GACTGTTCAATGCAGG 4903 CA CTG C
 CACAG GATT CAATGCAGG
 ||| ||| |||||
 GTGTC CTGA GTTACGTCC
 CAA I
 GAM320 ANK1 CACAGCAGAGTCT---ATACAG 4900 T GCA G
 CACAGCAGA TCT ATGCAG
 ||||| ||| ||||
 GTGTCGTCT AGA TATGTC
 C _ I
 GAM320 AOA H CAACTGAGGGATGCTG-GAG 4887 TGACAA A_ C G
 CTGAGGGA CTG GAG
 ||||| ||| ||
 GACTCCCT GAC CTC
 AC _ G
 GAM320 ATOX1 GACAACTGAGGG-TCTCCGCAGG 4912 TG AA_ G
 ACAACTGAGGG CTGC AGGG
 ||||| ||| ||||
 TGTGACTCCC GGCG TCCT
 AGA _
 GAM320 ATP6V1A1 CAGAGCTG-TTCTGCAATATGCAG 4895 C AGA _ GCI
 CA AGC TTCTGCA ATGCAG
 || ||| ||||| |||||
 GT TCG AAGACGT TACGTC
 C AC_ TA |||
 GAM320 B3GALT5 CACCAGATTCTGACAGTGC 4906 CACAG _ A AGG
 CAGATTCTG CA TGC
 ||||| ||| |||
 GTCTAAGAC GT ACG
 G_ T C AGI
 GAM320 B3GALT5 CAGCAGATTCTGCACTCCAGG 4908 CACA ATG C
 GCAGATTCTGCA CAGG
 ||||| ||| |||
 CGTCTAAGACGT GTCC
 GAG A
 GAM320 BCL7A CACAGCAGAGTTCTTCAGTG 4890 _ G ATGCAGG
 CACAGCAGA TTCT CA
 ||||| ||| ||

	GTGTCGTCT AAGA GT		
	C A CACIIIC		
GAM320 BTD	GACA-CTGAGGGAATCTGC 4910 TG A _ GAG		
	ACA CTGAGGGAA CTGC		
	TGT GACTCCCTT GACG		
	_ _ A GII		
GAM320 CASP8	ACAGCAGATGCTCCAGAAATGC 4877 CA T G _ AGGC		
	CAGCAGAT CT CA ATGC		
	GTCGTCTA GA GT TACG		
	_ C G CTT AII		
GAM320 E2F1	CACCAGATTCTGGGA-GCAGGC 4909 CACAG CAAT		
	CAGATTCTG GCAGGC		
	GTCTAAGAC CGTCCG		
	G _ CCT _		
GAM320 GADD45B	CAACAGATTCTGC--TGCTGG 4907 CACA AA A		
	GCAGATTCTGC TGC GG		
	TGTCTAAGACG ACG CC		
	_ _ A		
GAM320 GNAI3	AGCACATTCTGCAA---AGGC 4886 CACAGCAG TGC		
	ATTCTGCAA AG		
	TAAGACGTT TC		
	TG _ _		
GAM320 GSPT1	ACTGAGGGAAGGCGGCGGGG 4881 TGACAACT AACT A		
	GAGGG GCG GG		
	CTTCC CGC CC		
	CC _ GC _ _		
GAM320 GSTM5	GCGGATTCTGC-AGACAGGC 4914 CACAGCAG AT		
	ATTCTGCA GCAGG		
	TAAGACGT TGTCC		
	_ C _		
GAM320 HLCS	GACAACTGAGTCTCCTGCGTGAGGG 4911 TG GGAA _ II		
	ACAACTGAG CTGC GAGGG		
	TGTTGACTC GACG CTCCC		
	_ AGAG CA TI		
GAM320 IL1RAP	CACAGCAGATGC--CACTGCA 4899 T TG AA GG		
	CACAGCAGAT C C TGCA		
	GTGTCGTCTA G G ACGT		
	C GT _ II		
GAM320 LIG1	CACAGCAGATTTGCTAAAAAGCA 4892 C AAT _ GGCI		
	CACAGCAGATT TGC GCA		

	GTGTCGTCTAA ACG CGT	
	_ ATTTTT IIIC	
GAM320 LNK	CACAGCAGA-CCTGCCATG 4897 T A CAG	
	CACAGCAGAT CTGC ATG	
	GTGTCGTCTG GACG TAC	
	_ G III	
GAM320 LPIN2	ACAACTGAGGATGCTGCAGGAGG 4876 TGAC AA _ I	
	AACTGAGGG CTGC GAGGG	
	TTGACTCCT GACG CTCCT	
	_____ AC TC G	
GAM320 MAPT	CAATTAACCGAACTGCGAGG 4888 TGACAACTGAGG	
	GAACTGCGAGG	
	CTTGACGCTCC	
	AATTGG_____	
GAM320 MMP16	ACAGCAGATACTG---TGCA 4880 CA T CAA G	
	CAGCAGAT CTG TGCA	
	GTCGTCTA GAC ACGT	
	_ T _ A	
GAM320 NCAM2	CAGAGCAGGTTTCTGCAATG 4893 C A_ CAGG	
	CA AGCAG TTCTGCAATG	
	GT TCGTC AAGACGTTAC	
	C CA IIIC	
GAM320 NEDD4L	CACGACA-ATTCTGCAATGGAG 4901 A A C GC	
	CAC GCAG TTCTGCAATG AG	
	GTG TGTT AAGACGTTAC TC	
	C _ C II	
GAM320 OGDH	ACAGCAGATAATGGACACTGCAG 4878 CA TCT_ A CI	
	CAGCAGAT GCA TGCAGG	
	GTCGTCTA TGT ACGTCT	
	_ TTACC G II	
GAM320 PAG	CATAGCTCACTCTGCAATGTCAG 4898 CAC AG _ GCI	
	AGC ATTCTGCAATG CAG	
	TCG TGAGACGTTAC GTC	
	GTA AG A III	
GAM320 PEA15	ACAACTGAGTGGA---GAGGG 4875 TGAC _ CTGC	
	AACTGAG GGAA GAGG	
	TTGACTC CCTT CTCC	
	_____ A _____	
GAM320 PKIA	AGCAGGTTTCCTGCAATGCAG 4883 CACAGCAGA G	
	TTCTGCAATGCAG	

AGGACGTTACGTC
 TCCA_____ G
 GAM320 PPARG AGCAGAATGCAGAAATGCAGGC 4882 CACA_ TTCTGC
 GCAGA AATGCAGGC
 ||||| |||||
 CGTCT TTACGTCCG
 TCTTA _____
 GAM320 PPP1R2 CACAGCAGAGACTCGC-AGGCAG 4894 TT GCAA
 CACAGCAGA CT TGCAGGC
 ||||| || |||||
 GTGTCGTCT GA GCGTCCG
 CT _____
 GAM320 PRKY CACAGCAGATTTGAGCAATGC 4891 CT_ AGGC
 CACAGCAGATT GCAATGC
 ||||| |||||
 GTGTCGTCTAA CGTTACG
 ACT IIIC
 GAM320 PTPRF CACACCATA--CTGCAATGCTGG 4902 G GATT A C
 CACA CA CTGCAATGC GG
 ||| || ||||| ||
 GTGT GT GACGTTACG CC
 G AT_ A I
 GAM320 RHO AGCAGATTCTCCAGAATGGAG 4884 CACAGC G _ C C
 AGATTCT CA ATG AGG
 ||||| || ||| ||
 TCTAAGA GT TAC TCT
 _____ G CT C T
 GAM320 SF3B2 TGACAAGTCCTTGGAAGTGCAG 4916 _ GA AGGG
 TGACAA CT GGGAAGTGCAG
 ||||| || |||||
 ACTGTT GG CCCTTGACGC
 CA AA IIIG
 GAM320 SLC4A10 CACA-CAGATTCTGCATTG 4896 G ATGCAG
 CACA CAGATTCTGCA
 ||| |||||
 GTGT GTCTAAGACGT
 _ AACII
 GAM320 SWAP70 AGGACATTCTGCAAAAGTGCAGG 4885 CACAGCAG _ CI
 ATTCTGCAA TGCAGG
 ||||| |||||
 TAAGACGTT ACGTCC
 TG_____ TTC TG
 GAM320 TAF1C TGAGAACTGAGGGACCTGCCTGAGG 4917 C A _ GII
 TGA AACTGAGGGA CTGC GAGG
 ||| ||||| ||| |||
 ACT TTGACTCCCT GACG CTCC
 C G GA III
 GAM320 TCF2 CACAGCAGAGGCATTCT--AATCCAGGC4889 _ CA G II
 CACAGCAGA TTCTG AT CAGGC
 ||||| ||| ||| |||

	GTGTCGTCT AAGAT TA GTCCG	
	CCGT _ G II	
GAM320 TGM4	CAGATTCTCTCCTGCAATGCCAGG 4905 CACAGCAGA _ CI	
	TTCTGCAATGC AGG	
	AGGACGTTACG TCC	
	AGAG_____ G CT	
GAM320 TSTA3	CAGAGCGGAT---GGAATGCAGGC 4904 C A TTC C	
	CA AGC GA TG AATGCAGGC	
	GT TCG CT AC TTACGTCCG	
	C C _ C	
GAM320 WBP2	TGCCAGACTGAGGGAGCTG 4915 TGA _ A CGAGG	
	CA ACTGAGGGA CTG	
	GT TGA TCCCT GAC	
	ACG C C IIIGG	
GAM321 GABRA2	GCAGCCAAGAGAGCGTGGAGCG 4920 AGGC AA _	
	AGCCAAGAGG GTGG GCGG	
	TCGGTTCTCT CACC CGCT	
	_____ CG T	
GAM321 GABRA2	GCAGCCAAGAGAGCGTGGAGCG 4920 C AA _ I	
	AGCCAAGAGG GTGG GC	
	TCGGTTCTCT CACC CG	
	_ CG T I	
GAM321 TCEA1	GCTGGCAAGGGGAAGTGGGCG 4921 A GCCA A	
	GGCA AG GGAAGTGGGCGG	
	CCGT TC CCTTCACCCGCT	
	A _ C	
GAM321 TCEA1	GCTGGCAAGGGGAAGTGGGCG 4921 CAGC A I	
	CAAG GGAAGTGGGC	
	GTTC CCTTCACCCG	
	GACC C I	
GAM321 TSN	GGCGGCCAAG--GAAGTGGACG 4922 _ A AG I	
	GC GCCA AGGAAGTGGGC	
	CG CGGT TCCTTCACCTG	
	C C _ I	
GAM321 TSN	GGCGGCCAAG--GAAGTGGACG 4922 AG A AG	
	GC GCCA AGGAAGTGGGCG	
	CG CGGT TCCTTCACCTGC	
	_ C _	
GAM322 ALDH1A3	TAAAAATAACAAGGCTGTGT 4938 CTCT GG	
	TAAAAATAACAA TTGTG	

	ATTTTATTGTT GACAC		
	CC__ AI		
GAM322 AXUD1	TAAAAATAAGCCTCTTTATTGG 4940	CAA	_ GCI
	TAAAAATAA CTCTTTGT GG		
	II		
	ATTTTATT GAGAAATA CC		
	TCG A III		
GAM322 AXUD1	TAAAAATAAGCCTCTTTATTGG 4940	CAA	GGI
	AAAAATAA CTCTTTGT		
	TTTTTATT GAGAAATA		
	TCG ACI		
GAM322 CDKN1B	TAAAAATAAC-ACTTTCCTGTGG 4937	AC_	T GC
	TAAAAATAACA TCTT GTGG		
	ATTTTATTGT AGGA CACC		
	GAA _ II		
GAM322 CDKN1B	TAAAAATAAC-ACTTTCCTGTGG 4937	AC_	T I
	AAAAATAACA TCTT GTG		
	TTTTTATTGT AGGA CAC		
	GAA _ I		
GAM322 CHN2	AAAATAACAACATTCTCGTG GG 4927 A	TC_	I
	AATAACAAC TTTGTGG		
	TTATTGTTG GAGCACC		
	_ TAA I		
GAM322 CHN2	AAAATAACAACATTCTCGTG GG 4927 TAAA	TC_	C
	AATAACAAC TTTGTGGG		
	TTATTGTTG GAGCACCC		
	_____ TAA A		
GAM322 GABRE	AAAGAGCAGC-CTTTGTGGG 4930 AATAACAAC		I
	TCTTTGTGG		
	GGAAACACC		
	TTTCTCGTC I		
GAM322 GABRE	AAAGAGCAGC-CTTTGTGGG 4930 TAAAAATAACAAC		
	TCTTTGTGGG		
	GGAAACACCC		
	CTCGTC_____		
GAM322 GPC4	TAACACAAACAACCTCTTTGTGGG 4936 AA__	AA	I
	AAATAAC CTCTTTGTGG		
	TTTGTTG GAGAAACACC		
	TGTG _ I		
GAM322 GPC4	TAACACAAACAACCTCTTTGTGGG 4936 TAA__	AA	CI
	AAATAAC CTCTTTGTGGG		

	TTTGTTG GAGAAACACCC		
	ATTGTG _ II		
GAM322 HGF	AAAATAACATTTAATTTGTGG 4928 TAAA	ACTC_ GC	
	AATAACA TTTGTGG		
	TTATTGT AAACACC		
	_ AAATT AA		
GAM322 HIP2	TAAAAATAACAGATGTTGGTG 4939	ACTCTT G C	
	TAAAAATAACA TGT GG		
	II		
	ATTTTATTGT ACA CC		
	CT_ A A		
GAM322 MEN1	TAAAAATAACAGTACACCTTGT 4934	_ T GGGC	
	TAAAAATAACA AC CTTTGT		
	ATTTTATTGT TG GGAACA		
	CA T IIIC		
GAM322 MGAT4A	TAACAATATGTACAACTCTTATGT 4933 TAAAAATA	TI	
	ACAACTCTT		
	TGTTGAGAA		
	ATACA_ TA		
GAM322 MGAT4A	TAACAATATGTACAACTCTTATGT 4933 TAAAAATA_	T GGCI	
	ACAACTCTT GTG		
	TGTTGAGAA TAC		
	ATTGTTATACA _ AIII		
GAM322 MTRR	TAAAAATAA-ATCCCTCTGTAGGC 4941	CAA I	
	TAAAAATAA CTCTTTGTGGGC		
	ATTTTATT GGGAGACATCCG		
	TA_ I		
GAM322 MTRR	TAAAAATAA-ATCCCTCTGTAGGC 4941_	CAA I	
	AAAAATAA CTCTTTGTGGG		
	TTTTTATT GGGAGACATCC		
	A TA_ I		
GAM322 OPTN	AAAAGCACAACCTCTTGGAGG 4929 AAAATA	TGTI	
	ACAACTCTT		
	TGTTGAGAA		
	TTCG_ CCTC		
GAM322 OPTN	AAAAGCACAACCTCTTGGAGG 4929 TAAAAATA	T TG	
	ACAACTCTT G GG		
	I		
	TGTTGAGAA C CC		
	TTCG_ _CT		
GAM322 PCDHB9	AAAAATAGTACCTTCTTTGTGG 4925 TA	_ AAC GC	
	AAAATA AC TCTTTGTGG		

	TTTTAT TG AGAAACACC		
	___ CA GA_ AI		
GAM322 TJP1	TAAAAATGTAACAACTCTGTG 4932	___	TT GGC
	TAAAAA TAACAACTCT GTG		
	ATTTTT ATTGTTGAGA CAC		
	AC ___ III		
GAM322 TJP1	TAAAAATGTAACAACTCTGTG 4932	___	TTIII
	TAAAAA TAACAACTCT		
	ATTTTT ATTGTTGAGA		
	AC CACII		
GAM322 TWIST	TAAAAATAAAAACATTCTTCGT 4935	C ___	GGGC
	TAAAAATAA AAC TCTTTGT		
	ATTTTTATT TTG AGAAGCA		
	T TA IIIC		
GAM322 VBP1	TAAAAAAGCTCACAACCTCTT 4931	TA___	GTGGGC
	TAAAAA ACAACTCTTT		
	ATTTTT TGTTGAGAAA		
	TCGAG IIICGG		
GAM322 VBP1	TAAAAAAGCTCACAACCTCTT 4931	TA___	III
	TAAAAA ACAACTCTT		
	ATTTTT TGTTGAGAA		
	TCGAG AII		
GAM322 XRCC5	AAAATAACAATGACTCTTT 4926	___	III
	AAAATAACA ACTCTT		
	TTTTATTGT TGAGAA		
	TAC AII		
GAM322 XRCC5	AAAATAACAATGACTCTTT 4926	TAAA ___	GGG
	AATAACA ACTCTTTGT		
	TTATTGT TGAGAAATA		
	___ TAC III		
GAM323 BCL11B	TGTGTTCCACG-AGACCTT 4956	AATGA	A A G
	GTTCCACGA GA CTT		
	CAAGGTGCT CT GAA		
	A___ _ G G		
GAM323 DDX3	GAGATCTCGCGA-GAACTTGC 4951	AATGAG	CA A
	TTC CGA GAACTTGC		
	GAG GCT CTTGAACG		
	TA___ C_ _		
GAM323 DHCR24	AATGAGTTCTAAACGGGGAAC 4944	C___ AA	TGCC
	AATGAGTTC ACG GAACT		

	TTACTCAAG TGC CTTGA		
	ATT CC IIIC		
GAM323 FACL6	TTACTGAGAAGAACTTTCC 4957 AATGAGTTCCAC	G	
	GAAGAACTT CC		
	II		
	CTTCTTGAA GG		
	ACT_____ A		
GAM323 FMR2	AATGAGTTCCCCAATAGGAAC 4946	A A__ TTGCC	
	AATGAGTTCC CGA GAAC		
	III		
	TTACTCAAGG GTT CTTG		
	G ATC IIIC		
GAM323 IL13RA1	AATGAGTTCCCCTACAAATAA 4945	__ GAACTTGCC	
	AATGAGTTCC ACGAA		
	TTACTCAAGG TGTTT		
	GGA ATIIICCG		
GAM323 MAPRE1	GAGGTCCAGAAAGAACTTGC 4952 AATGAGT	C	
	TCCA GAAGAACTTGC		
	AGGT TTTCTTGAACG		
	C_____ C		
GAM323 PMM2	AGTTTCACGAAGAACGTGC 4949 AATGAGTTC	T	
	CACGAAGAAC TGC		
	III		
	GTGCTTCTTG ACG		
	A_____ C		
GAM323 RAD52	GACTCCACGCTAGAACTTGCC 4953 AATGAG	A	
	TTCCACG AGAACTTGCC		
	AGGGTGC TCTTGAACGG		
	_____ A		
GAM323 RBM3	TGAGCCCTCCCACGAAGAGCTTTCC 4954 AATGAG	A G II	
	TTCCACGAAGA CTT CC		
	III II		
	AGGGTGCTTCT GAA GG		
	TCGGG_ C A AA		
GAM323 STARD4	AATGGGT---ATGAAGAACTT 4948	A TCCAC G	
	AATG GT GAAGAACTT		
	II		
	TTAC CA CTTCTTGAA		
	C TA__ I		
GAM323 TEM6	AATGAGTT-CAAAAAGCACGTTTGC 4947	CAC A __ CI	
	AATGAGTTC GAAG AC TTGC		
	II		
	TTACTCAAG TTTC TG AACG		
	TT_ G CA II		
GAM323 TRIP12	ATAATTTAAAC-AAGAACTTGC 4950 AATGAGTTCCACG	C	
	AAGAACTTGC		

		TTCTTGAACG			
		ATTAAATTTG_____A			
GAM323 XT3		TGAGTTCCATGAGCAAAACT	4955	AATG C _____	TGCC
		AGTTCCA GA AGAACT			
		TCAAGGT CT TTTTGA			
		_____ A CGT TAlI			
GAM324 ABCA1		TGAGAATACACAGGAACAAAA	4968	CTGAAAC	CCGT
		TGAGAATAC CAAA			
		ACTCTTATG GTTT			
		TGTCCTT TIII			
GAM324 CACNA1C		AATACAAGAAAACCAAACC	4960	TGAGAATACCT	G
		GAAACCAAACC			
		TTTTGGTTTGG			
		GTTC_____ G			
GAM324 CNTN3		AGCATACC-AAACCAAAC	4964	TGAGA TG	C
		ATACC AAACCAAAC			
		TATGG TTTGGTTTG			
		G_____ T			
GAM324 DDX6		GAGACTTCAACCTGAAACCAAA	4967	TG AT_____	CCGT
		AGA ACCTGAAACCAAA			
		TCT TGGACTTTGGTTT			
		___ GAAGT TIII			
GAM324 HTN3		TGAGAATACACGAGTCCAAAGCG	4969	C AA C TI	
		TGAGAATAC TGA CCAA CG			
		ACTCTTATG GCT GGTTT GC			
		T CA C II			
GAM324 PDGFRA		GAAAACCTGTCAAACCAAAC	4966	TGAGAAT _____	CGT
		ACCTG AAACCAAAC			
		TGGAC TTTGGTTTG			
		T_____ AGT AAA			
GAM324 PRDM1		AATCCCTGAAACCTCACAGT	4962	TGAGAATA	AA C
		CCTGAAACC AC G			
		GGACTTTGG TG C			
		_____ AG T			
GAM324 RAB11A		AGACATAC-TGAAACCAAA	4963	TGAGA C	CC
		ATAC TGAAACCAAA			
		TATG ACTTTGGTTT			
		TG_____ CT			
GAM324 STCH		AATACCTGACATCAACACGGT	4961	TGAGAATA	AAC AC T
		CCTGA CAA CG			

		GGACT GTT GC		
		_____ GTA GT C		
GAM324 STIM1		AGAA-ACAAGAAACCAAACC	4965 TGAGAAT CT	G
		AC GAAACCAAACC		
		TG CTTTGGTTTGG		
		TT_____ TT A		
GAM325 COL4A6		AAACTAAACACTGCTTCTAGAT	4973 TAAAAGTAAAA	CCTG
		CTTCTAGAT		
		GAAGATCTA		
		TGATTTGTGAC TTII		
GAM325 F8		AAAAGTAAAATTTCT-GAT	4972 C AGAI	
		AAAAGTAAAA TTCT		
		TTTTCATTTT AAGA		
		A CTAI		
GAM325 F8		AAAAGTAAAATTTCT-GAT	4972 TA C A CC	
		AAAGTAAAA TTCT GAT		
		TTTTCATTTT AAGA CTA		
		_____ A _ AI		
GAM326 HAO2		GTGGTGGTATTAGAAATGTG	4976 C_ TG CCI	
		GTGG GTATTAGAA GTG		
		CACC CATAATCTT CAC		
		AC TA		
GAM326 TTC3		GTGGGGAAGGAGAATGGTG	4978 CGTATT CC	
		GTGG AGAATGGTG		
		CACC TCTTACCAC		
		CCTTCC II		
GAM326 USP14		GTGGC-TAC-AGAATGGTG	4977 GTAT C	
		GTGGC TAGAATGGTG		
		CACCG GTCTTACCAC		
		AT_____ I		
GAM327 ADRA1A		TCACCAGTCACCATGGAGAGAA	4985 TCACCC AI	
		CACCATGGAGA		
		GTGGTACCTCT		
		GTCA_____ CT		
GAM327 ADRA1A		TCACCAGTCACCATGGAGAGAA	4985 TGTC C_ AAAGA	
		ACC CACCATGGAGA		
		TGG GTGGTACCTCT		
		_____ TCA CTTAC		
GAM327 CHD4		CCCCAAAAAGGAGAAAAGA	4982 CCAT II	
		CCCCA GGAGAAAAG		

	GGGGT CCTCTTTTC			
	TTTT TI			
GAM327 FTH1	GTCACCCACGGCTATGGGGAAA	4983 TCA	C___ A I	
	CCCCAC ATGG GAA			
	GGGGTG TACC CTT			
	___ CCGA C I			
GAM327 FTH1	GTCACCCACGGCTATGGGGAAA	4983 TG	C___ A AGAI	
	TCACCCAC ATGG GAAA			
	AGTGGGGTG TACC CTTT			
	___ CCGA C AIII			
GAM327 MGAT5	TCACTCCCACCATGAGGCAAA	4984 C _	AGAAAI	
	AC CCCACCATGG			
	TG GGGTGGTACT			
	_ A CCGTTI			
GAM327 MGAT5	TCACTCCCACCATGAGGCAAA	4984 TGTC _	AGAAAAGA	
	AC CCCACCATGG			
	TG GGGTGGTACT			
	___ A CCGTTTTA			
GAM327 MUC4	ACCCACCAAGGAAAGAAAA	4981 T	AAII	
	ACCCACCA GGAGA			
	TGGGGTGGT CCTTT			
	_ CTTT			
GAM327 MUC4	ACCCACCAAGGAAAGAAAA	4981 TGTCACCC	T AAAG	
	CACCA GGAGA			
	GTGGT CCTTT			
	___ _ CTTT			
GAM327 SEPN1	TGTCTACCCGCCACCATGGAGCCAAG	4986 _ _	AA AII	
	TGTC ACCC CACCATGGAG AAG			
	ACAG TGGG GTGGTACCTC TTC			
	A CG GG			
GAM327 SEPN1	TGTCTACCCGCCACCATGGAGCCAAG	4986 TCA _	AAI	
	CC CCACCATGGAG			
	GG GGTGGTACCTC			
	G_ C GGT			
GAM328 ATP2A3	TGCAGA--CAGCGCGGCGGCCGC	4998 AAAC	G	
	TGCA CAGCGTGGCGGCCGC			
	ACGT GTCGCGCCGCGGCG			
	CT_ I			
GAM328 CHRNA7	TGCAAAACCAACTGTCTCGG	4995 _ GG	CCGC	
	TGCAAAACCAGC GT CGG			

		ACGTTTTGGTTG CA GCC			
		A GA III G			
GAM328 CUGBP1		GCAAAACCAATTTGGCAGC 4992 TG CG CGC			
		CAAAACCAG TGGCGGC			
		GTTTTGGTT ACCGTCG			
		— AA TII			
GAM328 FLNB		GCAAAACCA---TGA CTGCCG 4993 TG GCG G			
		CAAAACCA TGGC GCCG			
		GTTTTGGT ACTG CGGC			
		— — A			
GAM328 GRLF1		GCAAAACCAAGGCGGTGGAGGC 4991 TG C C CC			
		CAAAACCAG GTGG GG GCG			
		GTTTTGGTT CGCC CC CGT			
		— C A TC			
GAM328 HNF3A		TGCGAAGCGA-CG-GGCGGCCGCG 5000 AAAACCA T			
		TGC GCG GGCGGCCGCG			
		ACG TGC CCGCCGGCGC			
		CTTCGC_ _			
GAM328 JUND		TGCAA---CA-CGGGGCGGCCGCG 4999 AACCA T			
		TGCAA GCG GGCGGCCGCG			
		ACGTT TGC CCGCCGGCG			
		G_ _ C			
GAM328 MECP2		TGCAAAACCTGGGT-GCTGCC 4997 AGCG CG C			
		TGCAAAACC TGG GC GC			
		ACGTTTTGG ACC CG CG			
		— CA A			
GAM328 PACE		CAAAACCAGCCGGGCTGGCCACG 4989 TGCA GT _ I			
		AAACCAGC GGC GGCCGCG			
		TTTGGTCG CCG CCGGTGC			
		— GC A T			
GAM328 PDGFB		TGAAAAATGGGCGCTGGCGGCCG 4996 TGCAAAACCA _ CGI			
		GCG TGGCGGCCG			
		CGC ACCGCCGGC			
		ACTTTTACC G			
GAM328 SCA1		TGCACAGAAACCAGCGTGG 4994 _ CGGCCGC			
		TGCA AAACCAGCGTGG			
		ACGT TTTGGTCGCACC			
		GTC GCGC			
GAM328 TNFRSF6B		GCAGAAACCAGCGTGCGCG 4990 TGCA _ CCGC			
		AAACCAGCGTG GCGG			

	TTTGGTCGCAC CGCT	
	GTC_ G III G	
GAM329 DBP	CCTGCAAATCTAGGAGCACGGAT 5003 C GA GA_ I	
	TGCAAAT AGGAG GGA	
	ACGTTTA TCCTC CCT	
	_ GA GTG I	
GAM329 DBP	CCTGCAAATCTAGGAGCACGGAT 5003 GTCC GA GA_ I	
	TGCAAAT AGGAG GGAT	
	ACGTTTA TCCTC CCTA	
	_____ GA GTG A	
GAM329 NPDC1	TGCCAAGGAGGAGGAGGAGGA 5004 AAAT A III	
	TGC GA GGAGGAGG	
	ACG CT CCTCCTCC	
	GTTC _ TCC	
GAM329 SLC2A2	TGCAT-TGCAGGAGGAGGA 5005 AA A I	
	TGCA TG AGGAGGAGG	
	ACGT AC TCCTCCTCC	
	A_ G T	
GAM329 SLC2A2	TGCAT-TGCAGGAGGAGGA 5005 GTCCTGCAAA A	
	TG AGGAGGAGG	
	AC TCCTCCTCC	
	A_____ G	
GAM330 ABCC1	GGTGGCGCGGGCGGCGGCGGCA 5031 TGGGC A_ I	
	GGCGCGGGCGGCG GGGCA	
	CCGCGCCCGCCGC CCCGT	
	A_____ CG G	
GAM330 ABCC1	GGCGCGGGCGGCGGCGGCA 5019 T _ G A GC	
	GGGCGGCG CGGGCG CG GG	
	CCCGCCGC GCCCGT GC CC	
	_ C G _ II	
GAM330 ABCC1	GGCGGCGGGCACCGGGCGGCG 5021 TG _ _ A GCA	
	GGCGG CGC GGGCGGCG GG	
	CCGCC GTG CCCGCCGC CC	
	G_ C G _ III	
GAM330 ADAM12	CGGGCCCGGCGGCGAGCGC 5012 TGGGCGGCGCG G	
	GGCGGCGAG GC	
	CCGCCGCTC CG	
	GGG_____ G	
GAM330 ARHC	GGCGGCGTGGGC---GAGGGCA 5045 TGGG C GGC	
	CGGCG GGGC GAGGGC	

	GCCGC CCG CTCCG		
	_____ A _____		
GAM330 ARHC	GGGCGGCGCCGAGGCGGCGTTGGGCA 5050 TG	___ A_ II	
	GGCGGCGC GGGCGGCG GGGCA		
	CCGCGCG TCCGCGC CCCGT		
	_____ GC AA CI		
GAM330 ARHC	TGGAGCGGCGGCGGGCGGCG 5070 _ _ AGGGC		
	TGG GCGGCG CGGGCGGCG		
	ACC CGCCGC GCCCGCCGC		
	T C IIIAC		
GAM330 BACE	GGCGGCGCGGGCAGGGGCAAGGGC 5026 TGGG	___ AI	
	CGGCGCGGGC GCGAGGGC		
	GCCGCGCCCG CCGTTCCCG		
	_____ TCC AG		
GAM330 BACE	GCGGGCGGCGGCGCGGGCA 5013 TGGG CGA		
	CGGCGCGGGCGG GGGC		
	GCCGCGCCCGTC CCG		
	_____ _____		
GAM330 BACH2	TGGGCAGGCG-GGGTGGCGAGGGC 5073 _ C C AI		
	TGGGC GGCG GGG GGCGAGGGC		
	ACCG CGC CCC CCGCTCCCG		
	T _ A II		
GAM330 BCL11A	GCGGGGCGGGCGGCGGCGGC 5017 T C G AG		
	GGGCGG GCGG CGGCG GGC		
	CCCGCC CGCC GCCGC CCG		
	_____ CG		
GAM330 BMP1	GGCGGGGCGG-CGGCGAGGG 5039 TG C GCG C		
	GG GGC GGCGGCGAGGG		
	CC CCG CCGCGCTCCC		
	G_ _ _ T		
GAM330 BTEB1	CGACGCGGGTGGCGAGGGC 5011 TGGGCGGC C		
	GCGGG GGCGAGGGC		
	CGCCC CCGCTCCCG		
	_____ A		
GAM330 CAPN7	GGCGGCCCGGCGGCGGCGAGG 5024 TGGG G _ A		
	CGGC CGG GCGGCGAGGGC		
	GCCG GCC CGCCGCTCCTG		
	_____ G GC I		
GAM330 CD81	GGCGGCGCGGGCGGCGGGCGGC 5032 TGGG GA A		
	CGGCGCGGGCGGC GGGC		

		GCCGCGCCCCGCG CCGG			
		_____ C			
GAM330 CDK2AP1		GGCGGCGGCGGCGGCGAGG	5035 TG	GCG	GC
		GGCGGC GGCGGCGAGG			
		CCGCCG CCGCCGCTCC			
		G_ _____ GG			
GAM330 CREBBP		GGGCGGC-CGGGCCGGCGAGGGC	5058 TG	G _	A
		GGCGGC CGGGC GGCGAGGGC			
		CCGCCG GCCCG CCGCTCCCG			
		_____ G G			
GAM330 CSNK2A2		GGGCGGCGCGGGGCGCAGAGGG	5053 TG	CG _	CA
		GGCGGCGCGGG GC GAGGG			
		CCGCCGCGCCC CG CTCCC			
		_____ CG T AI			
GAM330 DLK1		GGGGGCGCGGGCGCGCAGCGAGGG	5027 T _	C G	CAI
		GG GCGG GCG GCGGCGAGGG			
		CC CGCC CGC CGTCGCTCCC			
		C G _ G CTI			
GAM330 DUSP7		TGGGGAGCGCGGGCGGCCCGGG	5077 C	GA	CA
		TGGG GGCGCGGGCGGC GGG			
		ACCC TCGCGCCCGCCG CCC			
		C GG II			
GAM330 DVL3		GGCGGCGC--GCGGCGCGG	5034 TG	G _	GAGGG
		GGCG CGCGG GCGGC			
		CCGC GCGCC CGCCG			
		G_ _ G GIIIA			
GAM330 FASN		GGCGGTGCGGGCGGCGGAGAGC	5030 TGGG	C _	A
		CGG GCGGGCGGCG AGGGC			
		GCC CGCCCGCCGC TCTCG			
		_____ A C C			
GAM330 FKBP1A		GGGCGGCGCGACGGGCGGCGTGG	5049 TG	_____	A CAI
		GGCGGCGC GGGCGGCG GGG			
		CCGCCGCG CCCGCCGC CCT			
		_____ CTG A III			
GAM330 FOXG1B		GGGGGGCGGCGGGCGGC-AGCGGC	5051 T C _	G _	AI
		GGG GGCG CGGGCGGC AG GGC			
		CCC CCGC GCCCGCCG TC CCG			
		_____ C _ G CI			
GAM330 FOXG1B		GGCGGCGCGGG-AGCG-GGACA	5042 TGGG	C A	
		CGGCGCGGG GGCG GGGC			

GCCGCGCCC TCGC CCTG

GAM330 FOXG1B	GGCG-CGCGGGCGGCGCGG	5033 TGGGCG	AG
	GCGCGGGCGGCG GG		
	CGCGCCCGCCGC CC		
	G_____ G_		
GAM330 G6PD	GGGCGGGGCGGG--GCGAGGGCA	5069 TG C CG	
	GGCGG GCGGG GCGAGGGCA		
	CCGCC CGCCC CGCTCCCGT		
	_____ C _____		
GAM330 GAD2	GCGGGGCCGAGCGGCGAGGGC	5014 TGGGC G A	
	GGC CGGGCGGCGAGGGC		
	CCG GCTCGCCGCTCCCG		
	C_____ _ C		
GAM330 GATA2	GGCCGCGCGGGCGGCTCAGGG	5060 TG G G_ CA	
	G CGGCGCGGGCGGC AGGG		
	C GCCGCGCCCGCCG TCCC		
	___ G AG AI		
GAM330 GPC1	GGCGGCGCGGGGCGCGCGGG	5037 TGGG _ _ A C	
	CGGCGCGGG CG GCG GGG		
	GCCGCGCCC GC CGC CCC		
	_____ C G _ A		
GAM330 GRB14	TGGGGCGCGCGGGCGGCGAGG	5076 T_ G GCA	
	GGGCG CGCGGGCGGCGAGG		
	CCCGC GCGCCGCGCTCC		
	AC _		
GAM330 GTF2IRD1	GGACGGCG-GCGCGGCGAGGGC	5065 TG_ GGGC A	
	GGCGGCGC GCGAGGGC		
	CCGCCGCG CCGCTCCCG		
	CTG _____ C		
GAM330 GTF2IRD1	GGGCGGCGCGG--GGAGAGG	5061 TG C C	
	GGCGGCGCGGG GG GAGGG		
	CCGCCGCGCCC CT CTCCT		
	_____ _		
GAM330 GTF2IRD1	CGGCGCGGGCTGCGGCGGAGGGC	5009 TGG C GG _ AI	
	GCGG GC GCGGCG AGGGC		
	CGCC CG CGCCGC TCCCG		
	_____ _ A_ C CC		
GAM330 HDAC4	TGGGAGGCTGTTCGGGCGGCGGCGGC	5074 C G_ AG AI	
	TGGG GGC CGGGCGGCG GGC		

	ACCC CCG GCCCGCCGC CCG		
	T ACAA CG III		
GAM330 HDAC4	GGGCTCGGGCTCGGGCGGCGA 5047 TG ____ G	GGGCA	
	GGC GGC CGGGCGGCGA		
	III III IIIIIIIII		
	CCG CCG GCCCGCCGCT		
	__ AGC A GIIIA		
GAM330 HDAC4	GGCGGCGCGGGCGGGTGC GCGGGC 5028 TGGG	__ A AI	
	CGGCGCGGGCG GCG GGGC		
	IIIIIIII III III		
	GCCGCGCCCGC CGC CCCG		
	____ CCA G AG		
GAM330 HDAC5	GGCTTCGCGGGCGGCGGCGGCA 5046 TGGGCGG	AG	
	CGCGGGCGGCG GGCA		
	IIIIIIII III		
	GCGCCCGCCGC CCGT		
	GAA____ CG		
GAM330 HSF4	TGCGCAGGCGCGGGCAGTGC GCGC 5072 G _	__ AGG AI	
	TG GC GGCGCGGGCG GCG GC		
	II IIIIIIIII III II		
	AC CG CCGCGCCCGT CGC CG		
	G T CA G__ II		
GAM330 IGFBP4	GGCGGCGGGGGGCGGCGAGGG 5025 TG CGC	_ A	
	GGCGG GGGCGGCGAGGG C		
	IIII IIIIIIIII I		
	CCGCC CCCGCCGCTCCC G		
	G_ C__ CI		
GAM330 JAG2	GGCGGCGCGGGCGGGGTGAGCGCA 5029 TGGG	__ G II	
	CGGCGCGGGCGG CGAG GCA		
	IIIIIIII III III		
	GCCGCGCCCGCC GCTC CGT		
	____ CCA G CG		
GAM330 JAG2	TGGGCG--GCGGGCGTGCAGGGGC 5075 GC	_ A A	
	TGGGCGGC GGGCG GCG GGGC		
	IIIIII IIII III III		
	ACCCGCCG CCCGC CGT CCCG		
	__ A C I		
GAM330 LBX1	TGGGCAGGGCGCGGGCCGGCGCGGG 5071	__ _ A CAII	
	TGGGC GGCGCGGGC GGCG GGG		
	IIII IIIIIII III III		
	ACCCG CCGCGCCCG CCGC CCC		
	TC G G IIIA		
GAM330 LBX1	GGACGGCGCGGGCCAGGC-AGCGGC 5057 TG	__ G _ AI	
	GGCGGCGCGGGC GGC AG GGC		
	IIIIIIII III II III		
	CTGCCGCGCCCG CCG TC CCG		
	__ GT _ G CI		
GAM330 MADH3	GGGCGT-GCGGGCGGCGAGG 5062 TG GC	C	
	GGCG GCGGGCGGCGAGGG		
	III IIIIIIIIIII		

	CCGC CGCCCGCCGCTCCT		
	__ A_ I		
GAM330 MAF	GGGCGTCTGTCCGGGCGGCGCGGGC 5048 TG	GCG__	A All
	GGCG CGGGCGGCG GGGC		
	CCGC GCCCGCCGC CCCG		
	__ AGACAG G GII		
GAM330 MAF	GGGCGGCGCGGGCCTTGGCACGGG 5056 TG	__	A CAI
	GGCGGCGCGGGC GGCG GGG		
	CCGCCGCGCCCG CCGT CCC		
	__ GAA G CII		
GAM330 MAFF	GGGCGGCGCAGGGGGCCGAGG 5052 TG	C GA	A
	GGCGGCGCGGG GGC GGGC		
	CCGCCGCGTCC CCG TCCG		
	__ C GC I		
GAM330 MAP4K2	GGGCGGCGCGGGGCGGGGCGGGC 5054 TG	_ CGA	AI
	GGCGGCGCGGG CGG GGGC		
	CCGCCGCGCCC GCC CCCG		
	__ C CCG CI		
GAM330 MAP4K2	CGGCGCGGGGCGGCGCGGG 5008 T__	_	CGAGGGC
	GGGCGGCGCGGG CGG		
	CCCGCCGCGCCC GCC		
	CGC C IIIACGG		
GAM330 MET	GGGCGCCGCGGGCGGCGAGGGC 5066 TG	G	A
	GGCG CGCGGGCGGCGAGGGC		
	CCGC GCGCCCGCCGCTCCCG		
	__ G I		
GAM330 MSI1	GGGAGCCGCGGGCGGCGCGGGCA 5068 T	GG	A I
	GGGC CGCGGGCGGCG GGGCA		
	CTCG GCGCCCGCCGC CCCGT		
	C __ G C		
GAM330 MSI1	GGGCGGCGCGGGCAGCGGAGCGGC 5059 TG	__	AI
	GGCGGCGCGGGCGGCG AG GGC		
	CCGCCGCGCCCGTCGC TC CCG		
	__ C G CI		
GAM330 NFATC2	GCGGGGCGGGGGCGAGGGC 5016 TGGGC	G C	
	GGC CGGG GGCGAGGGC		
	CCG GCCC CCGCTCCCG		
	C__ _ _		
GAM330 PABPC4	CGG-GCGGGCGGCGAAGGGCA 5010 T	C_	AGGGC
	GGGCGGCG GGGCGGCG		

	CCCGCCGC CCCGTCGT			
	G TT GIIIA			
GAM330 PABPC4	GGTGGCACCGGCGCGGCGAGG 5022 TGGGC	_ _		A
	GGCGC GG GCGGCGAGGGC			
	CCGTG CC CGCCGCTCCTG			
	A_ G G I			
GAM330 PDXK	GGCGGCGCGGGGCCGAGGCGGGGGCA 5023 TGGG	_ _	A	II
	CGGCGCGGG C GGCG GGGCA			
	GCCGCGCCC G CCGC CCCGT			
	C GCT C GC			
GAM330 PK428	GGCGGCGCGGGCGGCTCTGGCA 5044 TGGG		GAG	
	CGGCGCGGGCGGC GGCA			
	GCCGCGCCCCGCG CCGT			
	AGA			
GAM330 PK428	GGCGGGCTGCGGGCGGCACTGGCA 5020 T GGC		AG	I
	GGGC GCGGGCGGCG GGCA			
	CCCG CGCCCGCCGT CCGT			
	G A_ GA G			
GAM330 PLCD1	GGGCGGCGC-GGCGG-GAGGG 5064 TG		G C C	
	GGCGGCGCGG CGG GAGGG			
	CCGCCGCGCC GCC CTCCC			
	C			
GAM330 SCN8A	GGCAGCGGCGGCGGCGAGGG 5036 TG	GCG		C
	GGCGGC GGCGGCGAGGG			
	TCGCCG CCGCCGCTCCC			
	G_ T			
GAM330 SLBP	GGCGGCGCGGGCAGAGAGCGCA 5043 TGGG		C G	
	CGGCGCGGGCGG GAG GCA			
	GCCGCGCCCGTC CTC CGT			
	T G			
GAM330 SLC6A8	GGCGCGGGCCGGCCGGGGGC 5018 T G	G C GA C		
	GG CGGC CGGG GGC GGG			
	CC GCCG GCCC CCG CCC			
	C G _ _ G_ C			
GAM330 SLC6A8	GCGGCTCGGGCGGCGGCGGC 5015	GCG	GAGG	
	TGGGCGGC GGCGGC GC			
	GCCCGCCG CCGCCG CG			
	CGA A_			
GAM330 SRM	GGGCGG-GCGGGCGGCGCGGG 5063 TG	C	A C	
	GGCGG GCGGGCGGCG GGG			

	CCGCC CGCCCGCCGC CCC			
	— — G C			
GAM330 SRM	GGGCGGCGCGG--GGCGCGGGC 5067 TG	CG	A	
	GGCGGCGCGGG GCG GGGC			
	CCGCCGCGCCC CGC CCCG			
	— — G			
GAM330 TFAP4	GGCGGCGGCGGCGGCGAGGG 5038 TG	GCG		C
	GGCGGC GGCGGCGAGGG			
	CCGCCG CCGCCGCTCCC			
	G_ — C			
GAM330 TFDP1	GGGCGGCGCGGAGAGGCGCGGGC 5055 TG	_C	A	AI
	GGCGGCGCGG G GGCG GGGC			
	CCGCCGCGCC C CCGC CCCG			
	— T T G AI			
GAM330 THBS1	GGTGGCGAGGGCGGCGAGGGC 5041 TGGGC	C		A
	GGCG GGGCGGCGAGGGC			
	CCGC CCCGCCGCTCCCG			
	A — T A			
GAM330 ZNF219	GGCGGAGCGGGCGGCGGCGGC 5040 TGGG	C	AG	A
	CGG GCGGGCGGCG GGC			
	GCC CGCCCGCCGC CCG			
	— T CG C			
GAM331 ADRA2A	GGCCGCA-GGGAGGCCGGGCCCG 5092 TG	T	C_	C
	GCCGTG GGGA CCGGGCCCG			
	CGGCGT CCCT GGCCCGGGC			
	— — CC T			
GAM331 AIM1	TGGCCGTGTGCG--CTGCGCC 5101	GGACCCGG		G
	TGGCCGTGTG GCCC			
	ACCGGCACAC CGGG			
	GCGACG_ I			
GAM331 AIRE	TGGGCGCG-GGGACCCGGG 5099	C	T	CCC
	TGG CGTG GGGACCCGGG			
	ACC GCGC CCCTGGGCCC			
	C _			
GAM331 ALPL	GGGCTTGTGGGTGCCCGGGCCC 5091	T	CG	A_ GC
	GGC TGTGGG CCGGGGCC			
	CCG ACACCC GGGCCCGGG			
	_ A_ AC AI			
GAM331 ARSB	GCCGCCTCCGACCCGGGCCC 5084 TG	GTGTGG		G
	GCC GACCCGGGCCC			

	CGG CTGGGCCCGGG			
	G_ AGG_ G			
GAM331 BCAT1	TGGCCGTGT-GGA-CCGGGTCTGC	5103	AC	CCC
	TGGCCGTGTGGG CCGGG GC			
	ACCGGCACACCT GGCCC CG			
	_ AGA			
GAM331 CELSR1	GCCGTGTGGCAACCGTGCCC	5085	TGGC	_ CGG G
	CGTGTGG GACC GCCC			
	GCACACC TTGG CGGG			
	_ G CA_ G			
GAM331 CHRNA4	GGCCGCTTCGGCCGCCGGGCCCG	5093	TG	GTG AC_ CI
	GCCGT GG CCGGGCCCG			
	CGGCG CC GGCCCGGGC			
	_ AAG GGC CI			
GAM331 CLTB	GCCGCG-GGGAGCCGGGCCCG	5086	TGGC	T C
	CGTG GGA CCGGGCCCG			
	GCGC CCCT GGCCCGGGC			
	_ _ C			
GAM331 DIA1	TGGCCGTGT--GACCGGTGCCCG	5102	GAC	_ C
	TGGCCGTGTGG CCGG GCCCG			
	ACCGGCACACT GGCC CGGGC			
	_ A I			
GAM331 DXYS155E	TGTGGGACCTCCGGGACCG	5104	TG	GTG C CCCG
	GCC TGGGACC GGG			
	TGG GCCCTGG CCC			
	_ AG_ _ ACAC			
GAM331 FGFR1	GCCCTGCGGAGGCCCGGGGCCCGC	5082	TGG	_ TG A I
	CC GTG GG CCCGGGGCCCGC			
	GG CGC CC GGGCCCGGGCG			
	_ A CT G C			
GAM331 FHIT	TGGCCGCCTGAGGGACCCGGG	5097	G_	CCCGC
	TGGCCGT T GGGACCCGGG			
	ACCGGCG A CCCTGGGCC			
	G CT CG			
GAM331 GNA11	GGCCGAGCGGGGACCCGGCGGCTCGC	5090	TG	T _ _ C
	GCCG GTGGG ACCCGG GC CGC			
	CGGC CGCCC TGGGCC CG GCG			
	_ T C GC A GI			
GAM331 HPN	GGCCAGGGTGGGACCCTGG	5087	TG	T_ _ CCCG
	GCCG GTGGGACCC GGG			

	CGGT CACCCTGGG CCC		
	___ CC A IIIC		
GAM331 IRS2	GGTCCTGTGGGACCCCCGCC 5094 TGG G GG CG		
	CC TGTGGGACCC GCC		
	GG ACACCCTGGG CGG		
	CA_ _ GG TI		
GAM331 IRS2	GGCCGCGCGG--CCCGGGCCCC 5096 TG GA		
	GCCGTGTGG CCCGGGCCCCG		
	CGGCGCGCC GGGCCCGGGC		
	___ _		
GAM331 MSF	CCG-GCGGGGCCCGGGCCC 5080 TGGCCGT A		
	GTGGG CCCGGGCCC		
	CGCCC GGGCCCGGG		
	___ C		
GAM331 NEK4	GGCTGTTGAGGCAGCCGGGCCCG 5088 TG C GT AC_ CI		
	GC GT GGG CCGGGCCCCG		
	CG CA TCC GGCCCGGGC		
	___ A AC GTC CI		
GAM331 NFRKB	GGCCGTGACGGCGGCTCCGGGCCCG 5089 TG _ _ AC CII		
	GCCGTG TGG G CCGGGCCCCG		
	CGGCAC GCC C GGCCCGGGC		
	___ T GC GA CII		
GAM331 PAFAH1B1	TGGC-GCGCTGGG-CCCGGGCCCCG 5098 _ G A C		
	TGGC CGT TGGG CCCGGGCCCCG		
	ACCG GCG ACCC GGGCCCGGGC		
	C _ _ I		
GAM331 SLC25A13	TGGC-GTTTGGGACCCGGGC 5100 C G CCG		
	TGGC GT TGGGACCCGGGC		
	ACCG CA ACCCTGGGCCCG		
	_ A		
GAM331 SMURF1	GCCGTGTGGCACACACCTGGC 5083 TGGC G _ G CCGC		
	CGTGTGG AC CC GGC		
	GCACACC TG GG CCG		
	___ G TGT A ACII		
GAM331 TBX1	GGCAGGGTGG--CCGGGCCCG 5095 TG CGT GAC		
	GC GTGG CCGGGCCCCG		
	CG CACC GGCCCGGGC		
	_ TCC _		
GAM331 ZNF9	CCGCGTCGGAGC-GGGCCCCG 5081 TGGCCGT G CC		
	GT GGA CCGGCCCG		

	CA CCT GCCCGGGC		
	G_____ G C_		
GAM332 AKAP2	GGCAGAGCTGTGCGCACGGC 5117	C G I	
	GCGGAGCTGTGC CA GG		
	CGTCTCGACACG GT CC		
	C G I		
GAM332 AKAP2	GGCAGAGCTGTGCGCACGGC 5117 TG	C G TG	
	GCGGAGCTGTGC CA GGC		
	CGTCTCGACACG GT CCG		
	_____ C G CI		
GAM332 FRAT2	CGGAGCTGTGC---GGGCT 5107	CCA	
	CGGAGCTGTGC GGGC		
	GCCTCGACACG CCCG		

GAM332 FRAT2	CGGAGCTGTGC---GGGCT 5107 TGGCGG	CCA	
	AGCTGTGC GGGC		
	TCGACACG CCCG		

GAM332 GGT2	TGGAAGAGGCGAGCCCAGGGCAGC 5122	C C T T I	
	TGG GGAG TG GCCCAGGGC GC		
	ACC TCTC GC CGGGTCCCG CG		
	T C T T I		
GAM332 GGT2	TGGAAGAGGCGAGCCCAGGGCAGC 5122	C C T TGI	
	GG GGAG TG GCCCAGGGC		
	CC TCTC GC CGGGTCCCG		
	T C T TCI		
GAM332 LOXL1	GGCAGGGGCGGTGCCAGGGCTGC 5114	GC A T I	
	GG GC GTGCCAGGGCTG		
	CC CG CACGGGTCCCGAC		
	GT C C I		
GAM332 LOXL1	GGCAGGGGCGGTGCCAGGGCTGC 5114 TG	A_ T I	
	GCGG GC GTGCCAGGGCTGC		
	CGTC CG CACGGGTCCCGACG		
	_____ CC C T		
GAM332 MARK3	TGGCGGAGCCGAGCCTGCGGGCGGC 5121	T CA_ T II	
	TGGCGGAGCTG GCC GGGC GC		
	ACCGCCTCGGC CGG CCCG CG		
	T ACG C II		
GAM332 MARK3	TGGCGGAGCCGAGCCTGCGGGCGGC 5121	T CA_ TGI	
	GCGGAGCTG GCC GGGC		

	CGCCTCGGC CGG CCCG			
	T ACG CII			
GAM332 OXTR	GCGGAGCTGGTTGCCCCAGCGTTG	5109 GG	___	GGCTI
	AGCTG TGCCAG			
	TCGAC GCGGGTC			
	___ CAA GCAII			
GAM332 OXTR	GCGGAGCTGGTTGCCCCAGCGTTG	5109 TGGC	___	GGCTGCI
	GGAGCTG TGCCAG			
	CCTCGAC GCGGGTC			
	___ CAA GCAACCA			
GAM332 P2RX7	GCGGAGCTG-GACCAGAGCT	5112_	TG C	I
	CGGAGCTG CC AGGGC			
	GCCTCGAC GG TCTCG			
	C CT _ I			
GAM332 P2RX7	GCGGAGCTG-GACCAGAGCT	5112 TGGC	TG C	G
	GGAGCTG CC AGGGCT			
	CCTCGAC GG TCTCGA			
	___ CT _ G			
GAM332 PIM2	GCGCAGCTGGGGAGCCAGGGCTG	5111 CGG	TGC___	I
	AGCTG CCAGGGCT			
	TCGAC GGTCCCGA			
	G___ CCCTC I			
GAM332 RBBP9	GCGGAGCTGAGCCCA-GCCTGC	5113_	T G G	I
	CGGAGCTG GCCCA G CTG			
	I			
	GCCTCGAC CGGGT C GAC			
	C T _ G I			
GAM332 RBBP9	GCGGAGCTGAGCCCA-GCCTGC	5113 TGGC	T G G	
	GGAGCTG GCCCA G CTGC			
	I			
	CCTCGAC CGGGT C GACG			
	___ T _ G			
GAM332 SLC1A2	GAGCGATGCGCCCAGGGCTGC	5108	___	III
	GAGC TGTGCCAGGGCTG			
	CTCG ACGCGGGTCCCGAC			
	CT GII			
GAM332 SLC1A2	GAGCGATGCGCCCAGGGCTGC	5108 TGGCGGAGC		
	TGTGCCAGGGCTGC			
	ACGCGGGTCCCGACG			
	T_____			
GAM332 SLC22A12	TGGCGG-CTGTGGGATGCCAGGGCTGC	5120	GA C___	II
	TGGCG GCTGTG CCAGGGCTGC			

	ACCGC CGACAC GGTCCCGACG	
	___ CCTAC II	
GAM332 SLC22A12	TGGCGG-CTGTGGGATGCCAGGGCTGC5120_ GGAGCT C I	
	GGC GTGCC AGGGCTG	
	III IIII IIIII	
	CCG TACGG TCCCGAC	
	G ACACCC _ I	
GAM332 SYN1	GGCGGACTGCGCGGTGCCAGG 5115 ___ T IIIC	
	GGCGGA GC GTGCCAG	
	IIII II IIIII	
	CCGCCT CG CACGGGTC	
	GACG C CII	
GAM332 SYN1	GGCGGACTGCGCGGTGCCAGG 5115 TG ___ T CTGC	
	GCGGA GC GTGCCAGGG	
	IIII II IIIII	
	CGCCT CG CACGGGTCCT	
	___ GACG C IIIC	
GAM332 TADA2L	TGGTAGAGCTACGCGCTCCAGGGCTG 5119 CG _ _ CII	
	TGG GAGCT GTGC CCAGGGCTG	
	III IIII III IIIII	
	ACC CTCGA CGCG GGTCCCGAC	
	AT TG A III	
GAM332 TADA2L	TGGTAGAGCTACGCGCTCCAGGGCTG 5119 GGC _ _ I	
	GGAGCT GTGC CCAGGGCT	
	IIII III IIIII	
	TCTCGA CGCG GGTCCCGA	
	___ TG A I	
GAM332 TIRAP	TGGCAGAGCAACTG-GCACAGGGCTGC5118 ___ T C II	
	TGGCGGAGC TG GC CAGGGCTGC	
	IIIIII II II IIIII	
	ACCGTCTCG AC CG GTCCCGACG	
	TTG _ T II	
GAM332 TIRAP	TGGCAGAGCAACTG-GCACAGGGCTGC5118 GG ___ T C I	
	CGGAGC TG GC CAGGGCTG	
	IIII II II IIIII	
	GTCTCG AC CG GTCCCGAC	
	___ TTG _ T I	
GAM332 TRPC6	GGCAGACCGGTGCCAGGG 5116 G _ II	
	GGCGGA CTG TGCCAGG	
	IIII III IIIII	
	CCGTCT GGC ACGGGTCC	
	_ C CI	
GAM332 TRPC6	GGCAGACCGGTGCCAGGG 5116 TG G _ CTG	
	GCGGA CTG TGCCAGGG	
	IIII III IIIII	
	CGTCT GGC ACGGGTCCC	
	___ _ C CII	
GAM332 UNG	GCGGA-CAGTAAGAGCCCAGGGCTG 5110_ AGCTGT I	
	CGG GCCCAGGGCT	
	III IIIIIII	

	GTC CGGGTCCCGA	
	T ATTCT_ I	
GAM332 UNG	GCGGA-CAGTAAGAGCCCCAGGGCTG 5110 T AGCTGT CI	
	GGCGG GCCCAGGGCTG	
	CTGTC CGGGTCCCGAC	
	C ATTCT_ CC	
GAM333 CASP8	CCAGCTA---AAAACATTCTCA 5127 GCCT TGA	
	GCTA AAAACATTCTCA	
	CGAT TTTTGTAAGAGT	
	GT_ _	
GAM333 DCK	CCTGCTATGAGAAATAATGTC 5126 GC AAAACATTCTCAC	
	CTGCTATGA	
	GACGATACT	
	_ CTTTATTACAGAI	
GAM333 EYA1	GCTGTGCTAAAACATTCTCA 5132 GCC TGAA	
	TGCTA AAACATTCTCA	
	ACGAT TTTGTAAGAGT	
	_ _	
GAM333 F11	TGTTATGTAA--CATTCTC 5133 GCCTGC AAA	
	TATG AACATTCTC	
	ATAC TTGTAAGAG	
	_ _ A_	
GAM333 MAP3K9	GCCT-CT-TGGCGAACATTCTC 5131 G A AAA A	
	GCCT CT TG AACATTCTC	
	CGGA GA AC TTGTAAGAG	
	_ _ CGC I	
GAM333 PSMB2	CCTGTCTCTATGAAAAACA 5125 GC_ G TCTCA	
	CT CTATGAAAAACAT	
	GA GATACTTTTTGTG	
	GACA _ CA	
GAM333 SYT4	TGATATCAAACACATTCTCA 5134 GCCTGC G A	
	TAT AAA ACATTCTCA	
	ATA TTT TGTAAGAGT	
	_ _ G G	
GAM333 TEM5	CTGCTA-GAAA-ACATTCT 5128 GCCT T A C	
	GCTA GAAAA CATTCT	
	CGAT CTTTT GTAAGA	
	_ _ _ T	
GAM333 ZNF132	CTTCTAC-AGAAACATTCT 5129 GC TATGAA C	
	CTGC AAACATTCT	

		GATG TTTGTAAGA		
		A_ TC_____ C		
GAM333 ZNF133		GCCTG-TAACACAAAACATTC	5130	CT A TCA
		GCCTG ATG AAAACATTC		
		CGGAC TGT TTTTGTAAAG		
		AT G		
GAM334 B3GALT2		ATTGTCTCTCTTGTAGTCA	5137 TA	CTTTCGCCACCT
		TTGTCTCTC		
		AACAGAGAG		
		____ AACATCAGTAII		
GAM334 CEP1		GTCTCTCCTTCCTCTGGCCAC	5139 TATTG TC	C CTC
		TC TCCTTT GCCAC		
		AG AGGAGA CGGTG		
		G_____ GA C TAC		
GAM334 FKRP		TTGTCTCTCCAGTCCCCAC	5143 TATT	TT G CT
		GTCTCTCC TC CCAC		
		CAGAGAGG AG GGTG		
		_____ TC G TT		
GAM334 GAB2		TTGTCTCT-CTATTGCTAGCCTC	5142 TATT	CT C CA_
		GTCTCTC TT GC CCTC		
		CAGAGAG AA CG GGAG		
		_____ AT _ ATC		
GAM334 HYAL3		TCTCACTCAGTCGCCACCTC	5140 TATTGTCT	CTT
		CTC TCGCCACCT		
		GAG AGCGGTGGA		
		_____ TC_		
GAM334 IHPK3		TTGTCTCTCAGTGC-CCACC	5144 TATT	CTTTCG T
		GTCTCTC CCACC		
		CAGAGAG GGTGG		
		_____ TCACG_ T		
GAM334 MECP2		GTCTCTCCTCCTCGCCTCCTC	5138 TATTGTCT	_ A
		CTCCTT TCGCC CCTC		
		GAGGAG AGCGG GGAG		
		_____ G A		
GAM334 ZIC1		TCTCTCCTTTCTCTCACGCTC	5141 TATTG	CT_ ACCTC
		TCTCTC TTCGCC		
		AGAGAG GAGCGG		
		GGAA_ TGC AG		
GAM335 ACHE		GGGAGGGGAGGACGGCACGA	5156	CA I
		GGAGGGGAGGGC CACG		

	CCTCCCCTCCTG GTGC		
	CC I		
GAM335 ACHE	GGGAGGGGAGGACGGCACGA 5156 TG	CA	TG
	GGAGGGGAGGGC CACGA		
	CCTCCCCTCCTG GTGCT		
	CC CI		
GAM335 BCL7A	GGAGGGGAGAG-CACAGCGAGTGC 5151	C _	TGI
	AGGGGAGGGC ACA CGA		
	TCCCCTCTCG TGT GCT		
	C CAI		
GAM335 BCL7A	GGAGGGGAGAG-CACAGCGAGTGC 5151 TGGG	C _ _	I
	AGGGGAGGGC ACA CGA TGC		
	TCCCCTCTCG TGT GCT ACG		
	C C G		
GAM335 CELSR1	GGCGGGGAGGGCCACACCAT 5150 GA	_	GAI
	GGGGAGGGCC ACAC		
	CCCCTCCCGG TGTG		
	G_ G GTI		
GAM335 CELSR1	GGCGGGGAGGGCCACACCAT 5150 TGGGA	_	G GC
	GGGGAGGGCC ACAC AT		
	CCCCTCCCGG TGTG TA		
	G_ G G GG		
GAM335 CNTN2	TGGGAGCAGGCAGGGCCACA 5158	_ _	CGATG
	TGGGAG GGG AGGGCCACA		
	ACCCTC TCC TCCCGGTGT		
	G G IIICG		
GAM335 CNTN2	TGGGAGCAGGCAGGGCCACA 5158	_ _	III
	TGGGAG GGG AGGGCCAC		
	ACCCTC TCC TCCCGGTG		
	G G TII		
GAM335 CRHR2	GGGAGGGGA---CACAGGA 5154	GGGC	C
	GGGAGGGGA CACA		
	CCCTCCCCT GTGT		
	C		
GAM335 CRHR2	GGGAGGGGA---CACAGGA 5154 TG	GGGC	C
	GGAGGGGA CACA GA		
	CCTCCCCT GTGT CT		
	C		
GAM335 DRPLA	GGGAGGGGCAGGGGTGGCACACGATGC5153 _ _	AG	C I
	GG AGGGG GGC ACACGATG		

	CC TCCCC CCG TGTGCTAC		
	C G A_ _ I		
GAM335 DRPLA	GGGAGGGGGCAGGGGTGGCACACGATGC5153 TG	_ C___	III
	GGAGGGG AGGG CACACGATGC		
	CCTCCCC TCCC GTGTGCTACG		
	_ G CACC AII		
GAM335 GFPT2	GGAGGGATGTGGGCCACAC 5148 A__		III
	GGAGGGG GGGCCACA		
	CCTCCCT CCCGGTGT		
	ACA GII		
GAM335 GFPT2	GGAGGGATGTGGGCCACAC 5148 T GGGGA		ATG
	GGGA GGGCCACACG		
	CCCT CCCGGTGTGT		
	T ACA__ GII		
GAM335 KIAA0857	GGGAGGGGAAGACAGCAGGA 5155	CA CGI	
	GGAGGGGAGGGC CA		
	CCTCCCCTTCTG GT		
	TC CCI		
GAM335 KIAA0857	GGGAGGGGAAGACAGCAGGA 5155 TG	CA C TG	
	GGAGGGGAGGGC CA GA		
	CCTCCCCTTCTG GT CT		
	_ TC C TI		
GAM335 KIAA0857	TGGGAGGGGGACGCCACAC 5160 A _		GATG
	TGGGAGGGG GG GCCACAC		
	ACCCTCCCC CT CGGTGTG		
	_ G IIIC		
GAM335 KIAA0857	TGGGAGGGGGACGCCACAC 5160 A _		II
	TGGGAGGGG GG GCCACA		
	ACCCTCCCC CT CGGTGT		
	_ G GI		
GAM335 MEF2D	GGGAGGGGGAGGGGCCATTAGATG 5152 GA		CAC I
	G GGGGAGGGCCA GAT		
	I		
	C CCCCTCCCGGT CTA		
	TC AAT I		
GAM335 MEF2D	GGGAGGGGGAGGGGCCATTAGATG 5152 T GA		CAC CI
	GG GGGGAGGGCCA GATG		
	CC CCCCTCCCGGT CTAC		
	_ TC AAT TI		
GAM335 MTM1	GGGAGGGGAAGCCAACACCAT 5157	G _	GAI
	GGAGGGGAGG CCA CAC		

	CCTCCCCTTC GGT GTG		
	_ T GTI		
GAM335 MTM1	GGGAGGGGAAGCCAACACCAT	5157 TG	G _ G GC
	GGAGGGGAGG CCA CAC AT		
	CCTCCCCTTC GGT GTG TA		
	_ _ T G AI		
GAM335 SOX13	TGGGAGGGGTGTTGGTCCCACA	5159	A__ G_ IIIT
	TGGGAGGGG GG CCAC		
	ACCCTCCCC CC GGTG		
	ACAA AG TIII		
GAM335 SOX13	TGGGAGGGGTGTTGGTCCCACA	5159	AG__ _ A ATGC
	TGGGAGGGG GG CC CACG		
	ACCCTCCCC CC GG GTGT		
	ACAA A _ IIIC		
GAM335 STIM1	GGAGGTTTGGGGGCCACACGCTG	5149 GAGG A	AI
	GG GGGCCACACG		
	CC CCCGGTGTGC		
	CAAA _ GA		
GAM335 STIM1	GGAGGTTTGGGGGCCACACGCTG	5149 T AGG A	AT_ I
	GGG GG GGGCCACACG GC		
	TCC CC CCCGGTGTGC CG		
	_ AAA _ GAC I		
GAM335 TLR9	AGGGGAGGGTCAGACCAGGC	5147	C C GATGI
	GGGGAGGG CA AC		
	CCCCTCCC GT TG		
	A C GTCCI		
GAM335 TLR9	AGGGGAGGGTCAGACCAGGC	5147 TGG	GA CA ATG
	GAGGG GGGCCA CG		
	CTCCC TCTGGT GT		
	_ AG CC CCG		
GAM336 AMPD1	TAGCACAGT---AGAAAAGA	5174	TGTC C T
	TAGCACAGT AGA AAGA		
	ATCGTGTCA TCT TTCT		
	_ T I		
GAM336 AMPD1	TAGCACAGT---AGAAAAGA	5174	TGTC_ CAI
	TAGCACAGT AGA		
	ATCGTGTCA TCT		
	TCTTT		
GAM336 B4GALT5	CACAGCAATCAAAGACAAGATT	5168 AC T _	I
	AGT GTCA GACAAGAT		

	TCG TAGT CTGTTCTA	
	___ T TT I	
GAM336 B4GALT5	CACAGCAATCAAAGACAAGATT 5168 TAGCAC T ___ C	
	AGT GTCA GACAAGATT	
	TCG TAGT CTGTTCTAA	
	_____ T TT T	
GAM336 EIF4A2	AGCA---TTG--AGACAAGATTC 5167_ CAG TC	
	GCA TTG AGACAAGAT	
	CGT AAC TCTGTTCTA	
	T _____	
GAM336 EIF4A2	AGCA---TTG--AGACAAGATTC 5167 TAGCACA TC	
	GTTG AGACAAGAT	
	TAAC TCTGTTCTA	
	CG_____	
GAM336 EN2	AGCACAGTTGTAAATAGA-AACATTC 5165 C CA TTI	
	ACAGTTGT AGA AGA	
	TGTCAACA TTT TCT	
	_ A_ TTG	
GAM336 EN2	AGCACAGTTGTAAATAGA-AACATTC 5165 TA C___ C G II	
	GCACAGTTGT AGA AA ATTC	
	CGTGTCAACA TCT TT TAAG	
	_____ TTTA _ G TI	
GAM336 HSD17B1	TATCACAGTTGTC---CATGCTTC 5175 AG AGACAAI	
	CACAGTTGTC	
	GTGTCAACAG	
	A_ GTACGAA	
GAM336 HSD17B1	TATCACAGTTGTC---CATGCTTC 5175 TAG AGACAAGATTC	
	CACAGTTGTC	
	GTGTCAACAG	
	ATA GTACGAAGIII	
GAM336 IFNG	CACAGTTGTCA-ACAATATT 5171_ A GATI	
	ACAGTTGTCAG CAA	
	TGTCAACAGTT GTT	
	G _ ATAI	
GAM336 IFNG	CACAGTTGTCA-ACAATATT 5171 TAGCAC A G	
	AGTTGTCAG CAA ATT	
	TCAACAGTT GTT TAA	
	_____ _ A	
GAM336 M11S1	CACAGTTGTTTGCCAGAT 5169 _____ CAAGAI	
	CACAGTTGT CAGA	

	GTGTCAACA GTCT		
	AACCG AIIIAGA		
GAM336 MCF2	TAGCACAG-TGGCAG-CAA 5173	TT A GAT	
	TAGCACAGT G CAG CAA		
	I		
	ATCGTGTCA C GTC GTT		
	C _ _		
GAM336 MCF2	TAGCACAG-TGGCAG-CAA 5173	TT A I	
	TAGCACAGT G CAG CA		
	I		
	ATCGTGTCA C GTC GT		
	C _ _ T		
GAM336 MOCS2	AGCACAGTTCT-TCACAAGAATTC 5166	G_ AG TTI	
	GCACAGTT TC ACAAGA		
	CGTGTCAA AG TGTTCT		
	GA _ TAA		
GAM336 MOCS2	AGCACAGTTCT-TCACAAGAATTC 5166 TA	G_ AG TTCI	
	GCACAGTT TC ACAAGA		
	CGTGTCAA AG TGTTCT		
	_ GA _ TAAG		
GAM336 PLAC1	AGCACTTATTTGTCAGACA 5164	AG_	
	AGCAC TTGTCAGAC		
	TCGTG AACAGTCTG		
	AATA TII		
GAM336 PLAC1	AGCACTTATTTGTCAGACA 5164 TA	AG_ AGATT	
	GCAC TTGTCAGACA		
	CGTG AACAGTCTGT		
	_ AATA AIIIC		
GAM336 RDX	CACATTTGTCAGACGTGAT 5170	G AAGAI	
	CACA TTGTCAGAC		
	GTGT AACAGTCTG		
	A CACTAI		
GAM336 RDX	CACATTTGTCAGACGTGAT 5170 TAGCACAG	AA T	
	TTGTCAGAC GAT		
	AACAGTCTG CTA		
	TA_ CA T		
GAM336 SLC7A9	AGCAGCAG----CAGACAAGA 5163	GCA T T	
	CAGT G CAGACAAG		
	I		
	GTCG C GTCTGTTC		
	TC_ T_		
GAM336 SLC7A9	AGCAGCAG----CAGACAAGA 5163 TAGCA	T T	
	CAGT G CAGACAAGAT		
	I		

		GTCTGTTCTG			
		C_____ T_			
GAM336 STAU	CAGTC-TCAGACAAGTTTC	5172	G	ATTI	
	CAGTT TCAGACAAG				
	GTCAG AGTCTGTTC				
	_____ AAAG				
GAM337 ALCAM	TAACAGCAA--CTCCCAGAACAAA	5196		GT AG	
	TAACAGCAAT TC GGAACAAA				
	ATTGTCGTTG AG TCTTGTTT				
	_____ GG				
GAM337 ALCAM	TAACAGCAA--CTCCCAGAACAAA	5196	_____	GT AG	I
	AACAGCAAT TC GGAACAA				
	TTGTCGTTG AG TCTTGTT				
	A _____ GG I				
GAM337 ATP1A2	ACAGGAAGGTTTCAGGGAAC	5186	C T	II	
	ACAG AA GTTCAGGGAA				
	TGTC TT CAAGTCCCTT				
	C C GI				
GAM337 ATP1A2	ACAGGAAGGTTTCAGGGAAC	5186	TAACAGCAAT	AA	
	GTTCAGGGAAC				
	CAAGTCCCTTG				
	TCCTTC_____ AA				
GAM337 CDC23	AAAAGCA---TTCAGGGAAGAA	5181	C_____	ATG	CI
	AGCA TTCAGGGAA				
	TCGT AAGTCCCTT				
	TTT _____ CI				
GAM337 CDC23	AAAAGCA---TTCAGGGAAGAA	5181	TAAC	ATG	CAA
	AGCA TTCAGGGAA				
	TCGT AAGTCCCTT				
	TT_____ CTT				
GAM337 CLASP1	TAACAGCAAAGCATCA-GCAACA	5193		T TCA G	AA
	TAACAGCAA GT GG AACA				
	ATTGTCGTT CG TC TTGT				
	T TAG G II				
GAM337 CLASP1	TAACAGCAAAGCATCA-GCAACA	5193	T _____	G ACI	
	AACAGCAA GT TCAG GA				
	TTGTCGTT CG AGTC TT				
	T T G GII				
GAM337 FLNB	AACAGCAATATTTTAGGGA	5178	C_____	II	
	AACAGCAATGTT AGGG				

	TTGTCGTTATAA TCCC			
	AA TI			
GAM337 FLNB	AACAGCAATATTTTAGGGA 5178 TA	C_	ACAA	
	ACAGCAATGTT AGGGA			
	TGTCGTTATAA TCCCT			
	___ AA A			
GAM337 GJB3	CAGCGAAAATGTTTCAGGGAA 5187 ___			
	CAGC AATGTTTCAGGGGA			
	GTCG TTACAAGTCCCT			
	CTT T			
GAM337 GJB3	CAGCGAAAATGTTTCAGGGAA 5187 TAACAGC		CAA	
	AATGTTTCAGGGAA			
	TTACAAGTCCCTT			
	GCTT___ TTA			
GAM337 GTF2E2	TAACAG-AAGGTTAACAGGGAACA 5194	C T ___	AAI	
	TAACAG AA GTT CAGGGAACA			
	ATTGTC TT CAA GTCCCTTGT			
	_ C TT			
GAM337 GTF2E2	TAACAG-AAGGTTAACAGGGAACA 5194 A	C T ___	I	
	ACAG AA GTT CAGGGAAC			
	TGTC TT CAA GTCCCTTG			
	_ _ C TT I			
GAM337 HNF3B	AACAGCAATG--GAGGAGAACAA 5180 _	TTC _	I	
	ACAGCAATG AGG GAACA			
	TGTCGTTAC TCC CTTGT			
	T C_ T I			
GAM337 HNF3B	AACAGCAATG--GAGGAGAACAA 5180 TA	TTC _	A	
	ACAGCAATG AGG GAACAA			
	TGTCGTTAC TCC CTTGTT			
	___ C_ T G			
GAM337 IL12RB2	ACAGCCAT---CAGGGAAC 5185 AATGT			
	ACAGC TCAGGGAA			
	TGTCG AGTCCCTT			
	GT___			
GAM337 IL12RB2	ACAGCCAT---CAGGGAAC 5185 TAAC AATGT			
	AGC TCAGGGAA			
	TCG AGTCCCTTG			
	___ GT___			
GAM337 MCF2	CAGCAATGTTGGGAGGAAAAAA 5189 A	CA	ACAAI	
	GCAATGTT GGGA			

	CGTTACAA CCCT			
	— CCTTT			
GAM337 MCF2	CAGCAATGTTGGGAGGAAAAAA	5189	TAACAG	CA ACAAA
	CAATGTT GGG			
	GTTACAA CCCT			
	— CCTTT			
GAM337 NLGN3	CAGCAATGT--AGAGAGCA	5190	TC	ACI
	CAGCAATGT AGGGA			
	GTCGTTACA TCTCT			
	— CGT			
GAM337 NLGN3	CAGCAATGT--AGAGAGCA	5190	TAACAG	TC A
	CAATGT AGGGA CA			
	GTTACA TCTCT GT			
	— C			
GAM337 NPTX2	AACAG-AATATTGGTAGGGAACAAA	5179	A C	C__ I
	CAG AATGTT AGGGAACAA			
	GTC TTATAA TCCCTTGTT			
	— CCA I			
GAM337 NPTX2	AACAG-AATATTGGTAGGGAACAAA	5179	TA C	C__ I
	ACAG AATGTT AGGGAACAAA			
	TGTC TTATAA TCCCTTGTTT			
	— CCA G			
GAM337 PPP2R4	TAAAAGCAATGGACAGTTCAGGGA	5192	C	_____ ACAA
	TAA AGCAAT GTTCAGGGA			
	ATT TCGTTA CAAGTCCCT			
	T CCTGT IIIAA			
GAM337 PPP2R4	TAAAAGCAATGGACAGTTCAGGGA	5192	C	_____ IIIT
	TAA AGCAAT GTTCAGGG			
	ATT TCGTTA CAAGTCCC			
	T CCTGT TIII			
GAM337 PPP2R4	AACAGCAATG---AGGGTGCAA	5182	TTC	AAI
	AACAGCAATG AGGG			
	TTGTCGTTAC TCCC			
	— ACG			
GAM337 PPP2R4	AACAGCAATG---AGGGTGCAA	5182	TA	TTC AA
	ACAGCAATG AGGG CAA			
	TGTCGTTAC TCCC GTT			
	— AC			
GAM337 PTPRN	ACAG--ATGTTTCAGGGAAC	5184	CA	I
	ACAG ATGTTTCAGGGAA			

	TGTC TACAAGTCCCTT		
	— G		
GAM337 PTPRN	ACAG--ATGTTTCAGGGAAC 5184 TAACAGCA A		
	ATGTTTCAGGGAAC		
	TACAAGTCCCTTG		
	TC— A		
GAM337 RNPEP	AACAGGAAT-TT--GGGAACAAA 5183 C GTTCA I		
	AACAG AAT GGGAACA		
	TTGTC TTA CCCTTGT		
	C AA— T		
GAM337 RNPEP	CAGGAAGTTGATCAGGGAACA 5188 CAGCAA— T III		
	TG TCAGGGAAC		
	AC AGTCCCTTG		
	GTCCTTCA T TII		
GAM337 RNPEP	CAGGAAGTTGATCAGGGAACA 5188 TAACAGCAA T AA		
	TG TCAGGGAACA		
	AC AGTCCCTTGT		
	CTTCA— T CC		
GAM337 ZFX	TAA-AGCACAGCTCAGGGAACA 5195 AAC AT I		
	AGCA GTTCAGGGAAC		
	TCGT CGAGTCCCTTG		
	ATT GT I		
GAM337 ZFX	TAA-AGCACAGCTCAGGGAACA 5195 TAAC AT AA		
	AGCA GTTCAGGGAACA		
	TCGT CGAGTCCCTTGT		
	ATT_ GT II		
GAM337 ZNF215	GCAATGGT--GGGAACAAA 5191 TTCA I		
	GCAATG GGGAACAA		
	CGTTAC CCCTTGTT		
	CA— T		
GAM338 APOD	AGTGGGTGCA-GCCTCCCTG 5206 _ _ CAT I		
	GTGGG GC GCCTCCCT		
	CACCC CG CGGAGGGA		
	T A T— I		
GAM338 APOD	AGTGGGTGCA-GCCTCCCTG 5206 TACAAGT G CAT		
	GG GC GCCTCCCT		
	CC CG CGGAGGGA		
	— A T—		
GAM338 ATP2B2	AGTGGGGCCCATGCTGCTCCCTG 5204 GT G _ I		
	GGG CCATGC CTCCCT		

	CCC GGTACG GAGGGA	
	___ G AC I	
GAM338 ATP2B2	AGTGGGGCCCATGCTGCTCCCTG 5204 TACAAGT G ___ I	
	GGG CCATGC CTCCCTG	
	CCC GGTACG GAGGGAC	
	_____ G AC C	
GAM338 ATP2B4	ACCAGTGTCTCC-TGCCTCCCTG 5202 CA_ GGG A I	
	AGTG CC TGCCTCCCT	
	TCAC GG ACGGAGGGA	
	TGG AGA _ I	
GAM338 ATP2B4	ACCAGTGTCTCC-TGCCTCCCTG 5202 TACA GGG A	
	AGTG CC TGCCTCCCTG	
	TCAC GG ACGGAGGGAC	
	GG_ AGA _	
GAM338 CALM1	TACCAGTGGGGCCACGTCTC 5211 A C CCT	
	TAC AGTGGGGCCATG CTC	
	ATG TCACCCCGGTGC GAG	
	G A	
GAM338 CALM1	TACCAGTGGGGCCACGTCTC 5211 A C I	
	AC AGTGGGGCCATG CT	
	TG TCACCCCGGTGC GA	
	G A I	
GAM338 CD79B	TGGAGGCCAGGGCCTCCCTG 5212 _ T_	
	TGG GGCCA GCCTCCCT	
	ACC CCGGT CGGAGGGA	
	T CC C	
GAM338 GAB2	ACAAGCTGTCAGCCATGCCT 5199 GG_	
	ACAAGT GGCCATGCC	
	TGTTTCG TCGGTACGG	
	ACAG A	
GAM338 GAB2	ACAAGCTGTCAGCCATGCCT 5199 TA GG_ CCCT	
	CAAGT GGCCATGCCT	
	GTTCG TCGGTACGGA	
	_ ACAG C	
GAM338 KCNQ1	CAGGTGGGGCCACTCTTGGCCTCCC 5207 TACAA _____ G	
	GTGGGGCCAT GCCTCCCT	
	CACCCCGGTG CGGAGGGG	
	C_ AGAAC A	
GAM338 NUMA1	ACAGGTGGGGCCA---CTCACTG 5201 A GC_ CCI	
	ACA GTGGGGCCAT CT	

	TGT CACCCCGGTG GA		
	C AGT CII		
GAM338 NUMA1	ACAGGTGGGGCCA---CTCACTG	5201 TA A	TGC C
	CA GTGGGGCCA CTC CT		
	II IIIIIII III II		
	GT CACCCCGGT GAG GA		
	__ C __ T		
GAM338 PTPRO	CATGTGTGGCCATGCCTCC	5208 CAA G	II
	GTG GGCCATGCCTC		
	III IIIIIIIII		
	CAC CCGGTACGGAG		
	GTA A GI		
GAM338 PTPRO	CATGTGTGGCCATGCCTCC	5208 TACAA G	CT
	GTG GGCCATGCCTCC		
	III IIIIIIIII		
	CAC CCGGTACGGAGG		
	A__ A AA		
GAM338 RNASE1	GTGGAGCTTCCATGCCTCCCTG	5209 __	III
	GTGGGGC CATGCCTCCCT		
	IIIIII IIIIIIIII		
	CACCTCG GTACGGAGGGA		
	AAG CII		
GAM338 RNASE1	GTGGAGCTTCCATGCCTCCCTG	5209 TACAAGTGGGG	
	CCATGCCTCCCTG		
	IIIIIIIIII		
	GGTACGGAGGGAC		
	CGAA_____		
GAM338 RNMT	GTGGCTCCAGTAAGCCTCCCTG	5210 GG T__	III
	GTGG CCA GCCTCCCT		
	III III IIIIIII		
	CACC GGT CGGAGGGA		
	GA CATT CII		
GAM338 SURF5	AGTGGA---AGGCCTCCCTG	5205 _ CCAT	
	GTGGGG GCCTCCCT		
	IIIIII IIIIIII		
	CACCTT CGGAGGGA		
	T C__		
GAM338 TM7SF2	AGTGGGGGCCATGGTCTCC	5203 _ C_ III	
	AGTGGGG CCATG CTC		
	IIIIII IIIII III		
	TCACCCC GGTAC GAG		
	C CA GII		
GAM338 TM7SF2	AGTGGGGGCCATGGTCTCC	5203 TACAAGT	C_ _
	GGGGCCATG CTCC CT		
	IIIIII IIIII II		
	CCCCGGTAC GAGG GA		
	_____ CA C		
GAM338 TNNC2	ACAAG--GGGCCGCGCCTCCCTG	5200 CAAGT	A I
	GGGGCC TGCCTCCCT		
	IIIIII IIIIIII		

	CCCCGG GCGGAGGGA	
	TGTT_ C I	
GAM338 TNNC2	ACAAG--GGGCCGCGCCTCCCTG 5200 TACAAGT A	
	GGGGCC TGCCTCCCTG	
	CCCCGG GCGGAGGGAC	
	GTT____ C	
GAM339 C4BPB	TCACTCAGAAGCAA-CAGC 5217 TTAA I	
	TCACTCAGA AGCAG	
	AGTGAGTCT TTGTC	
	TCG_ G	
GAM339 ITGA4	TATCAAGAGCCACAGATTAAA 5215 TCA_ _ GCAGC	
	TATCA CT CAGATTAAA	
	ATAGT GG GTCTAATTT	
	TCTC T IIICG	
GAM339 ITGA4	TATCAAGAGCCACAGATTAAA 5215 TCA_ _ III	
	TATCA CT CAGATTAA	
	ATAGT GG GTCTAATT	
	TCTC T TII	
GAM339 KRTHA7	TCCTCAGCTCA--TTAAAGCA 5218 CA A _ I	
	TC CTCAG ATTAAAGC	
	AG GAGTC TAATTTTCG	
	_ _ GAG I	
GAM339 NOS1	TATCATCACTGAAACGAATTAGCAG 5216 AT C T _ I	
	CATCACT AGAT AA AGCA	
	GTAGTGA TTTG TT TCGT	
	_ C C AA I	
GAM339 NOS1	TATCATCACTGAAACGAATTAGCAG 5216 C T _ CII	
	TATCATCACT AGAT AA AGCAG	
	ATAGTAGTGA TTTG TT TCGTC	
	C C AA III	
GAM339 USH3A	TCCTCAC--AGCACTAAAGCAGC 5219 CA_ TC _ I	
	TCAC AG ATTAAAGCAG	
	AGTG TC TGATTTTCGTC	
	AGG _ G I	
GAM339 USH3A	TCCTCAC--AGCACTAAAGCAGC 5219 TATCA TC _	
	TCAC AG ATTAAAGCAGC	
	AGTG TC TGATTTTCGTCG	
	G____ _ G	
GAM340 ADAMTS8	ATCGGGTGCAAGGCCGA-CTCGG 5222 TATG _ G G	
	GGGTGCAAG TCGA TTCGG	

	CCCACGTTC GGCT GAGCC	
	AG__ C _ G	
GAM340 ADAMTS8	ATCGGGTGCAAGGCCGA-CTCGG 5222 TG _ G I	
	GGGTGCAAG TCGA TTCG	
	CCCACGTTC GGCT GAGC	
	AG C _ I	
GAM340 EPHA1	TGGGGTGCAAGCAGGGTTC 5227 AGTC TII	
	TGGGGTGCA GAGT	
	ACCCACGT CTCG	
	_____ TCC	
GAM340 EPHA1	TGGGGTGCAAGCAGGGTTC 5227 TATG AGTC TC	
	GGGTGCA GAGT GG	
	CCCACGT CTCG CC	
	_____ T_	
GAM340 LARGE	GGTGCCAAGCACAGAGTTCGGG 5224 _ C__ III	
	GGTGC AAGT GAGTTCGG	
	CCACG TTCG CTCAAGCC	
	G TGT CII	
GAM340 LARGE	GGTGCCAAGCACAGAGTTCGGG 5224 TATG TG AGTC	
	GGG CA GAGTTCGGG	
	TTC GT CTCAAGCCC	
	G__ GT _____	
GAM340 PDE4D	TATAAGGTGCAAGTAAAATTC 5225 C GGG	
	TATGGGGTGCAAGT GAGTTC	
	ATATTCCACGTTCA TTAAAG	
	T III	
GAM340 PDE4D	TATAAGGTGCAAGTAAAATTC 5225 C I	
	ATGGGGTGCAAGT GAGTT	
	TATTCCACGTTCA TTAA	
	T I	
GAM340 PPARGC1	ATGGGGTGCA---CGTGTTC 5223 A CGAGTI	
	ATGGGGTGCA GT	
	TACCCACGT CA	
	G CAAGII	
GAM340 PPARGC1	ATGGGGTGCA---CGTGTTC 5223 TA AGT A	
	TGGGGTGCA CG GTTCG	
	ACCCACGT GC CAAGT	
	_____ A	
GAM340 SHANK2	TATGGGGTGAGG--GACTCCGGG 5226 CA TC G	
	TATGGGGTG AG GA TTCGGG	

	ATACCCAC TC CT AGGCC	
	C_ C_ G	
GAM340 SHANK2	TATGGGGTGGAGG--GACTCCGGG 5226_ CA TC G I	
	ATGGGGTG AG GA TTCGG	
	TACCCAC TC CT AGGCC	
	A C_ C_ G I	
GAM341 ACK1	GAAAACATGGAACCGCGTGG 5240 _ TCTTGII	
	GAAAACATGGA CC	
	CTTTTGTACCT GG	
	T CGCACCI	
GAM341 ACK1	GAAAACATGGAACCGCGTGG 5240 TG _ TCT AAG	
	AAAACATGGA CC TGG	
	TTTTGTACCT GG ACC	
	_ T CGC CII	
GAM341 ADA	TGAGATCATGGTCTTCTTGGAAGG 5247 AAA ACC I	
	TGA CATGG TCTTGGAAGG	
	ACT GTACC AGAACCTTCC	
	CTA AGA I	
GAM341 ADA	TGAGATCATGGTCTTCTTGGAAGG 5247 GAAAA ACC I	
	CATGG TCTTGGAAG	
	GTACC AGAACCTTC	
	CTCTA AGA I	
GAM341 ADAMTS1	AACTATAGTCCTTCTTGGAAGG 5236 AC A _ I	
	ATGG CCT CTTGGAAG	
	TATC GGA GAACCTTC	
	A_ A A I	
GAM341 ADAMTS1	AACTATAGTCCTTCTTGGAAGG 5236 TGAAAAC A _	
	ATGG CCT CTTGGAAGG	
	TATC GGA GAACCTTCC	
	_ A A	
GAM341 COL15A1	GAAAACATGAAGGACATCTT 5239 _ C	
	GAAAACAT GGAC TCT	
	CTTTTGTA CCTG AGA	
	CTT T AII	
GAM341 COL15A1	GAAAACATGAAGGACATCTT 5239 TG _ C GAAG	
	AAAACAT GGAC TCTTG	
	TTTTGTA CCTG AGAAT	
	_ CTT T IIIG	
GAM341 ITGB4BP	CATGGAACAACCTTGGAAGG 5238 _ CT II	
	CATGGA C CTTGGAAG	

	GTACCT G GAACCTTC		
	T TT CI		
GAM341 KCNK10	TGATCACATGGACC-CTTG 5244 AA T GAA		
	TGA ACATGGACC CTTG		
	ACT TGTACCTGG GAAC		
	AG _		
GAM341 KCNK10	TGATCACATGGACC-CTTG 5244 AA CTTI		
	TGA ACATGGACCT		
	ACT TGTACCTGGG		
	AG AACI		
GAM341 KCNS2	TGAAACACAAAAGGACCTCTTAAGAAG5242 _ T_ _ G		
	TGAAA ACA GGACCTCTTG GAAG		
	ACTTT TGT CCTGGAGAAT CTTC		
	G TTT T G		
GAM341 KCNS2	TGAAACACAAAAGGACCTCTTAAGAAG5242 GAAA T_ _ I		
	ACA GGACCTCTTG GAA		
	TGT CCTGGAGAAT CTT		
	G_ TTT T I		
GAM341 LNK	AAAAATTTGACCTCTTGGA 5232 AAAACATG II		
	GACCTCTTGGA		
	CTGGAGAACC		
	TTTTTAAA TI		
GAM341 LNK	AAAAATTTGACCTCTTGGA 5232 TGAAAACATG AG		
	GACCTCTTGGA		
	CTGGAGAACCT		
	TTTAAA_ CG		
GAM341 MBL2	TGAAAACATTGACTTTTACAAG 5246 G CTC G GI		
	TGAAAACAT GAC TTG AAG		
	ACTTTTGTA CTG AAT TTC		
	A AAA G II		
GAM341 MBL2	TGAAAACATTGACTTTTACAAG 5246 G CTCTTGGAII		
	GAAAACAT GAC		
	CTTTTGTA CTG		
	A AAAATGTTI		
GAM341 MLLT4	GAAAACAT-GACC-CTTGAAA 5241 G T I		
	GAAAACATG ACC CTTGG		
	CTTTGTAC TGG GAACT		
	_ _ T		
GAM341 MLLT4	GAAAACAT-GACC-CTTGAAA 5241 TG G T G		
	AAAACATG ACC CTTGGAA		

	TTTTGTAC TGG GAACTTT	
	— — — A	
GAM341 PSG11	TGAAAACATTATCCTTTTG 5243	GGA C GAAG
	TGAAAACAT CCT TTG	
	ACTTTTGTA GGA AAC	
	ATA A IIIG	
GAM341 PSG11	TGAAAACATTATCCTTTTG 5243	GGA CTTII
	TGAAAACAT CCT	
	ACTTTTGTA GGA	
	ATA AAACI	
GAM341 PSG9	TGAAAACATTATCCTTTTG 5243	GGA C GAAG
	TGAAAACAT CCT TTG	
	ACTTTTGTA GGA AAC	
	ATA A IIIG	
GAM341 PSG9	TGAAAACATTATCCTTTTG 5243	GGA CTTII
	TGAAAACAT CCT	
	ACTTTTGTA GGA	
	ATA AAACI	
GAM341 RAG1	AAAAAAAGG--CTCTTGGAAG 5233	AAACAT_ AC I
	GG CTCTTGGAAG	
	CC GAGAACCTT	
	TTTTTTT _ I	
GAM341 RAG1	AAAAAAAGG--CTCTTGGAAG 5233	TGAAAACAT AC
	GG CTCTTGGAAG	
	CC GAGAACCTTC	
	TTTTT _ _	
GAM341 RFC1	AAAACATGGTTGCTCTGGGAA 5230	A AC_ T I
	AACATGG CTCT GGA	
	TTGTACC GAGA CCT	
	_ AAC C I	
GAM341 RFC1	AAAACATGGTTGCTCTGGGAA 5230	TGAA AC_ T
	AACATGG CTCT GGAAGG	
	TTGTACC GAGA CCTTTT	
	_ AAC C	
GAM341 ROBO1	TGAAAACATTAATCACATGGA 5245	GGACCTCT AGG
	TGAAAACAT TGGA	
	ACTTTTGTA ACCT	
	ATTAGTGT III	
GAM341 SH2D1A	AAAAAAAGG--CTCTTGGAAG 5233	AAACAT_ AC I
	GG CTCTTGGAAG	

	CC GAGAACCTT		
	TTTTTT _ I		
GAM341 SH2D1A	AAAAAAAGG--CTCTTGGAAG 5233 TGAAAACAT AC		
	GG CTCTTGGAAG		
	II		
	CC GAGAACCTTC		
	TTTTT _ _		
GAM341 SLC13A1	AAAACATGGGCTTCTTGATGAAGG 5231 AA ACC _ I		
	ACATGG TCTTG GAAG		
	TGTACC AGAAC CTTC		
	_ CGA TA I		
GAM341 SLC13A1	AAAACATGGGCTTCTTGATGAAGG 5231 TGAA ACC _ I		
	AACATGG TCTTG GAAGG		
	TTGTACC AGAAC CTTC		
	_ CGA TA G		
GAM341 TRIM34	AAACATGGATAAATGGGAAGG 5235 CCTCTT I		
	AACATGGA GGAAG		
	TTGTACCT CCTTC		
	ATTAC I		
GAM341 TRIM34	AAACATGGATAAATGGGAAGG 5235 TGAAAA CCTCTT		
	CATGGA GGAAGG		
	GTACCT CCTTC		
	_ ATTTAC		
GAM341 TRPM2	AAACATGGAGGCCCTCTTGG 5234 _ III		
	AAACATGGA CCTCTTG		
	TTGTACCT GGAGAAC		
	CCG CII		
GAM341 TRPM2	AAACATGGAGGCCCTCTTGG 5234 TGAAAA _ AAG		
	CATGGA CCTCTTGG		
	GTACCT GGAGAACC		
	_ CCG CCT		
GAM341 WISP1	ACA-GTACCTCTTGGCAGG 5237 TGG AAGI		
	ACA ACCTCTTGG		
	TGT TGGAGAACC		
	CA_ GTCC		
GAM342 ATP5J	AGAAGCCAAACAGGAGGAGGA 5256 _ AGIII		
	AGAAGCCAA GGGGGGA		
	TCTTCGGTT TCCTCCT		
	TG CCTII		
GAM342 ATP5J	AGAAGCCAAACAGGAGGAGGA 5256 TGAG _ AGTT		
	AAGCCAA GGGGGGAAG		

		TTCGGTT TCCTCCTTC		
		____ TGTCC IIIT		
GAM342 BCL9		AGAAACTGAGGGGGGAA-AGT 5259 _ CA AGI		
		GAAGC AGGGGGGAAG		
		CTTTG TCCCCCCTTT		
		T AC CII		
GAM342 BCL9		AGAAACTGAGGGGGGAA-AGT 5259 TGAG CA A		
		AAGC AGGGGGGA GAGT		
		TTTG TCCCCCCT TTCA		
		____ AC _		
GAM342 CHRN4		TGGGAAGCCCTGGG-GGAAGAG 5282 A AAG TT		
		TG GAAGCC GGGGGAAGAG		
		AC CTTCGG CCCCCTTCTC		
		C GA_ II		
GAM342 CHRN4		TGGGAAGCCCTGGG-GGAAGAG 5282 _ A AAG I		
		G GAAGCC GGGGGAAGA		
		C CTTCGG CCCCCTTCT		
		A C GA_ I		
GAM342 CISH		GAGAAGCCA----GGGCAGAGTT 5267 A G AGI		
		GAGAAGCCA GGG GGA		
		CTCTTCGGT CCC TCT		
		_ G CAA		
GAM342 CISH		GAGAAGCCA----GGGCAGAGTT 5267 TG A G AGAGT		
		AGAAGCCA GGG GGA		
		TCTTCGGT CCC TCT		
		_ _ G CAACI		
GAM342 COL1A1		TGAGAAGCCAGAGGCAGGTGGAGAG 5273 _ G AA TTII		
		TGAGAAGCCA AGG GGG GAG		
		ACTCTTCGGT TCC TCC CTC		
		C G AC TCII		
GAM342 COL1A1		TGAGAAGCCAGAGGCAGGTGGAGAG 5273 G _ G AAGAI		
		AAGCCA AGG GGG		
		TTCGGT TCC TCC		
		_ C G ACCTI		
GAM342 CR1		AAACTAAGGGGGGAAAAGT 5251 C II		
		AAGC AAGGGGGGAAGAG		
		TTTG TTCCCCCCTTTTC		
		A AI		
GAM342 CR1		AAACTAAGGGGGGAAAAGT 5251 TGAGAAGCC		
		AAGGGGGGAAGAGT		

		TTCCCCCCTTTTCA	
		A_____	
GAM342 DBY	AAGC--AGGAGGGGAAGAGTT	5250 _ CA _ I	
	AGC AGG GGGGAAGAGT		
	TCG TCC CCCCTTCTCA		
	T _ T I		
GAM342 DGKB	AAGGAAATTGGGGAAGAGTT	5252 AGCCAAGG I	
	GGGGAAGAGT		
	CCCCTTCTCA		
	TCCTTTAA I		
GAM342 DGKB	AAGGAAATTGGGGAAGAGTT	5252 TGAGAAGCCAAGG	
	GGGGAAGAGT		
	CCCCTTCTCA		
	TTTAA_____		
GAM342 DHCR24	TGAGATCCCAGGGTGGGGAAGAG	5275 AG A _ TTI	
	TGAGA CCA GG GGGGAAGAG		
	ACTCT GGT CC CCCCTTCTC		
	AG C A		
GAM342 DHCR24	TGAGATCCCAGGGTGGGGAAGAG	5275 G AG A _ I	
	AGA CCA GG GGGGAAGA		
	TCT GGT CC CCCCTTCT		
	_ AG C A I		
GAM342 DSCR5	TGGGGAGCCGCAGTGGGGAAGAG	5274 GAGA A_ G I	
	AGCC AG GGGGAAGA		
	TCGG TC CCCCTTCT		
	CCC_ CG A I		
GAM342 DSCR5	TGGGGAGCCGCAGTGGGGAAGAG	5274 TGAGA A_ G TTI	
	AGCC AG GGGGAAGAG		
	TCGG TC CCCCTTCTC		
	ACCC CG A		
GAM342 EGR3	TGGGGACCCGAGGTGGGGAAGAGTT	5276 GA AG A _ I	
	GA CC AGG GGGGAAGAGT		
	CT GG TCC CCCCTTCTCA		
	CC G_ C A I		
GAM342 EGR3	TGGGGACCCGAGGTGGGGAAGAGTT	5276 TGA_ AG A _ II	
	GA CC AGG GGGGAAGAGTT		
	CT GG TCC CCCCTTCTCAA		
	ACCC G_ C A II		
GAM342 FGF5	GAGAAGGGGAGAGGGGAAGAG	5265 CCA I	
	AGAAG AGGGGGGAAGA		

	TCTTC TCTCCCCTTCT			
	CCC I			
GAM342 FGF5	GAGAAGGGGAGAGGGGAAGAG 5265 TG CCA TT			
	AGAAG AGGGGGGAAGAG			
	TCTTC TCTCCCCTTCTC			
	__ CCC TI			
GAM342 FOSB	TGAGGGGGCCAAGGGGTGGGAGAAGTT 5277 AA __ AG II			
	TGAG GCCAAGGGG GGA AGTT			
	ACTC CGGTTCCCC CCT TCAA			
	CC AC CT II			
GAM342 FOSB	TGAGGGGGCCAAGGGGTGGGAGAAGTT 5277 AGAA _ A TI			
	GCCAAGGGG GG AGAG			
	CGGTTCCCC CC TCTT			
	CCC_ A C CI			
GAM342 GDI2	GCGAAGGAAAGGGGAAGAG 5269 C __ III			
	GC AAGG GGGGAAGA			
	CG TTCC CCCCTTCT			
	C TTT CII			
GAM342 GDI2	GCGAAGGAAAGGGGAAGAG 5269 TGAGAAGCCA T			
	AGGGGGGAAGAG			
	TTTCCCCTTCTC			
	C_____ T			
GAM342 GJA5	TGAACAGCCAAGGGAGAAAG 5279 A AGT			
	TGAG AGCCAAGGGGGGAAG			
	ACTT TCGGTTCCCTCTTTC			
	G III			
GAM342 GJA5	TGAACAGCCAAGGGAGAAAG 5279 A I			
	GAG AGCCAAGGGGGGAAG			
	CTT TCGGTTCCCTCTTT			
	G I			
GAM342 HD	TGACAGGCACATGGGGGAAGAG 5281 GA C AG_ TT			
	TGA AG CA GGGGAAGAG			
	ACT TC GT CCCCCTTCTC			
	G_ C GTA II			
GAM342 HD	TGACAGGCACATGGGGGAAGAG 5281 GAGA C AG_ I			
	AG CA GGGGAAGA			
	TC GT CCCCCTTCT			
	CTG_ C GTA I			
GAM342 HOXA4	TGAGCTGCCTTAATGGGGGAAGAG 5272 AA AAG_ TTI			
	TGAG GCC GGGGAAGAG			

	ACTC CGG CCCCTTCTC		
	GA AATTA III		
GAM342 HOXA4	TGAGCTGCCTTAATGGGGGAAGAG 5272 GAGAA AAG__ I		
	GCC GGGGGAAGA		
	III		
	CGG CCCCTTCT		
	CGA__ AATTA I		
GAM342 MAP1A	GAGAAGCCAAGCAGGGGATGAG 5263 A _ A I		
	GAAGCCAAG GGGGGA GA		
	II		
	CTTCGGTTC TCCCCT CT		
	_ G A I		
GAM342 MAP1A	GAGAAGCCAAGCAGGGGATGAG 5263 TG _ A TT		
	AGAAGCCAAG GGGGGA GAG		
	III		
	TCTTCGGTTC TCCCCT CTC		
	_ G A TI		
GAM342 MAPK14	GAGAAGCCAAAGTGGCAAAAG 5264 _ G AI		
	AGAAGCCAAGG GG GAAG		
	TCTTCGGTTTC CC TTTT		
	A G II		
GAM342 MAPK14	GAGAAGCCAAAGTGGCAAAAG 5264 TG G G T		
	AGAAGCCAAGG GG AAGAGT		
	TCTTCGGTTTC CC TTTTCG		
	_ A G I		
GAM342 MYCL2	TGAGAAGCCAAAGGTGCCAGA 5280 GGGA GTT		
	TGAGAAGCCAAGGG AGA		
	III		
	ACTCTTCGGTTTCC TCT		
	ACGG III		
GAM342 MYCL2	TGAGAAGCCAAAGGTGCCAGA 5280 GGGAAGI		
	GAGAAGCCAAGGG		
	CTCTTCGGTTTCC		
	ACGGTCI		
GAM342 NDP	TGAGA-GCCAAGGGGGAAA 5278 A GAG		
	TGAGA GCCAAGGGGGGAA		
	ACTCT CGGTTCCCCCTTT		
	_ III		
GAM342 NDP	TGAGA-GCCAAGGGGGAAA 5278 A I		
	TGAGA GCCAAGGGGGGA		
	ACTCT CGGTTCCCCCTT		
	_ T		
GAM342 NESH	GAAGCCAAGGTCGGGGCAG 5261 _ AAIII		
	GAAGCCAAGG GGGG		

	CTTCGGTTCC CCCC			
	AG GTCII			
GAM342 NESH	GAAGCCAAGGTCGGGGCAG	5261	TGAGAA	___ A AGT
	GCCAAGG GGGG AG			
	CGGTTCC CCCC TC			
	_____ AG G GAC			
GAM342 NONO	GAGAGGTGAAAGGGGGAAGAG	5266	AGCC	I
	AGA AAGGGGGGAAGA			
	TCT TTTCCCCCTTCT			
	CCAC I			
GAM342 NONO	GAGAGGTGAAAGGGGGAAGAG	5266	T AAGCC	TT
	GAG AAGGGGGGAAGAG			
	CTC TTTCCCCCTTCTC			
	T CAC___ TI			
GAM342 NRG1	AGATGC-AAGGGGGGAAGA	5258	A C	I
	AGA GC AAGGGGGGAAG			
	TCT CG TTCCCCCCTTC			
	A _ T			
GAM342 NRG1	AGATGC-AAGGGGGGAAGA	5258	TGAGAA C	
	GC AAGGGGGGAAGAG			
	CG TTCCCCCCTTCTT			
	TA_____			
GAM342 PABPN1	TGAGCAGGCCCAAGGGGGTGAAG	5271	AA_ _ _	AGTTI
	TGAG GCC AAGGGGG GAAG			
	ACTC CGG TTCCCCC CTTC			
	GTC G A IIIT			
GAM342 PABPN1	TGAGCAGGCCCAAGGGGGTGAAG	5271	GAGAAG	_ I
	CCAAGGGGG GAA			
	GGTTCCCCC CTT			
	GTCCG_ A I			
GAM342 PAK1	TGAGAGTCCAAGGGGGGAAGGCGT	5283	AG	G A TI
	TGAGA CCAAGGGGG AAG GT			
	ACTCT GGTTCCTTTC CG			
	CA _ _ CA			
GAM342 PAK1	TGAGAGTCCAAGGGGGGAAGGCGT	5283	AG	AGAGI
	GAGA CCAAGGGGGGA			
	CTCT GGTTCCTTTC			
	CA CCGCI			
GAM342 RECQL5	GAGAAGCCAAAGCGCTGGGAA	5262	_____	
	GAGAAGCCAAAGG GGGGA			

	CTCTTCGGTTTC CCCTT		
	GCGA III		
GAM342 RECQL5	GAGAAGCCAAAGCGCTGGGA 5262 TG	G__	GAGTT
	AGAAGCCAAGG GGGAA		
	TCTTCGGTTTC CCCTT		
	__ GCGA AIIIT		
GAM342 SLC3A2	AGAAGCCAAAGGGCCTGGGAAG 5255	__	IIIC
	AGAAGCCAAGGGG GGAA		
	TCTTCGGTTTCCC CCTT		
	GGAC CIII		
GAM342 SLC3A2	AGAAGCCAAAGGGCCTGGGAAG 5255 TGAG	__	AGTT
	AAGCCAAGGGG GGAAG		
	TTCGGTTTCCC CCTTC		
	__ GGAC CTII		
GAM342 SNRPA	AGAAGGCCCCCAAGGGGGGA 5254	__	IIIT
	AGAAG CCAAGGGGGG		
	TCTTC GGTTCCCCC		
	CGGG TIII		
GAM342 SNRPA	AGAAGGCCCCCAAGGGGGGA 5254 TGAGAAG		AGAGT
	CCAAGGGGGGA		
	GGTTCCCCCCT		
	TTCCGGG GAIII		
GAM342 STX1A	TGAGAAGCCCCAAGGTGGTGAGGAG 5270	A_ _ _ A	TTII
	TGAGAAGCC AGGG GG GA GAG		
	ACTCTTCGG TTCC CC CT CTC		
	GG A A C IIIT		
GAM342 STX1A	TGAGAAGCCCCAAGGTGGTGAGGAG 5270 AG	A_ _ GA	AI
	AAGCC AGGG GG AG		
	TTCGG TTCC CC TC		
	__ GG A AC CI		
GAM342 SURF6	AGAAGCCAAGAGAGCGGGGAGGAG 5257	__ _ CAA	AGI
	AGA AGC GGGGGGA		
	TCT TCG CCCTCCT		
	GT C C__ CII		
GAM342 SURF6	AGAAGCCAAGAGAGCGGGGAGGAG 5257 TGAG	__	A I
	AAGCCAAGG GGGGA GAGTT		
	TTCGGTTCT CCCCT CTCGG		
	__ CTCG C I		
GAM342 TAGLN2	AGAACAGGCCA--GGGGGAAGA 5253 TGAGAA	AG	T
	GCCA GGGGGAAGAG		

	CGGT CCCCCTTCTT			
	TTGTC_ _ C			
GAM342 TAGLN2	AGAACAGGCCA--GGGGGAAGA	5253	_ AG	II
	AGAA GCCA GGGGGAAG			
	TCTT CGGT CCCCCTTC			
	GTC _ TI			
GAM342 TMOD	GAGAAGCCAAATGGGGATG-GTT	5268	G AGAGI	
	AGAAGCCAAG GGGGA			
	TCTTCGGTTT CCCCT			
	A ACCAI			
GAM342 TMOD	GAGAAGCCAAATGGGGATG-GTT	5268 TG	G AGAGTT	
	AGAAGCCAAG GGGGA			
	TCTTCGGTTT CCCCT			
	_ A ACCAAC			
GAM342 XBP1	GATGCCAAAAAGGGGGAAGAG	5260 GAA	_ III	
	GCCAA GGGGGGAAGA			
	CGGTT TCCCCCTTCT			
	CTA TT CII			
GAM342 XBP1	GATGCCAAAAAGGGGGAAGAG	5260 TGAGAA	_ TT	
	GCCAA GGGGGGAAGAG			
	CGGTT TCCCCCTTCTC			
	_ TT TT			
GAM343 DYRK1A	AAACTG---CTTTAGTTTT	5286	TATC	
	AAACTG CTTTAGTT			
	TTTGAC GAAATCAA			
	_			
GAM343 GRIN2A	TAAACTGTATCC-ACAGTTT	5290 _	TT I	
	AAACTGTATCC TAGTT			
	TTTGACATAGG GTCAA			
	A T_ I			
GAM343 GRIN2A	TAAACTGTATCC-ACAGTTT	5290 TGTA	TT T	
	AACTGTATCC TAGTTT			
	TTTGACATAGG GTCAAA			
	_ T_ C			
GAM343 HMGN2	AAACTGTATCC---AGCTTTA	5288 TGTA	TTT	
	CTGTATCC AGTTT			
	GACATAGG TCGAA			
	_ _			
GAM343 HMGN2	AAACTGTATCC---AGCTTTA	5288	TTT I	
	AAACTGTATCC AGTTT			

	TTTGACATAGG TCGAA		
	_____ A		
GAM343 MRE11A	TAAACTGTAAACTCTTAGCTT 5289 A TC _ I		
	AACTGTA CTTT AGTT		
	TTGACAT GAGA TCGA		
	_ TT A I		
GAM343 MRE11A	TAAACTGTAAACTCTTAGCTT 5289 TGTA TC _ TA		
	AACTGTA CTTT AGTTT		
	TTGACAT GAGA TCGAA		
	_____ TT A CA		
GAM343 PPP2R2C	TGTATCCTTCGGGCCTTTTA 5295 A_		
	TGTATCCTTT GTTTT		
	ACATAGGAAG CGGAA		
	CC AAT		
GAM343 PTPRG	TGTAATACAGAGTTATCCTTTATTTT 5292 _ TG___ GTTTTAl		
	TGTAA AC TATCCTTTA		
	ACATT TG ATAGGAAAT		
	A TCTCA AAAA A		
GAM343 PTPRG	TGTAATACAGAGTTATCCTTTATTTT 5292 GTAAACTG GI		
	TATCCTTTA		
	ATAGGAAAT		
	GTCTCA_ AA		
GAM343 SLA	TAGACTGTATCCATTTCCTTT 5291 AA TTTAGTTI		
	ACTGTATCC		
	TGACATAGG		
	C_ TAAAGAAA		
GAM343 SLA	TAGACTGTATCCATTTCCTTT 5291 TGTA _ AG A		
	ACTGTATCC TTT TTTT		
	TGACATAGG AAA AAAG		
	C_ T GA A		
GAM343 YWHAG	TGTCACCTGTATCCTGTTA 5293 AAA TTAGTTTT		
	TGT CTGTATCCT		
	ACA GACATAGGA		
	GTG CAAT A		
GAM343 YWHAG	TGTCACCTGTATCCTGTTA 5293 AAA TTII		
	TGT CTGTATCCT		
	ACA GACATAGGA		
	GTG CAAT		
GAM343 YWHAG	TGTAAACTGCA--ATTTAGTGTTA 5294 TCC TTI		
	TGTAAACTGTA TTTAGT		

	ACATTTGACGT AAATCA		
	T__ CAA		
GAM343 YWHAG	TGTAAACTGCA--ATTTAGTGTTA 5294	TCC	TTTA
	TGTAAACTGTA TTTAGT		
	ACATTTGACGT AAATCA		
	T__ CAAT		
GAM343 ZNF189	AAACTGTATACTT-GTTTTA 5287	C	TAGTTTI
	AAACTGTAT CTT		
	TTTGACATA GAA		
	T CAAAATI		
GAM344 ADRA1A	GGGTGGGCTCTGAGTGGTTGGG 5303	TAG T	T_ ATG
	GG GCTCTGAGT TTGGG		
	CC CGAGACTCA AACCC		
	CA_ _ CC CAI		
GAM344 AKAP4	GGGTGCTCTG-G-CTGGGATG 5304	TAGG	A TT
	GTGCTCTG GT TGGGAT		
	CACGAGAC CG ACCCTA		
	_____ - -		
GAM344 ASGR2	AGGTTGCTCTGAGGGCTGGG 5299	TA G	TT AT
	GG TGCTCTGAG TTGGG		
	CC ACGAGACTC GACCC		
	_ A CC CI		
GAM344 DLST	AGGCTGCTCTGAG-CTTGGA 5300	TA G	T T
	GG TGCTCTGAGTTT GGGA		
	CC ACGAGACTCGAA CCCT		
	_ G _ C		
GAM344 PCDHA12	AGGGC-CTCTGAG--TTGGGA 5301	TA G	TT
	GGGT CTCTGAGT TGGGA		
	CCCG GAGACTCA ACCCT		
	_____ - -		
GAM344 PDE4B	GGTGCTCTG---CCTGGGATG 5305	TAGGGT	AGT
	GCTCTG TTTGGGA		
	CGAGAC GGACCCT		
	_____ - -		
GAM344 PIGA	AGGGTAGCAGCTG-GTTTTGGGATG 5298	TA _ T_ A	I
	GGGT GC CTG GTTTTGGGATG		
	CCCA CG GAC CAAAACCCTAC		
	_ T TC _ C		
GAM344 RAD50	AGAGAGCTCTGAGTCT--GGATG 5302	TA T	TG
	GGG GCTCTGAGTTT GGATG		

	CTC CGAGACTCAGA CCTAC	
	— T —	
GAM345 ACCN1	CAGAGTGTGACTCATCTCT 5324 AGTACAGATC TT	
	GT CTCATCTCT	
	CA GAGTAGAGA	
	CA_____ CT	
GAM345 ADAR	AAAAACCAACGAAGTCCCTTC 5309 — III	
	AAAAACCAA AGTCTCTT	
	TTTTTGGTT TCAGGGAA	
	GCT GII	
GAM345 BCL9	CAAAGACTAAAGTCTCTGCT 5323 A C TCI	
	AAA AC AAAGTCTCT	
	TTT TG TTTCAGAGA	
	C A CGI	
GAM345 BCL9	CAAAGACTAAAGTCTCTGCT 5323 TGACAAAA C T	
	AC AAAGTCTCT CT	
	TG TTTCAGAGA GA	
	TC_____ A C	
GAM345 CAPZB	ACAAAAACCACACGGTCTCT 5316 AA_ III	
	ACAAAAACCA GTCTC	
	TGTTTTTGGT CAGAG	
	GTGC AII	
GAM345 CAPZB	ACAAAAACCACACGGTCTCT 5316 TGAC AA_ TCT	
	AAAAACCA GTCTCT	
	TTTTTGGT CAGAGA	
	_____ GTGC TAI	
GAM345 CD36	TACAAGCTCTGGTTCCTCATCTCT 5329 AGTACAGATC AI	
	GTTTCTCATCTCT	
	CAAGGAGTAGAGA	
	GTTCGAGAC_ GA	
GAM345 CHRNA10	AGTACAGTTCAGTTTCTCAT 5320 A _ CTCT	
	AGTACAG TC GTTTCTCAT	
	TCATGTC AG CAAAGAGTA	
	A T IIIA	
GAM345 CLECSF5	TACAGAAGCGGACCTCATCTCTA 5330 AGTA T_ TT I	
	CAGA CG TCTCATCTCTA	
	GTCT GC GGAGTAGAGAT	
	_____ TC CT A	
GAM345 CNR1	CAGAAACCAAAGTACTCTCCT 5322 AA _ I	
	AAACCAAAGT CTCTTC	

	TTTGGTTTCA GAGAGG			
	C_ T I			
GAM345 CNR1	CAGAAACCAAAGTACTCTCCT 5322 TGACAA _ G			
	AAACCAAAGT CTCTTCT			
	TTTGGTTTCA GAGAGGA			
	_____ T A			
GAM345 COIL	TGACAAAAAACCAAAGATCT 5332 _ _ CTTCTG			
	TGACAAAA ACCAAAG TCT			
	ACTGTTTT TGGTTTC AGA			
	TT T GTC			
GAM345 COIL	TGACAAAAAACCAAAGATCT 5332 _ _			
	TGACAAAA ACCAAAG TC			
	ACTGTTTT TGGTTTC AG			
	TT T A			
GAM345 DMD	GACAAAAACCAA---TCTTC 5326 TG GTC			
	ACAAAAACCAA TCTTC			
	TGTTTTTGGTTT AGAAG			

GAM345 DMD	GACAAAAACCAA---TCTTC 5326 G CI			
	GACAAAAACCAA TCT			
	CTGTTTTTGGTTT AGA			
	_ AG			
GAM345 DNMT3B	GTAGCAGA-C--TTCTCATCT 5328 AGTA CGT C			
	CAGAT TTCTCATCT			
	GTCTG AAGAGTAGA			
	ATC_ _ C			
GAM345 EFNB2	AAAACCAAAGTGCTGTGCT 5313 _ CTTCT			
	AAAACCAAAGT CT			
	TTTTGGTTTCA GA			
	C CACGAI			
GAM345 EGFL5	AAAAACC-AAG-CCCTTCTG 5312_ A T I			
	AAAACCAA GTC CTTCT			
	TTTTGGTT CGG GAAGA			
	T _ _ I			
GAM345 FIGF	ACAGAAAACCAAATAATCAGTTCTG 5314 CA _ TC I			
	AAAACCAA GTC TTCT			
	TTTTGGTTT TAG AAGA			
	_ AT TC I			
GAM345 FIGF	ACAGAAAACCAAATAATCAGTTCTG 5314 TGACA _ TC			
	AAAACCAA GTC TTCTG			

	TTTTGGTTT TAG AAGAC			
	TC_____ AT TC TA			
GAM345 FUT8	AAAAACCAAACGTCCATTCT	5310	_ C II	
	AAAAACCAAA GTCT TTC			
	TTTTTGGTTT CAGG AAG			
	G T AI			
GAM345 FUT8	AAAAACCAAACGTCCATTCT	5310	TGACAAAA _ C	
	ACCAAA GTCT TTCT			
	TGGTTT CAGG AAGA			
	_____ G T			
GAM345 GBP1	AAAAATCCCATATTCTCTTCTG	5308	AAAA AAG I	
	CCA TCTCTTCT			
	GGT AGAGAAGA			
	TTAG ATA I			
GAM345 GBP1	AAAAATCCCATATTCTCTTCTG	5308	TGACAAAAA AAG	
	CCA TCTCTTCTG			
	GGT AGAGAAGAC			
	TAG_____ ATA			
GAM345 GPR44	GACAATAGACCAAAGTCCCT	5325	AA_ II	
	GACAA ACCAAAGTCTC			
	CTGTT TGGTTTCAGGG			
	ATC AI			
GAM345 GPR44	GACAATAGACCAAAGTCCCT	5325	TG AA_ TCT	
	ACAA ACCAAAGTCTCT			
	TGTT TGGTTTCAGGGA			
	_ ATC CII			
GAM345 HOXB7	AAAAACCAAATTTCTCCT	5311	C II	
	AAAAACCAAAGT TCTTC			
	TTTTTGGTTTTA AGAGG			
	A AI			
GAM345 HOXB7	AAAAACCAAATTTCTCCT	5311	TGACAAAA C	
	ACCAAAGT TCTTCT			
	TGGTTTTA AGAGGA			
	_____ A			
GAM345 IPF1	ACAAAAACCAATGGCTCTT	5317	AGT II	
	ACAAAAACCAA CTCT			
	TGTTTTTGGTT GAGA			
	ACC AI			
GAM345 IPF1	ACAAAAACCAATGGCTCTT	5317	TGAC AGT CT	
	AAAAACCAA CTCTT			

	TTTTTGGTT GAGAA		
	_____ ACC AA		
GAM345 JRKL	TATAAATC-TTTCTCATC-CTA 5331 AGTAC G CT		
	AGATC TTTCTCATCT		
	TTTAG AAAGAGTAGG		
	A_____ AT		
GAM345 KIF5C	TGAGAAAAGCCCAAAGTCTCCCCTG 5334 C A_ II		
	TGA AAAA CCAAAGTCTCTTCTG		
	ACT TTTT GGTTTCAGAGGGGAC		
	C CG II		
GAM345 KIF5C	TGAGAAAAGCCCAAAGTCTCCCCTG 5334 _ C AA I		
	GA AAA CCAAAGTCTCTTCT		
	CT TTT GGTTTCAGAGGGGA		
	T _ CG I		
GAM345 PCDHA11	ACATGATCTATTCTCATCTCT 5315 AGTACA GT A		
	GATC TTCTCATCTCT		
	CTAG AAGAGTAGAGA		
	A_____ AT C		
GAM345 PPARBP	CAAAATGACCAAAGTC-CTTC 5321 _ CTTII		
	CAAAA ACCAAAGTCT		
	GTTTT TGGTTTCAGG		
	AC AAGII		
GAM345 PPARBP	CAAAATGACCAAAGTC-CTTC 5321 TGACAAAA T T		
	ACCAAAGTC CTTC		
	TGGTTTCAG GAAG		
	TTAC_____ T		
GAM345 PTPN1	AGCAGAGATCAAAGTTTCTCATTTTC 5319 C _ C TAIL		
	AGTA AGATC GTTTCTCAT TC		
	TCGT TCTAG CAAAGAGTA AG		
	C TTT A IIIA		
GAM345 RAG1	ACAGATCTTTGCTCATCTCT 5318 AGTACA GTTT		
	GATC CTCATCTCT		
	CTAG GAGTAGAGA		
	_____ AAAC		
GAM345 RET	TGATGAAAACCAAA-TGTCTTC 5336 _ CA _ CTTI		
	GA AAAACCAAA GTCT		
	CT TTTTGGTTT CAGA		
	A AC A AIII		
GAM345 RET	TGATGAAAACCAAA-TGTCTTC 5336 CA GTC TG		
	TGA AAAACCAAA TCTTC		

		ACT TTTTGGTTT AGAAG		
		AC AC_ II		
GAM345 SET7		GAAAAAAACCAAAG-CCATTCT 5327 AC	TCTI	
		AAAAACCAAAGTC		
		TTTTTGGTTTCGG		
		T_ TAAG		
GAM345 SET7		GAAAAAAACCAAAG-CCATTCT 5327 TGAC	TC	
		AAAAACCAAAGTC TTCTG		
		TTTTTGGTTTCGG AAGAT		
		TT_ T_		
GAM345 SLC22A1LS		TGACAAAAAAAAGGTCTCT 5335	CC A TCT	
		TGACAAAAA AA GTCTCT		
		ACTGTTTTT TT CAGAGA		
		TT C III		
GAM345 SLC22A1LS		TGACAAAAAAAAGGTCTCT 5335	CC A I	
		GACAAAAA AA GTCTC		
		CTGTTTTT TT CAGAG		
		TT C I		
GAM345 YWHAG		TGACAAAAGCACAAAGGCTCATTC 5333	C_ T _ TGII	
		TGACAAAAA CAAAG CTC TTC		
		ACTGTTTTT GTTTC GAG AAG		
		CGT C T IIIG		
GAM346 ADD2		TCCAAGGCT---CCTTCTGT 5346	GTC A G	
		TCCAAGGCT CCT CTGT		
		AGGTTCCGA GGA GACA		
		_ A I		
GAM346 ATSV		TCCAAGGTGGCTGTCCCTGCCCTGCC 5344	_ A G III	
		TCCAA GGCTGTCCCT CT TGCC		
		AGGTT CCGACAGGGA GG ACGG		
		CCA C G III		
GAM346 DEC1		CCAAGGCTGT-TCTAGCTG 5343 TC	CC _ TGC	
		CAAGGCTGT CTA CTG		
		GTTCCGACA GAT GAC		
		_ A_ C TII		
GAM346 DMPK		TCCCTGGCTGTCCC--CTGGGCC 5347 AA	TA T	
		TCC GGCTGTCCC CTG GCC		
		AGG CCGACAGGG GAC CGG		
		GA _ C		
GAM346 FXD1		CCAATCGGGCTGTCCCCTGCTG 5342 TCCAA_	TA GCCI	
		GGCTGTCCC CTGT		

	CCGACAGGG GACG	
	GTTAGC ACTI	
GAM346 MEN1	TCCCAGGCATCTCCCTACTGT 5345	A TG_ GCC
	TCC AGGC TCCCTACTGT	
	AGG TCCG AGGGATGACA	
	G TAG	
GAM346 SIM2	CAGGGCAGGTCCCTACTGTG 5340	TCCA T_ CC
	GGC GTCCCTACTGTG	
	CCG CAGGGATGACAC	
	C_ TC AC	
GAM346 UBE2I	CAAGGCTGTCTCGCACTGGGC 5341	TCCA CC_ T C
	AGGCTGTC TACTG GC	
	TCCGACAG GTGAC CG	
	_____ AGC C A	
GAM346 WHSC1	AAGGCTGTCCCGTCCTGGTGC 5339	TCCAAG TA_ _ C
	GCTGTCCC CTG TGC	
	CGACAGGG GAC ACG	
	_____ CAG C A	
GAM347 ADAMTS5	CACAGACAAATGGCACTGGGATT 5352	TGAC C _ GCI
	ACAGA GG ACTGGGATTG	
	TGTTT CC TGACCCTAAT	
	TC_ A G AAI	
GAM347 ANGPT4	TGTCACAGACGGA-GGGGAGTTGG 5358	TGA CT _ CI
	CACAGACGGA GGGA TTGG	
	GTGTCTGCCT CCCT AACC	
	ACA C_ C II	
GAM347 AXL	ACTCAGAAGGTGAGGGATTGGC 5350	TGACA C ACT
	CAGA GG GGGATTGGC	
	GTCT CC CCCTAACCG	
	A_ T ACT	
GAM347 IL1B	ACAAAAGGGCTGGGGATTGGC 5351	TGACACAGAC A _
	GG CTGGG ATTGGC	
	CC GACCC TAACCG	
	TT_____ C C	
GAM347 PDGFB	GAGACAGACGGACGAGGGA 5355	TGAC T_ TTGG
	ACAGACGGAC GGGA	
	TGTCTGCCTG CCCT	
	TC_ CT T	
GAM347 RANBP3	TGACACAGAGGGCACAGTGGAGGGGC 5357	C _ TG_ TT II
	TGACACAGA GG AC GGA GGC	

	ACTGTGTCT CC TG CCT CCG		
	C G TCA CC II		
GAM347 SIRT7	TGACACAGA-GGCC--GGATGGGC 5359	C A G T	
	TGACACAGA GG CTGG AT GGC		
	II II		
	ACTGTGTCT CC GGCC TA CCG		
	_ _ _ C		
GAM347 SLC7A5	GACACAGACAGGGAGCAGGCA-TGGC 5354 TG	_ CT AT II	
	ACACAGAC GGA GGG TGGC		
	III III		
	TGTGTCTG CCT TCC ACCG		
	_ TC CG GT TI		
GAM347 TMPRSS2	CACAGACGGATCCTGCAAATGG 5353 TGACAC	_ G T C	
	AGACGGA CTG GA TGG		
	III II		
	TCTGCCT GAC TT ACC		
	_ AG G T C		
GAM347 TPM2	GAC-CGGACGGACTGGGCTGGG 5356 TGACACA	A C	
	GACGGACTGGG TTGG		
	CTGCCTGACCC GACC		
	TGGC_ _ C		
GAM348 CKMT2	TCAGAGTAGAGATTTATGTCTGTT 5367	_ TA_ A TTTTII	
	TCAGAGTAG G TATG CT		
	I II		
	AGTCTCATC C ATAC GA		
	T TAA A CAIII		
GAM348 CSNK1G3	AGAGAATGTTAATATGACTT 5362 TC	AGGT TTT	
	AGAGT ATATGACTT		
	TCTTA TATACTGAA		
	_ CAAT TAI		
GAM348 DTNA	CAAATTAG---TATGACTTTTTT 5365 TCA	A TA	
	GAGT GGTA TGACTTTTT		
	TTTA TCAT ACTGAAAAA		
	_ A _		
GAM348 EDNRA	TCAAAGT--GTA-ATGACTTTT 5368	AG T T	
	TCAGAGT GTA ATGACTTTT		
	III		
	AGTTTCA CAT TACTGAAAA		
	_ _ I		
GAM348 SFRS2IP	TCTGAGTA---ATATGACTTATT 5369 TCA	GGT TTT	
	GAGTA ATATGACTT		
	CTCAT TATACTGAA		
	AGA _ TAA		
GAM348 SLC4A10	CAAAGTGGTGTATATGACTT 5364 TC	G _ TTTT	
	AGA TAGGT ATATGACTT		

TTT ATCCA TATACTGAA
 _ G CA TIII
 GAM348 SLC4A4 CACAGTAGAGAAGATGACTTTT 5363 TCAG _TAT TT
 AGTAG G ATGACTTTT
 ||||| | |||||
 TCATC C TACTGAAAA
 TG_ T TTC TI
 GAM348 ZNF141 GAGGAG--ATATGACTTTT 5366 TCAGAGTA T
 GG ATATGACTTTT
 || |||||
 TC TATACTGAAAA
 C _ _
 GAM349 CAPN5 GCGGGTCCAGCCGGGCTCCCGGGA 5372 TG A A_ CI
 CGGGT CAGTT CTCCCGGGA
 ||||| ||||| |||||
 GCCCA GTCGG GAGGGCCCT
 _ G CCC AI
 GAM349 CTLA1 GGGTACAGTAACCTCAGAGAC 5374 TGCGGG TA_ CC
 TACAGT CTC GGGAC
 ||||| || |||||
 ATGTCA GAG CTCTG
 _ TTG T_
 GAM349 GGA3 TGGGGTCCATGT--TCCCGGGAC 5377 C A GTTAC
 TG GGGT CA TCCCGGGAC
 || ||||| || |||||
 AC CCCA GT AGGGCCCTG
 C G ACA_
 GAM349 IGHMBP2 TGTGGGG-CAGCTTTTCCCGGGAC 5378 C TA AC I
 TG GGG CAGTT TCCCGGGAC
 || ||||| ||||| |||||
 AC CCC GTCGA AGGGCCCTG
 A C_ AA I
 GAM349 TXNRD1 TGCAGG-ACAGTTCTCTTTCCCGGGAC5375 T AC_ II
 TGCGGG ACAGTT TCCCGGGAC
 ||||| ||||| |||||
 ACGTCC TGTCAA AGGGCCCTG
 _ GAGAA II
 GAM349 VENTX2 TGTGGGTACAG---TCCCGG 5376 C TTAC G
 TG GGGTACAG TCCCGG
 || ||||| |||||
 AC CCCATGTC AGGGCC
 A _ I
 GAM349 WISP3 GCGAGCACT-TTCCTCCCGGGAC 5373 TG AG A
 CGGGTAC TT CTCCCGGGAC
 ||||| || |||||
 GCTCGTG AG GAGGGCCCTG
 _ AA _
 GAM350 NT5M AGCGCGC-TGGCCCGTCGTGG 5382 TA CATC T
 GCGTT GCCCGTCGTGG
 ||||| |||||

	CGCGA CGGGCAGCACC		
	CG C__ C		
GAM350 SLC15A1	TAGCGTTCACGGCCGGGCGCGGT 5383	C CGT	CI
	TAGCGTTCAT GCC CGTGGT		
	ATCGCAAGTG CGG GCGCCA		
	C CCC II		
GAM350 TP53	AGCGTGTCA---CCGTCGTGG 5381 TA TCA C		
	GCGT TCGCC GTCGTGG		
	CGCA AGTGG CAGCACC		
	_ C _		
GAM351 BAALC	TGCCATGGGCAGTGGGTTGG 5398 GACAAGT	TGI	
	GCCGTGGGT		
	CGGTACCCG		
	_____ TCA		
GAM351 BAALC	TGCCATGGGCAGTGGGTTGG 5398 TGACAAG	__ CT	
	TGCCGTGGGT TGGG		
	ACGGTACCCG ACCC		
	_____ TC AA		
GAM351 BCL9	GAAAATGTGCCAGTGGGTTGG 5395 GACAA_ _		
	GTGCC GTGGGTTG		
	CACGG CACCCAAC		
	CTTTTA T CII		
GAM351 BCL9	GAAAATGTGCCAGTGGGTTGG 5395 TGACAA _	GCTT	
	GTGCC GTGGGTTGG		
	CACGG CACCCAACC		
	TTTTA_ T AIII		
GAM351 BRCA1	AGTGCCGTGGTATGATCTT 5393	GT GG II	
	AGTGCCGTGG TG CT		
	TCACGGCACC AC GA		
	AT TA AI		
GAM351 BRCA1	AGTGCCGTGGTATGATCTT 5393 TGACAA CC	GTTG	
	GTG GTGG GGCT		
	CAC TACT CCGA		
	G_____ CA AGAA		
GAM351 CDO1	TGGCAGAGTGCCGTGAGTT 5397 A _	GGGCT	
	TG CA AGTGCCGTGGGT		
	AC GT TCACGGCACTCAA		
	C C IIIT		
GAM351 CDO1	TGGCAGAGTGCCGTGAGTT 5397 A _	II	
	TG CA AGTGCCGTGGGT		

	AC GT TCACGGCACTCA			
	C C AI			
GAM351 FOXE1	AAGTGATCCCTGGGTTGGG	5386	__ G III	
	AAGTG CC TGGGTTGG			
	TTCAC GG ACCCAACC			
	TA G CII			
GAM351 FOXE1	AAGTGATCCCTGGGTTGGG	5386	TGACAAGTG G CT	
	CC TGGGTTGGG			
	GG ACCCAACCC			
	CTA_____ G CA			
GAM351 GBF1	AAGTGCAGAGTGGTTGGGCTT	5387	A CGTG_ I	
	GTGC GGTTGGGCT			
	CACG CCAACCCGA			
	_ TCTCA I			
GAM351 GBF1	AAGTGCAGAGTGGTTGGGCTT	5387	TGACAAGTGCC G	
	GTGG TTGGGCTT			
	CACC AACCCGAA			
	CGTCT_____ _			
GAM351 HLA-A	GACATGAGG-GTGGGTTGGTCT	5396	CAA CC_ GI	
	GTG GTGGGTTGG			
	TAC CACCCAACC			
	TG_ TCC AI			
GAM351 HLA-A	GACATGAGG-GTGGGTTGGTCT	5396	TGACAA CC_ G	
	GTG GTGGGTTGG CTT			
	TAC CACCCAACC GAG			
	TG_____ TCC A			
GAM351 MAP3K14	ACAGGTCAGCCTTGGGTTGGG	5390	TGACAAGT G CTT	
	GCC TGGGTTGGG			
	CGG ACCCAACCC			
	TCCAGT_ A CCI			
GAM351 MAP3K14	ACAGGTCAGCCTTGGGTTGGG	5390	A __ G III	
	ACA GT GCC TGGGTTGG			
	TGT CA CGG ACCCAACC			
	C GT A CII			
GAM351 PLAT	TGACAGGT-CAGGAGGTTGGGCTT	5400	A GCCGT I	
	TGACA GT GGGTTGGGCTT			
	ACTGT CA TCCAACCCGAA			
	C GTCC_ I			
GAM351 PLAT	TGACAGGT-CAGGAGGTTGGGCTT	5400	_ A GCCGT I	
	GACA GT GGGTTGGGCT			

	CTGT CA TCCAACCCGA		
	A C GTCC_ I		
GAM351 RS1	AACTCCCCTACGTTGGGCTT 5389 AGTG G G I		
	CC TG GTTGGGCT		
	II II IIIIIII		
	GG AT CAACCCGA		
	TGAG G G I		
GAM351 RS1	AACTCCCCTACGTTGGGCTT 5389 TGACAAGTG G G		
	CC TG GTTGGGCT		
	II II IIIIIII		
	GG AT CAACCCGA		
	G_____ G G		
GAM351 SIAT4C	AGTGCCGTGTCTAGGCCTT 5394 GG II		
	AGTGCCGTG TTGGGCT		
	IIIIIIII IIIIIII		
	TCACGGCAC GATCCGG		
	A_ AA		
GAM351 SLC12A7	AGTGCCGTGATGCTGTTGGGC 5391 _____ IIIG		
	AGTGCCGTGG GTTGGG		
	IIIIIIII IIIIIII		
	TCACGGCACT CAACCC		
	ACGA GIII		
GAM351 SOX12	AAGGGGTGGGGGTTGGGCT 5388 AA___ CCGT II		
	GTG GGGTTGGGC		
	III IIIIIII		
	CAC CCCAACCCG		
	TTCCC C___ AI		
GAM351 SOX12	AAGGGGTGGGGGTTGGGCT 5388 TGACAA CCGT		
	GTG GGGTTGGGCT		
	III IIIIIII		
	CAC CCCAACCCGA		
	C_____ C___		
GAM351 UCP2	TGACAAGTGGGCTAGGCTGGGCT 5399 CCG TI		
	TGACAAGTG TGGGTTGGGCT		
	IIIIIIII IIIIIIIII		
	ACTGTTTAC ATCCGACCCGA		
	CCG II		
GAM351 UCP2	TGACAAGTGGGCTAGGCTGGGCT 5399 CCG I		
	GACAAGTG TGGGTTGGGC		
	IIIIIIII IIIIIIIII		
	CTGTTTAC ATCCGACCCG		
	CCG I		
GAM351 WNT6	AGAGCCCTGGGAGTTGGGCTT 5392 T G ___ III		
	AG GCC TGGG TTGGGCT		
	II III III IIIIIII		
	TC CGG ACCC AACCCGA		
	T G TC AII		
GAM352 CAPN10	CTGACGGAGGCTTCCCGTGG 5409 _ G III		
	CTGA GGAGGCTTC TG		
	IIII IIIIIIIII II		

	GACT CCTCCGAAG GC		
	G G ACC		
GAM352 EHD2	AGCTGTGGGGAGGCTTCCAGGG 5406 GAT A__	GT I	
	CTG GGAGGCTTC GG		
	GAC CCTCCGAAG CC		
	C__ ACC GT I		
GAM352 EHD2	AGCTGTGGGGAGGCTTCCAGGG 5406 TGAGATC A	GT	
	TG GGAGGCTTC GGG		
	AC CCTCCGAAG CCC		
	GAC__ C GT		
GAM352 GJA5	TGAGTAATCTGAA-AGGCTTCGT 5414 __	G GGG	
	TGAG ATCTGAG AGGCTTCGT		
	ACTC TAGACTT TCCGAAGCA		
	AT _		
GAM352 GJA5	TGAGTAATCTGAA-AGGCTTCGT 5414 GA_	G I	
	GATCTGAG AGGCTTCG		
	TTAGACTT TCCGAAGC		
	TCA _ I		
GAM352 ITGB4	GAGTAGCTGAGGAGGCTCCG 5410 AT_	II	
	GAG CTGAGGAGGCTTC		
	CTC GACTCCTCCGAGG		
	ATC CI		
GAM352 ITGB4	GAGTAGCTGAGGAGGCTCCG 5410 TGAGAT	TGG	
	CTGAGGAGGCTTCG		
	GACTCCTCCGAGGC		
	TCATC_ CII		
GAM352 JAM2	TCTGAGGAGG--TCGAGGG 5413	CT T I	
	TCTGAGGAGG TCG GG		
	AGACTCCTCC AGC CC		
	_ T C		
GAM352 LAMC1	TGAGA-CTGAGGAGG-TTC 5415 T	C GTG	
	TGAGA CTGAGGAGG TTC		
	ACTCT GACTCCTCC AAG		
	_ _		
GAM352 LAMC1	TGAGA-CTGAGGAGG-TTC 5415 T	CTTI	
	TGAGA CTGAGGAGG		
	ACTCT GACTCCTCC		
	_ AAGI		
GAM352 LZTR1	GATTTGAGGAGGCTGCCCTGTGGG 5412 ATCT	_ _ I	
	GAGGAGGCT TC GTGG		

	CTCCTCCGA GG CACC		
	C_____ CG A I		
GAM352 LZTR1	GATTGGAGGAGGCTGCCCTGTGGG 5412 TGAGATCT	___ _	II
	GAGGAGGCT TC GTGGG		
	II		
	CTCCTCCGA GG CACCC		
	AAC_____ CG A AC		
GAM352 MEF2A	AGATCTGAGGTCCAGAGTTTCG 5403	___ GC	III
	AGATCTGAGG AG TTC		
	II		
	TCTAGACTCC TC AAG		
	AGG TC CII		
GAM352 MEF2A	AGATCTGAGGTCCAGAGTTTCG 5403 TGAG	___ GC	T G
	ATCTGAGG AG TTCG GG		
	II		
	TAGACTCC TC AAGC TC		
	_____ AGG TC _ I		
GAM352 MEIS1	ATGTAAGGAGGCTTC-TGG 5408 ATC		GTGI
	TGAGGAGGCTTC		
	ATTCCTCCGAAG		
	TAC ACCI		
GAM352 MEIS1	ATGTAAGGAGGCTTC-TGG 5408 TGAGATCT		G
	GAGGAGGCTTC TG		
	II		
	TTCCTCCGAAG AC		

GAM352 NGB	TGA-ATCTGAGGA-GCT--GTGG 5417 A		G TC
	TGAG TCTGAGGAG CT GTGG		
	II		
	ACTT AGACTCCTC GA CACC		

GAM352 NGB	TGA-ATCTGAGGA-GCT--GTGG 5417 A		G TC
	G GATCTGAGGAG CT GTG		
	I II		
	A TTAGACTCCTC GA CAC		
	C _____		
GAM352 NOS2A	TGAGA---GAGGAGGCTCCG 5416 TCT		TG
	TGAGA GAGGAGGCTTCG		
	ACTCT CTCCTCCGAGGC		
	_____ II		
GAM352 NOS2A	TGAGA---GAGGAGGCTCCG 5416 _ TCT		
	GAGA GAGGAGGCTTC		
	CTCT CTCCTCCGAGG		
	A _____		
GAM352 PCDHGA1	AGAACT-AGGAGGCTT-GTAGG 5405 _ T G		C I
	GA CT AGGAGGCTT GTGG		

	CT GA TCCTCCGAA CATC		
	T T _ _ I		
GAM352 PCDHGA1	AGAACT-AGGAGGCTT-GTAGG	5405 TGAGATCTG	C
	AGGAGGCTT GTGG		
	TCCTCCGAA CATC		
	TTGA_____		
GAM352 PCDHGA10	AGAACT-AGGAGGCTT-GTAGG	5405 _ T G	C I
	GA CT AGGAGGCTT GTGG		
	CT GA TCCTCCGAA CATC		
	T T _ _ I		
GAM352 PCDHGA10	AGAACT-AGGAGGCTT-GTAGG	5405 TGAGATCTG	C
	AGGAGGCTT GTGG		
	TCCTCCGAA CATC		
	TTGA_____		
GAM352 PCDHGA11	AGAACT-AGGAGGCTT-GTAGG	5405 _ T G	C I
	GA CT AGGAGGCTT GTGG		
	CT GA TCCTCCGAA CATC		
	T T _ _ I		
GAM352 PCDHGA11	AGAACT-AGGAGGCTT-GTAGG	5405 TGAGATCTG	C
	AGGAGGCTT GTGG		
	TCCTCCGAA CATC		
	TTGA_____		
GAM352 PCDHGA12	AGAACT-AGGAGGCTT-GTAGG	5405 _ T G	C I
	GA CT AGGAGGCTT GTGG		
	CT GA TCCTCCGAA CATC		
	T T _ _ I		
GAM352 PCDHGA12	AGAACT-AGGAGGCTT-GTAGG	5405 TGAGATCTG	C
	AGGAGGCTT GTGG		
	TCCTCCGAA CATC		
	TTGA_____		
GAM352 PCDHGA2	AGAACT-AGGAGGCTT-GTAGG	5405 _ T G	C I
	GA CT AGGAGGCTT GTGG		
	CT GA TCCTCCGAA CATC		
	T T _ _ I		
GAM352 PCDHGA2	AGAACT-AGGAGGCTT-GTAGG	5405 TGAGATCTG	C
	AGGAGGCTT GTGG		
	TCCTCCGAA CATC		
	TTGA_____		
GAM352 PCDHGA3	AGAACT-AGGAGGCTT-GTAGG	5405 _ T G	C I
	GA CT AGGAGGCTT GTGG		

	CT GA TCCTCCGAA CATC		
	T T _ _ I		
GAM352 PCDHGA3	AGAACT-AGGAGGCTT-GTAGG	5405 TGAGATCTG	C
	AGGAGGCTT GTGG		
	TCCTCCGAA CATC		
	TTGA_____		
GAM352 PCDHGA4	AGAACT-AGGAGGCTT-GTAGG	5405 _ T G	C I
	GA CT AGGAGGCTT GTGG		
	CT GA TCCTCCGAA CATC		
	T T _ _ I		
GAM352 PCDHGA4	AGAACT-AGGAGGCTT-GTAGG	5405 TGAGATCTG	C
	AGGAGGCTT GTGG		
	TCCTCCGAA CATC		
	TTGA_____		
GAM352 PCDHGA5	AGAACT-AGGAGGCTT-GTAGG	5405 _ T G	C I
	GA CT AGGAGGCTT GTGG		
	CT GA TCCTCCGAA CATC		
	T T _ _ I		
GAM352 PCDHGA5	AGAACT-AGGAGGCTT-GTAGG	5405 TGAGATCTG	C
	AGGAGGCTT GTGG		
	TCCTCCGAA CATC		
	TTGA_____		
GAM352 PCDHGA6	AGAACT-AGGAGGCTT-GTAGG	5405 _ T G	C I
	GA CT AGGAGGCTT GTGG		
	CT GA TCCTCCGAA CATC		
	T T _ _ I		
GAM352 PCDHGA6	AGAACT-AGGAGGCTT-GTAGG	5405 TGAGATCTG	C
	AGGAGGCTT GTGG		
	TCCTCCGAA CATC		
	TTGA_____		
GAM352 PCDHGA7	AGAACT-AGGAGGCTT-GTAGG	5405 _ T G	C I
	GA CT AGGAGGCTT GTGG		
	CT GA TCCTCCGAA CATC		
	T T _ _ I		
GAM352 PCDHGA7	AGAACT-AGGAGGCTT-GTAGG	5405 TGAGATCTG	C
	AGGAGGCTT GTGG		
	TCCTCCGAA CATC		
	TTGA_____		
GAM352 PCDHGA8	AGAACT-AGGAGGCTT-GTAGG	5405 _ T G	C I
	GA CT AGGAGGCTT GTGG		

		CT GA TCCTCCGAA CATC			
		T T _ _ I			
GAM352	PCDHGA8	AGAACT-AGGAGGCTT-GTAGG	5405	TGAGATCTG	C
		AGGAGGCTT GTGG			
		TCCTCCGAA CATC			
		TTGA_____			
GAM352	PCDHGA9	AGAACT-AGGAGGCTT-GTAGG	5405	_ T G	C I
		GA CT AGGAGGCTT GTGG			
		CT GA TCCTCCGAA CATC			
		T T _ _ I			
GAM352	PCDHGA9	AGAACT-AGGAGGCTT-GTAGG	5405	TGAGATCTG	C
		AGGAGGCTT GTGG			
		TCCTCCGAA CATC			
		TTGA_____			
GAM352	PCDHGB1	AGAACT-AGGAGGCTT-GTAGG	5405	_ T G	C I
		GA CT AGGAGGCTT GTGG			
		CT GA TCCTCCGAA CATC			
		T T _ _ I			
GAM352	PCDHGB1	AGAACT-AGGAGGCTT-GTAGG	5405	TGAGATCTG	C
		AGGAGGCTT GTGG			
		TCCTCCGAA CATC			
		TTGA_____			
GAM352	PCDHGB2	AGAACT-AGGAGGCTT-GTAGG	5405	_ T G	C I
		GA CT AGGAGGCTT GTGG			
		CT GA TCCTCCGAA CATC			
		T T _ _ I			
GAM352	PCDHGB2	AGAACT-AGGAGGCTT-GTAGG	5405	TGAGATCTG	C
		AGGAGGCTT GTGG			
		TCCTCCGAA CATC			
		TTGA_____			
GAM352	PCDHGB3	AGAACT-AGGAGGCTT-GTAGG	5405	_ T G	C I
		GA CT AGGAGGCTT GTGG			
		CT GA TCCTCCGAA CATC			
		T T _ _ I			
GAM352	PCDHGB3	AGAACT-AGGAGGCTT-GTAGG	5405	TGAGATCTG	C
		AGGAGGCTT GTGG			
		TCCTCCGAA CATC			
		TTGA_____			
GAM352	PCDHGB4	AGAACT-AGGAGGCTT-GTAGG	5405	_ T G	C I
		GA CT AGGAGGCTT GTGG			

		CT GA TCCTCCGAA CATC			
		T T _ _ I			
GAM352	PCDHGB4	AGAACT-AGGAGGCTT-GTAGG	5405	TGAGATCTG	C
		AGGAGGCTT GTGG			
		TCCTCCGAA CATC			
		TTGA_____			
GAM352	PCDHGB5	AGAACT-AGGAGGCTT-GTAGG	5405	_ T G	C I
		GA CT AGGAGGCTT GTGG			
		CT GA TCCTCCGAA CATC			
		T T _ _ I			
GAM352	PCDHGB5	AGAACT-AGGAGGCTT-GTAGG	5405	TGAGATCTG	C
		AGGAGGCTT GTGG			
		TCCTCCGAA CATC			
		TTGA_____			
GAM352	PCDHGB6	AGAACT-AGGAGGCTT-GTAGG	5405	_ T G	C I
		GA CT AGGAGGCTT GTGG			
		CT GA TCCTCCGAA CATC			
		T T _ _ I			
GAM352	PCDHGB6	AGAACT-AGGAGGCTT-GTAGG	5405	TGAGATCTG	C
		AGGAGGCTT GTGG			
		TCCTCCGAA CATC			
		TTGA_____			
GAM352	PCDHGB7	AGAACT-AGGAGGCTT-GTAGG	5405	_ T G	C I
		GA CT AGGAGGCTT GTGG			
		CT GA TCCTCCGAA CATC			
		T T _ _ I			
GAM352	PCDHGB7	AGAACT-AGGAGGCTT-GTAGG	5405	TGAGATCTG	C
		AGGAGGCTT GTGG			
		TCCTCCGAA CATC			
		TTGA_____			
GAM352	PCDHGC3	AGAACT-AGGAGGCTT-GTAGG	5405	_ T G	C I
		GA CT AGGAGGCTT GTGG			
		CT GA TCCTCCGAA CATC			
		T T _ _ I			
GAM352	PCDHGC3	AGAACT-AGGAGGCTT-GTAGG	5405	TGAGATCTG	C
		AGGAGGCTT GTGG			
		TCCTCCGAA CATC			
		TTGA_____			
GAM352	PCDHGC4	AGAACT-AGGAGGCTT-GTAGG	5405	_ T G	C I
		GA CT AGGAGGCTT GTGG			

		CT GA TCCTCCGAA CATC	
		T T _ _ I	
GAM352 PCDHGC4		AGAACT-AGGAGGCTT-GTAGG 5405 TGAGATCTG C	
		AGGAGGCTT GTGG	
		TCCTCCGAA CATC	
		TTGA_____	
GAM352 PCDHGC5		AGAACT-AGGAGGCTT-GTAGG 5405 _ T G C I	
		GA CT AGGAGGCTT GTGG	
		CT GA TCCTCCGAA CATC	
		T T _ _ I	
GAM352 PCDHGC5		AGAACT-AGGAGGCTT-GTAGG 5405 TGAGATCTG C	
		AGGAGGCTT GTGG	
		TCCTCCGAA CATC	
		TTGA_____	
GAM352 SACM2L		AGAGCTGAGGAGGCTTCATG 5404 T I	
		GA CTGAGGAGGCTTCGT	
		CT GACTCCTCCGAAGTA	
		C I	
GAM352 SACM2L		AGAGCTGAGGAGGCTTCATG 5404 TGAGAT G	
		CTGAGGAGGCTTCGTG	
		GACTCCTCCGAAGTAC	
		TC_____ G	
GAM352 SLA2		GAGATCTGAGAGCTAGGCTGGGTG 5411 GA _ TCGTI	
		TCTGAGG AGGCT	
		AGACTCT TCCGA	
		_ CGA CCCII	
GAM352 SLA2		GAGATCTGAGAGCTAGGCTGGGTG 5411 TG _ TC GGI	
		AGATCTGAGG AGGCT GTG	
		TCTAGACTCT TCCGA CAC	
		_ CGA CC GII	
GAM352 STIM1		ATCTGAGGAGGTTTGGGGG 5407 CTTCGTGII	
		ATCTGAGGAGG	
		TAGACTCCTCC	
		AAACCCCCI	
GAM353 ADRA2A		GGGAGGGCA-GG--C-AGGGC 5435 TG TG CA	
		GGAGGGCA GGT AGGGC	
		CCTCCCGT CCG TCCCG	

GAM353 AGXT		GGGTGGGCATGGGACAGGTGTGT 5440 TG A T A GCGTI	
		GG GGGCATGGG CA GG	

	CC CCCGTACCC GT CC		
	__ A __ T __ ACACA		
GAM353 ALPPL2	AGGGCGTGGTGTCAAGGGC	5420	TGGGAGGGCA __ G
	TGG GTCAAGGGC		
	ACC CAGTTCCCG		
	GC_____ A A		
GAM353 CALU	TGGGGTGTGATGGGTCAAAGGC	5455	AGGGC GT
	TGGG ATGGGTCAAAGGGC		
	ACCC TACCCAGTTTCCG		
	CACAC II		
GAM353 COL4A6	GGGAGGGCAAGGGGCAGAGTGGC	5429	TG T_ CA _ TI
	GGAGGGCA GGGT AG GGC		
	CCTCCCGT CCCG TC CCGT		
	__ TC TC A II		
GAM353 CYBA	GGGAGGGCA--GGTCCGGGGCG	5437	TG TG AA
	GGAGGGCA GGTC GGGCG		
	CCTCCCGT CCAG CCCGC		
	__ __ GC		
GAM353 DPH2L1	TGGGAGGGCATGGATGACGG	5450	CAAG
	TGGGAGGGCATGGGT GGC		
	ACCCTCCCGTACCTA CTGC		

GAM353 EHD2	GGGAGGGCA-GG--C-AGGGCGT	5439	TG TG CA
	GGAGGGCA GGT AGGGCG		
	CCTCCCGT CCG TCCCGC		
	__ __ __		
GAM353 EPB49	TGGGAGGGC-TGGGT---GGGCG	5457	A CAA
	TGGGAGGGC TGGGT GGGCG		
	ACCCTCCCG ACCCA CCCGC		
	__ __		
GAM353 ERBB2	TGGGAGGGCGCGGGGCGCGGG	5451	A TCAA CGT
	TGGGAGGGC TGGG GGG		
	ACCCTCCCG GCCC CCC		
	C CGCG		
GAM353 GNB2	TGGGAGGGCAGGGACCCAAGGC	5453	T GT A GT
	TGGGAGGGCA GG C AGGGC		
	ACCCTCCCGT CC G TTCCG		
	C TG G II		
GAM353 GRM4	TGGGTGGGCATGGG-C-AGGGC	5456	A CA G
	TGGG GGGCATGGGT AGGGC		

	ACCC CCCGTACCCG TCCCG			
	A _ I			
GAM353 ID3	GGGAGGGCA-GGGCCCAGG 5431 TG T AA			
	GGAGGGCA GGGTC GGGC			
	CCTCCCGT CCCGG TCCG			
	_ _ G_			
GAM353 IL24	TGGGACC-CATGGC-CAAGGGCGT 5458 GGG G			
	TGGGA CATGG TCAAGGGCGT			
	ACCCT GTACC GGTTCGCGCA			
	GG_ _			
GAM353 JUNB	GGGAGGGCAGGGGGCGGGGG 5434 TG T TCAA C			
	GGAGGGCA GGG GGG G			
	CCTCCCGT CCC CCC C			
	_ C CG_ C			
GAM353 KCNAB2	GGGTGGGTGGGGGTCAAGGGC 5436 _ A CATG GT			
	TGGG GGG GGTCAAGGGC			
	ACCC CCC CCAGTTCCCG			
	CC A _ GI			
GAM353 KCNMB1	TGGGAGGGCAGGTGGAGAAGG 5445 TG_ TC GCGT			
	TGGGAGGGCA GG AAGG			
	ACCCTCCCGT CC TTCC			
	CCA TC IIIT			
GAM353 KLK13	GGGAGGGCA-GGG-C--GGGCG 5438 TG T CAA			
	GGAGGGCA GGGT GGGC			
	CCTCCCGT CCCG CCCG			
	_ _ _			
GAM353 MEOX1	GGAAGG--TGGG-CAAGGGCGT 5423 TGG GCA T			
	GAGG TGGG CAAGGGCG			
	TTCC ACCC GTTCCCGC			
	_ _ _			
GAM353 MGAT1	GGGAGGGCA--GGCCAGGGG 5433 TG TG A C			
	GGAGGGCA GGTCA GGG			
	CCTCCCGT CCGGT CCC			
	_ _ C T			
GAM353 MSX1	GGGCATGGGCTC-CGGGCG 5441 TGGGA A_ CAA			
	GGGC TGGGT GGGC			
	CCCG GCCCG CCCG			
	A_ AG _			
GAM353 NEFH	GGGAGGGCATGGGGGCAGGGGC 5425 TG T_ A GT			
	GGAGGGCATGGG CA GGGC			

	CCTCCCGTACCC GT CCCG	
	___ CC C GI	
GAM353 OPCML	GGAAAGGGAAGGGTCAAGG 5430 T GG CAT GCG	
	G AGGG GGGTCAAGG	
	I	
	C TCCC CCCAGTTCC	
	TT TT AII	
GAM353 PLD2	TGGGAGGGGCCCTGGGACAGGGAGGGGGT5442 A_ T ___ C III	
	TGGGAGGGC TGGG CA AGGG GT	
	ACCCTCCCG ACCC GT TCCC CA	
	GG T CCC C III	
GAM353 PML	GGAGGGCATGG--CGAAGGCG 5421 TGGG GTCA	
	AGGGCATGG AGGGCG	
	TCCCGTACC TTCCGC	
	___ GC_	
GAM353 PPT2	TGGGAGGGC-TGATGTCAGGGG 5446 A _ A CGT	
	TGGGAGGGC TGG GTCA GGG	
	ACCCTCCCG ACT CAGT CCC	
	_ A C III	
GAM353 PRKCN	TGGGAGGGCTAAGGGT-AAG 5444 AT_ C GGCG	
	TGGGAGGGC GGGT AAG	
	ACCCTCCCG CCCA TTC	
	ATT _ IIIT	
GAM353 RARA	GGGAGGGCAGGTGGGGGCAGGGC 5424 TG ___ TCA GTI	
	GGAGGGCA TGGG AGGGC	
	CCTCCCGT ACCC TCCCG	
	___ CC CCG AII	
GAM353 RHCG	GGGAGGGCAGGGGTGGAGG 5432 TG T CAA G	
	GGAGGGCA GGGT GGGC	
	CCTCCCGT CCCA TCCG	
	___ C CC_ I	
GAM353 RNF4	TGGGAGGGCCCTGGGTCCAGCGC 5443 A_ A G GTI	
	TGGGAGGGC TGGGTC AG GC	
	ACCCTCCCG ACCCAG TC CG	
	GG G G III	
GAM353 SLC7A4	TGGGAGGGC--GGGGCAAG 5447 AT T GGC	
	TGGGAGGGC GGG CAAG	
	ACCCTCCCG CCC GTTC	
	C_ _ III	
GAM353 SORCS2	TGGGAGGGCCTGGCACCCGGGC 5454 ATG CAA_ GT	
	TGGGAGGGC GGT GGGC	

	ACCCTCCCG CCG CCG			
	GA_ TGGG II			
GAM353 SOX13	GGGAGGGCAGGAGGAGGTCA	5426 TG	T_____	AGGGCG
	GGAGGGCA GGGTCA			
	CCTCCCGT TCCAGT			
	___ CCTCC CIIITG			
GAM353 SOX13	GGGAGGGCAGGCAGGTGAGGGGC	5427 TG	___	CAA TI
	GGAGGGCA TGGGT GGGCG			
	CCTCCCGT GTCCA CCCGT			
	___ CC CTC II			
GAM353 SREBF2	GGGAGGGCATGCTGGGCACAGGC	5428 TG	___	T A GTI
	GGAGGGCA TGGG CA GGGC			
	CCTCCCGT ACCC GT TCCG			
	___ ACG _ G GII			
GAM353 TAGLN2	TGGGAGGGCA-GGGGCAAGG	5449	T T	GCG
	TGGGAGGGCA GGG CAAGG			
	ACCCTCCCGT CCC GTTCC			
	C _ III			
GAM353 TFAP4	GGCGGGCATGGG--AGGGGCG	5422 TGGGA		TCAA
	GGGCATGGG GGGCG			
	CCCGTACCC CCCGC			
	G_____ TC__			
GAM353 THRA	TGGGAGGGCTGGGGGCAAG	5448	A	TCAAG
	TGGGAGGGC TGGG GGGC			
	ACCCTCCCG ACCC CCGT			

GAM353 ZNF76	TGGGAGGGCA--GGAC-AGGGC	5452	T T A	G
	TGGGAGGGCA GGG CA GGGC			
	ACCCTCCCGT CCT GT CCCG			
	_____ I			
GAM354 BGN	GGGAACATGTGATGGGGGCC	5466		CGCTGCI
	GGAACATGTGGT			
	CCTTGTA CACTA			
	CCCCCGI			
GAM354 BGN	GGGAACATGTGATGGGGGCC	5466 TGCGGG		CGCT
	AACATGTGGT GCC			
	TTGTACACTA CGG			
	_____ CCCC			
GAM354 DDX20	TGAGGCAACTGGTGAGTCGCTGCC	5467 C G AT _		II
	TG GG AAC GTG GTCGCTGCC			
	II II III			

	AC CC TTG CAC CAGCGACGG	
	T G AC T II	
GAM354 DDX20	TGAGGCAACTGGTGAGTCGCTGCC	5467 GC G AT _ I
	GG AAC GTG GTCGCTGC	
	II III III IIIIIII	
	CC TTG CAC CAGCGACG	
	T_ G AC T I	
GAM354 EGFL5	GCCGGTACG-GTGGTCGCT	5462 G A AT I
	GC GG AC GTGGTCGC	
	II II II IIIIIII	
	CG CC TG CACCAGCG	
	G A C_ A	
GAM354 EGFL5	GCCGGTACG-GTGGTCGCT	5462 TG GA AT C
	CGG AC GTGGTCGCTG	
	III II IIIIIII	
	GCC TG CACCAGCGAT	
	G_ A_ C_ I	
GAM354 GGA3	GGGAACA--TGGTCTGTGCC	5465 TG _ _ GI
	GGGAACA TGGTC GCT	
	IIIIII IIII III	
	CCCTTGT ACCAG CGG	
	_ ACA II	
GAM354 GUCY2C	GGACACTTGAGGTCGCTGCC	5464 _ A T II
	GGA AC TG GGTGCTGC	
	III II II IIIIIII	
	CCT TG AC CCAGCGACG	
	G A T GI	
GAM354 GUCY2C	GGACACTTGAGGTCGCTGCC	5464 TGCGGGA A T
	AC TG GGTCGCTGCC	
	II II IIIIIII	
	TG AC CCAGCGACGG	
	_ _ _ A T	
GAM354 KCNAB2	GCGGGAACA-GAGGTGCCTGC	5463 _ TGT C GI
	CGGGAACA GGT GCT	
	IIIIII III III	
	GCCCTTGT CCA CGG	
	C CT_ _ AC	
GAM354 KCNAB2	GCGGGAACA-GAGGTGCCTGC	5463 TG TGT C _ C
	CGGGAACA GGT GC TGC	
	IIIIII III II III	
	GCCCTTGT CCA CG ACG	
	_ CT_ _ G T	
GAM354 KIF5B	TGAGGG--CTTGTGGTCGC	5468 C AACA TG
	TG GGG TGTGGTCGC	
	II III IIIIIII	
	AC CCC ACACCAGCG	
	T GA_ II	
GAM354 KIF5B	TGAGGG--CTTGTGGTCGC	5468 C AACA I
	TG GGG TGTGGTCG	
	II III IIIIIII	

	AC CCC ACACCAGC		
	T GA__ G		
GAM354 TLL1	CGGAAACATGTGGATGCCGCC 5461	TC	I
	GGGAACATGTGG GCTGC		
	CCTTTGTACACC CGGCG		
	TA I		
GAM354 TLL1	CGGAAACATGTGGATGCCGCC 5461	TGCG	TC
	GGAACATGTGG GCTGCC		
	CTTTGTACACC CGGCGG		
	TA		
GAM355 ADAM19	GCTCGGCGCTCACACGCCCTCAGCC 5489	TGCC	_ C__ II
	CGG GCTC CGCCCTCAGCC		
	GCC CGAG GCGGGAGTCGG		
	GA__ G TGT TI		
GAM355 AGTR1	CGGGTCTCCCGCCCGCCGCC 5487	TGCCCGGG	TCA
	CTCCCGCCC GCC		
	GAGGGCGGG CGG		
	A_____ CGG		
GAM355 BMPR1B	CCCGGCTCCCGCTCCTCAGC 5483	TGCCCG	_ C
	GGCTCCCGC CCTCAGC		
	CCGAGGGCG GGAGTCG		
	CA C		
GAM355 C18orf1	CCGGGCTCCCTGCGCCACAGC 5481	TGCCCG	_ T CI
	GGCTCCC GCCC CAGC		
	CCGAGGG CGGG GTCG		
	ACG T TC		
GAM355 CDR2	CCCGGCCCTCCGCCCTCAGCC 5475	TGCC	G _ I
	CGG CTC CCGCCCTCAGCC		
	GCC GGG GCGGGAGTCGG		
	G A T		
GAM355 CDS1	TGCCCGGGCTCCCGCAC-CAG 5501	_ _	TCAGCC
	TGCCCGGGC TCCCGC CC		
	ACGGGCCCG AGGGCG GG		
	G T TC C		
GAM355 CEBPA	CCGGGCTCCC-AGCTCAGCC 5485	TGCCCG	CC
	GGCTCCCG CTCAGC		
	CCGAGGGT GAGTCG		
	C_		
GAM355 CLDN5	CCCGGGCTCTGCATCCGCC 5474	TGCC	_ CAGCC
	CGGGCTC CCGCCCT		

	GCCCGAG GCGGGG		
	_____ ACGTA AIIIC		
GAM355 CLTCL1	TGCCTGCTCTGCAGCCCTCAGC 5506	CGG CC__	CI
	TGCC GCTC GCCCTCAGC		
	ACGG CGAG CGGGAGTCG		
	A__ ACGT II		
GAM355 EN2	CCCGGGCTCCCCGCTCCTC 5473	TGCC _ _	AGC
	CGGGCTCCC GC CCTC		
	GCCCGAGGG CG GGAG		
	_____ G A AGI		
GAM355 ENPP1	GCCGCGGCTCCCGCCCCCGC 5495	TGC _	A C
	CCG GGCTCCCGCCCTC GC		
	GGC CCGAGGGCGGGGG CG		
	_____ G G C		
GAM355 FKBP10	TGCCCTCCCTCCACCCCTCAGCC 5504	GGG _	II
	TGCCC CTCCCGCCC TCAGCC		
	ACGGG GAGGGTGGG AGTCGG		
	AGG G II		
GAM355 GALR1	TGCCC GGCGCCTCCGCCGCTGC 5502	_ _	TCA CII
	TGCCC GGCG TC CCGCCC GC		
	ACGGGCCCCG GG GGCGGG CG		
	C A CGA III		
GAM355 GNL1	CCGAGCTCCCGCCGCCTCA 5482	TGCCCG _	
	GGCTCCCGCC CTCAGC		
	TCGAGGGCGG GAGTTG		
	_____ CG		
GAM355 GORASP1	GCCCGGGCTGCCTGCCACA 5491	TG _ C	T GCC
	CCCGGGCT CC GCC CA		
	GGGCCCGA GG CGGG GT		
	_____ C A T AII		
GAM355 GYPC	CCCGGGCTCCTGACCCTCGGC 5478	TGCC C_	A C
	CGGGCTCC GCCCTC GC		
	GCCCGAGG TGGGAG CG		
	_____ AC C C		
GAM355 HNF4A	CCCGAAGGCCCGCCCTCCGCC 5471	TGCC	A I
	GGGCTCCCGCCCTC GCC		
	TCCGGGGGCGGGAG CGG		
	GCT__ G G		
GAM355 HRMT1L1	GCCTGAGCCACCGCCCTCAACC 5497	TG C TC	I
	CC GGGC CCGCCCTCAGCC		

	GG CTCG GGCGGGAGTTGG		
	__ A GT G		
GAM355 IKBKAP	TGTCCGCGGCTCCCGCTCTC 5499 C _ C AGCC		
	TG CCG GGCTCCCGC CTC		
	AC GGC CCGAGGGCG GAG		
	A G A C		
GAM355 KCNK1	CCTGGCTCCCGCCCGCCGCC 5486 TGCCCG TCA		
	GGCTCCCGCCC GCC		
	CCGAGGGCGGG CGG		
	CGG		
GAM355 KIF5C	CCCGGGCTCCTGCGCGCTCAGCC 5477 TGCC _ C I		
	CGGGCTCC CGC CTCAGCC		
	GCCCGAGG GCG GAGTCGG		
	AC C T		
GAM355 MAP3K11	CCGGGCCCTGGCCCTCAGCC 5484 TGCCCG CC		
	GGCTC GCCCTCAGCC		
	CCGGG CGGGAGTCGG		
	AC		
GAM355 MAPT	CCCGTGGCCTCCCGCCC-CACCC 5472 TGCCC G T G I		
	GG CTCCCGCCC CA CC		
	CC GAGGGCGGG GT GG		
	GCA__ G _ G G		
GAM355 MUCDHL	CGGGCTCCCGGCCGAGCC 5488 TGCCCGGG C T		
	CTCCCG CC CAGC		
	GAGGGC GG GTCG		
	C C		
GAM355 MYO5A	CCCGGGCTCGCCGCGAGCAGCC 5476 TGCC _ CCT I		
	CGGGCTC CCGC CAGCC		
	GCCCGAG GGCG GTCGG		
	C CTC C		
GAM355 NAGA	TGCCTGGCTAGCTCGGCCGCCCTCAACC5500 C _ _		
	TGCC GG GCTC CCGCCCTCAGCC G		
	ACGG CC CGAG GGCGGGAGTTGG C		
	A GAT CC		
GAM355 NEUROD2	GCCCGGGCTCCGGCGCCCT 5492 TG _ CAGC		
	CCCGGGCTCC CGCCCT		
	GGGCCCGAGG GCGGGA		
	CC T		
GAM355 PACSIN1	GCCCGGGCTGAGGGCCTGCATGCC 5493 TG CCC_ CT _		
	CCCGGGCT GCC CA GCC		

	GGGCCCGA CGG GT CGG	
	___ CTCC AC A GI	
GAM355 PITPN	GCCCGGCCTCCCGCCCGCTGCC 5496 TG G TCA I	
	CCCGG CTCCCGCCC GCC	
	GGGCC GAGGGCGGG CGG	
	___ G CGA G	
GAM355 PLXNA1	GCCCTGGCCTCAC-CCCTCAGCC 5490 TG _ G CCG I	
	CCC GG CTC CCCTCAGCC	
	GGG CC GAG GGGAGTCGG	
	___ A G TG_ G	
GAM355 POLH	TGCCCGGGCAACCGTCCCCAGC 5505 TC C CI	
	TGCCCGGGC CCG CCTCAGC	
	ACGGGCCCG GGC GGGGTCTG	
	TT A II	
GAM355 PVRL2	CCCGGGCTCCC-CATGCAGCC 5480 TGCC GCCCT	
	CGGGCTCCC CAGCC	
	GCCCGAGGG GTCGG	
	___ GTAC_	
GAM355 RASGRP2	GCCCTGGC-CCTGCCCTCAGC 5494 TG G T C C	
	CCC GGC CC GCCCTCAGC	
	GGG CCG GG CGGGAGTCG	
	___ A _ A A	
GAM355 SIAT4C	TGGCCGGGCTCCCACGGCTCCAGC 5503 C C_ _ CII	
	TG CCGGGCTCCCGC CTC AGC	
	AC GGCCCGAGGGTG GAG TCG	
	C CC G III	
GAM355 SLC19A1	TGCCCTGGGGCTCCCGGACCCGGCC 5498 _ CC A II	
	TGCC GGGCTCCCG CTC GCC	
	ACGGG CCCGAGGGC GGG CGG	
	AC CT C II	
GAM355 TP53BP2	CCCGGGCTCCCCCGCCCCGGCC 5479 TGCC _ CA I	
	CGGGCTCCC GCCCT GCC	
	GCCCGAGGG CGGGG CGG	
	___ GG C_ C	
GAM356 CTH	GAAGAAGAGAG-GAAAAGAAC 5510 T_ AT A T CT	
	GAA GA AG GAAAAGAAC	
	CTT CT TC CTTTTCTTG	
	TT _ C _ TI	
GAM356 DMPK	ATGAATTTCAAGAAGAACCTG 5509 TGAAATGAAAGT A	
	GA AAGAACCTG	

	TT TTCTTGGAC		
	TAAAG_____ C		
GAM356 DRD3	TGAAATGAACAG---AAAGAA 5511	AGT A CC	
	TGAAATGAA GAAA GAA		
	ACTTTACTT CTTT CTT		
	GT_ _ II		
GAM356 MELK	TGGAATTAGA---AAAAGAACCTG 5513	TGAAATGAA T	
	AG GAAAAGAACCTG		
	TC TTTTCTTGGAC		
	ACCTTAA_ _		
GAM356 NR1I2	TGATGTGAAAGTGAGCAAAG 5512	AA AA ACCT	
	TGA TGAAAGTGA AGA		
	ACT ACTTCACT TTT		
	AC CG C		
GAM357 B4GALT5	ACAGCA--TGAACAAACGGGGAC 5517	TA CC A	
	CAGTA TGGA AAACGGGGAC		
	GTCGT ACTT TTTGCCCTG		
	_ _ G		
GAM357 FBXO7	GTAGCTGAGGCGAAACGGGGA 5520	TACAGTACCT AA C	
	GG AAACGGGGA		
	CC TTTGCCCT		
	GACT_____ GC T		
GAM357 PIK3CG	AGTACCTGGGACTACAGGCAC 5518	TACAGT AAAA G	
	ACCTGG ACGGG AC		
	TGGACC TGTCC TG		
	_____ CTGA G		
GAM357 SERPINB5	ACAGTTATCCTGGAAAATGCGTGGA 5516	TA A_ A_ G C	
	CAGT CCTGGAAAA CG GGA		
	GTCA GGACCTTTT GC CCT		
	_ ATA AC A T		
GAM357 SLC1A4	GTAATTGGAAAAACATGGAC 5521	TACAGTACC G	
	TGGAAAAACG GGA		
	ACCTTTTGT CCT		
	A_____ A		
GAM357 TNFAIP2	CAGTACCTGGGAAAA-GGGGAC 5519	TACA A C	
	GTACCTGG AAAA GGGGAC		
	CATGGACC TTTT CCCCTG		
	_____ C _		
GAM358 ADAM11	TGACAGGGACAGCAGGACG 5538	C C _ C	
	TGACAGGGAC GC GG C		

	ACTGTCCCTG CG CC G		
	T T T CII		
GAM358 ADAM11	TGACAGGGACAGCAGGACG 5538	C C C CCCC	
	TGACAGGGAC GC GG CG		
	ACTGTCCCTG CG CC GC		
	T T T IIIG		
GAM358 ANK1	GACAAG---CGCCTAGGCCGCCCG 5530 _	GAC _ I	
	ACAGG CGCC GGCCGCCCG		
	TGTTT GCGG CCGGCGGGG		
	C _ AT I		
GAM358 ANK1	GACAAG---CGCCTAGGCCGCCCG 5530 TG	GAC _	
	ACAGG CGCC GGCCGCCCG		
	TGTTT GCGG CCGGCGGGG		
	_ _ AT		
GAM358 ANK1	GACAAGG--CGCCTAGGCCGCCCG 5531	AC _ I	
	ACAGGG CGCC GGCCGCCCG		
	TGTTCC GCGG CCGGCGGGG		
	_ AT I		
GAM358 ANK1	GACAAGG--CGCCTAGGCCGCCCG 5531 TG	AC _ I	
	ACAGGG CGCC GGCCGCCCG		
	TGTTCC GCGG CCGGCGGGG		
	_ _ AT C		
GAM358 BRF1	TGACAGGGAGCGCC-ACTGCCC 5539	C G C CG	
	TGACAGGGA CGCCG C GCCC		
	ACTGTCCCT GCGGT G CGGG		
	C _ A II		
GAM358 BRF1	TGACAGGGAGCGCC-ACTGCCC 5539 _	C _ GCCI	
	GACAGGGA CGCCG GCC		
	CTGTCCCT GCGGT CGG		
	A C GA IIIC		
GAM358 CACNA1A	GGGAGTCGCCGCGCGTGCCG 5536	C_ CC II	
	GGGA CGCCGGCCG CC		
	CCCT GCGGCCGGC GG		
	CA AC CI		
GAM358 CACNA1A	GGGAGTCGCCGCGCGTGCCG 5536 TGACAGGGAC	CC	
	CGCCGGCCG CC		
	GCGGCCGGC GG		
	A _ AC		
GAM358 CDC34	GACAGGTGG-GCCGGCCGCTCC 5534	GACC CI	
	ACAGG GCCGGCCGC		

		TGTCC CGGCCGGCG			
		ACC_ AG			
GAM358 CDC34		GACAGGTGG-GCCGGCCGCTCC	5534 TG	GACC	_ G
		ACAGG GCCGGCCGC CCC			
		TGTCC CGGCCGGCG GGG			
		_ ACC_ A I			
GAM358 COL18A1		CAGGGGCTGGCCGGCCGCTCC	5525 A	ACC	CCI
		GGG GCCGGCCGC			
		CCC CGGCCGGCG			
		C GAC AGI			
GAM358 COL18A1		CAGGGGCTGGCCGGCCGCTCC	5525 TGACA	ACC	_ G
		GGG GCCGGCCGC CCC			
		CCC CGGCCGGCG GGG			
		_____ GAC A A			
GAM358 FCN2		GACAGGGAC--ACGGCCCCC	5532	CGC	GI
		GACAGGGAC CGGCC			
		CTGTCCCTG GCCGG			
		T_ GG			
GAM358 FCN2		GACAGGGAC--ACGGCCCCC	5532 TG	CGC	G
		ACAGGGAC CGGCC CCC			
		TGTCCCTG GCCGG GGG			
		_ T_ _			
GAM358 GPC1		CAGAG-CCGCCGGCCCTCCC	5529 _ A	G_ CI	
		AGGG CCGCCGGCC CC			
		TCTC GGCGGCCGG GG			
		G _ GA II			
GAM358 GPC1		CAGAG-CCGCCGGCCCTCCC	5529 TGACAG	A	GC
		GG CCGCCGGCC CCC			
		TC GGCGGCCGG GGG			
		_____ GA			
GAM358 HDAC4		ACAGGGACCGCCGGGCTGCAGCCCC	5524 CAGG	_ C_	I
		GACCGCCGG C GCCC			
		CTGGCGGCC G CGGG			
		_____ C ACGT I			
GAM358 HDAC4		ACAGGGACCGCCGGGCTGCAGCCCC	5524 TGAC	_ C_	GII
		AGGGACCGCCGG C GCCCC			
		TCCCTGGCGGCC G CGGGG			
		_____ C ACGT ACI			
GAM358 MAD1L1		GAGAGGGT--GCTGGCCGCCCC	5535 AC_	ACC C	I
		AGGG GC GGCCGCCC			

	TCCC CG CCGGCGGG			
	CTC A__ A I			
GAM358 MAD1L1	GAGAGGGT--GCTGGCCGCCCC	5535	TGAC ACC C	
	AGGG GC GGCCGCCCC			
	TCCC CG CCGGCGGGG			
	TC__ A__ A			
GAM358 MAPRE3	CAGGG-CTGC-GGCCGCCC	5527	ACC C I	
	CAGGG GC GGCCGCC			
	GTCCC CG CCGGCGG			
	GA_ _ G			
GAM358 MLC1	TGGCAGGGTCTGCAGGCCGCCCC	5540	A ACC C	GI
	TG CAGGG GC GGCCGCCCC			
	AC GTCCC CG CCGGCGGGG			
	C AGA T II			
GAM358 MLC1	TGGCAGGGTCTGCAGGCCGCCCC	5540	GA ACC C	I
	CAGGG GC GGCCGCCCC			
	GTCCC CG CCGGCGGG			
	CC AGA T I			
GAM358 PAK4	GACAGGGACCATCTGTCCCCC	5533	CCGG_ G I	
	ACAGGGACCG CC CC			
	TGTCCCTGGT GG GG			
	AGACA _ I			
GAM358 PAK4	GACAGGGACCATCTGTCCCCC	5533	TG CCGGCCG G	
	ACAGGGACCG CCCC			
	TGTCCCTGGT GGGG			
	_ AGACA_ G			
GAM358 PPP5C	GGGAT-GCAGGCCGCCCCG	5537	CC C I	
	GGGA GC GGCCGCCCC			
	CCCT CG CCGGCGGGG			
	A_ T C			
GAM358 PPP5C	GGGAT-GCAGGCCGCCCCG	5537	TGA GA GG	
	CAGG CCGCC CCGCCC			
	GTCC GGCGG GGC GGG			
	C_ _ _			
GAM358 TBX2	CAGGGACCGCTGG--GCCC	5528	C_ GCCI	
	CAGGGACCGC GGCC			
	GTCCCTGGCG CCGG			
	AC G			
GAM358 TBX2	CAGGGACCGCTGG--GCCC	5528	TGACAG C CC	
	GGACCGC GG GCCC			

		CCTGGCG CC CGGG			
		_____ A _____			
GAM358 WHSC1		CAGGCAGGGCCGCGCCGCC	5526	GACC	II
		CAGG GCCGGCCGCC			
		GTCC CGGCCGGCGG			
		GTCC GI			
GAM358 WHSC1		CAGGCAGGGCCGCGCCGCC	5526	TGA GACC	C
		CAGG GCCGGCCGCC			
		GTCC CGGCCGGCGGG			
		C_____ A			
GAM359 ALDH3A2		AGGAAGTGAGCAGTGCCATTA	5550	AA_____ GATTI	
		GGAAGTGAG GTCA			
		CCTTCACTC CGGT			
		GTCA AAIII			
GAM359 ALDH3A2		AGGAAGTGAGCAGTGCCATTA	5550	TA AA_____ GATTACC	
		GGAAGTGAG GTCA			
		CCTTCACTC CGGT			
		_____ GTCA AATTIII			
GAM359 AQP8		AAGTGAGAATTGTCAGCTT	5544	_____ ATIII	
		AAGTGAGAA GTCAG			
		TTCACTCTT CAGTC			
		AA GAII			
GAM359 CD1A		AGGAAGTGAGGAGCACAG-TTA	5549	A _ ATTI	
		GGAAGTGAG AGT CAG			
		CCTTCACTC TCG GTC			
		C T AAII			
GAM359 CD1A		AGGAAGTGAGGAGCACAG-TTA	5549	TA A _ A CC	
		GGAAGTGAG AGT CAG TTA			
		CCTTCACTC TCG GTC AAT			
		_____ C T _ CI			
GAM359 EYA1		AAGTAGAGATGTACAGATTACC	5543	AGT A _ I	
		GAGA GT CAGATTAC			
		CTCT CA GTCTAATG			
		AT_ A T I			
GAM359 EYA1		AAGTAGAGATGTACAGATTACC	5543	TAGGAAGT A _	
		GAGA GT CAGATTACC			
		CTCT CA GTCTAATGG			
		T_____ A T			
GAM359 FACL6		GAAGTGAGAGGACAACTCTACC	5553	A AGT ACI	
		GTGAGA CAGATT			

	CACTCT GTTTGA		
	— CCT GAT		
GAM359	FACL6	GAAGTGAGAGGACAACTCTACC	5553 TAGGAA AGT — I
	GTGAGA CAGAT TACC		
	CACTCT GTTTG ATGG		
	— CCT AG G		
GAM359	GLP1R	GATGGGAGAAGTCAGAATTGCC	5552 TAGGAAGT TTA—
	GAGAAGTCAGA CC		
	CTCTTCAGTCT GG		
	CC — TAACG		
GAM359	GLP1R	GATGGGAGAAGTCAGAATTGCC	5552 GAAGT TTI
	GAGAAGTCAGA		
	CTCTTCAGTCT		
	C — TAA		
GAM359	HTN1	AGGAGAGTCAAGAAGTCAG	5545 — — III
	AGGA AGT GAGAAGTCAG		
	TCCT TCA TTCTTCAGT		
	C G CII		
GAM359	HTN1	AGGAGAGTCAAGAAGTCAG	5545 TA — — ATTAC
	GGA AGT GAGAAGTCAG		
	CCT TCA TTCTTCAGTC		
	— C G AIIIC		
GAM359	KRTHA4	TAGTAACTG-GAGCTCAGATTAC	5555 G G A AG C
	TAG AA TG GA TCAGATTAC		
	ATC TT AC CT AGTCTAATG		
	A G — CG I		
GAM359	KRTHA4	TAGTAACTG-GAGCTCAGATTAC	5555 — G G A AG I
	AG AA TG GA TCAGATTA		
	TC TT AC CT AGTCTAAT		
	A A G — CG I		
GAM359	MAD2L2	AGGAGGCTGAGAAGTCGAGGTT	5548 — AAG — ATI
	GG TGAGAAGTC AG		
	CC ACTCTTCAG TC		
	T G — C CAI		
GAM359	MAD2L2	AGGAGGCTGAGAAGTCGAGGTT	5548 TA A — — ATTACC
	GGA G TGAGAAGTC AG		
	CCT C ACTCTTCAG TC		
	— C G C CAACII		
GAM359	MET	AGGAACCAAGTGGAGAAGTCAG	5546 — — IIIC
	AGGA AGTG AGAAGTCA		

	TCCT TCAC TCTTCAGT		
	TGG C CIII		
GAM359 MET	AGGAACCAGTGGAGAAGTCAG	5546 TA	ATTACC
	GGA AGTG AGAAGTCAG		
	CCT TCAC TCTTCAGTC		
	__ TGG C GIIIC		
GAM359 PCDHGA12	GGACAGTTGGGAAGTCAGA	5554 AG__ A	
	GGA TG GAAGTCAG		
	CCT AC CTTTCAGTC		
	GTCA C TII		
GAM359 PCDHGA12	GGACAGTTGGGAAGTCAGA	5554 TAGGA GA_	TTAC
	AGT GAAGTCAGA		
	TCA CTTTCAGTCT		
	TG__ ACC CGII		
GAM359 PITPNB	AGGACTGTCAGCAAATCAGATTAC	5547 GGAA G _	I
	GT AG AAGTCAGATTA		
	CA TC TTTAGTCTAAT		
	TGA_ G G I		
GAM359 PITPNB	AGGACTGTCAGCAAATCAGATTAC	5547 TA A_ G _	CI
	GGA GT AG AAGTCAGATTAC		
	CCT CA TC TTTAGTCTAATG		
	__ GA G G AI		
GAM359 ZNF80	AGTGAGAAGTAGCAAGATT	5551 C ATIII	
	AGTGAGAAGT AG		
	TCACTCTTCA TC		
	_ GTTCT		
GAM360 ABCD3	TGATAGCATTGCA-TACTC	5565 AATG	AAGG
	ATAGCATTG ACTCG		
	TATCGTAAC TGAGT		
	__ GTA_		
GAM360 ABCD3	TGATAGCATTGCA-TACTC	5565	AAGG I
	TGATAGCATTG ACT		
	ACTATCGTAAC TGA		
	GTA_ G		
GAM360 ABCD3	TGATAGCATTGCA-TACTC	5565 AATG	AAGG
	ATAGCATTG ACTCG		
	TATCGTAAC TGAGT		
	__ GTA_		
GAM360 ABCD3	TGATAGCATTGCA-TACTC	5565	AAGG I
	TGATAGCATTG ACT		

	ACTATCGTAAC TGA		
	GTA_ G		
GAM360 ACPT	AAGGATAGCATT CAGCAGGA	5558 AAT	GA__ CTCGG
	GATAGCATT AGGA		
	CTATCGTAA TCCT		
	TTC GTCG GG		
GAM360 ACPT	AAGGATAGCATT CAGCAGGA	5558 AAT	GA__
	GATAGCATT AGG		
	CTATCGTAA TCC		
	TTC GTCG T		
GAM360 ACPT	AAGGATAGCATT CAGCAGGA	5558 AAT	GA__ CTCGG
	GATAGCATT AGGA		
	CTATCGTAA TCCT		
	TTC GTCG GG		
GAM360 ACPT	AAGGATAGCATT CAGCAGGA	5558 AAT	GA__
	GATAGCATT AGG		
	CTATCGTAA TCC		
	TTC GTCG T		
GAM360 AMY2B	GAAAGCACTTGAAGGACACGGG	5561 AATGAT	_ T
	AGCATT GAAGGAC CGGG		
	TCGTGA CTTCTG GCCC		
	_____ A T		
GAM360 AMY2B	GAAAGCACTTGAAGGACACGGG	5561 AT	_ T
	AGCATT GAAGGAC CGG		
	TCGTGA CTTCTG GCC		
	T_ A T		
GAM360 AMY2B	GAAAGCACTTGAAGGACACGGG	5561 AATGAT	_ T
	AGCATT GAAGGAC CGGG		
	TCGTGA CTTCTG GCCC		
	_____ A T		
GAM360 AMY2B	GAAAGCACTTGAAGGACACGGG	5561 AT	_ T
	AGCATT GAAGGAC CGG		
	TCGTGA CTTCTG GCC		
	T_ A T		
GAM360 APP	CTA-TTCATGCACTAGTTT	3499 ACTACTTC	CTC
	GCACTAGTTT		
	CGTGATCAAA		
	ATAAGTA_ C		
GAM360 APP	CTA-TTCATGCACTAGTTT	3499 CACTACTTC	CT
	GCACTAGTTT		

	CGTGATCAAA		
	TAAGTA__ CT		
GAM360 APP	CTA-TTCATGCACTAGTTT	3499	CTACTTC_ II
	GCACTAGTT		
	CGTGATCAA		
	GATAAGTA AI		
GAM360 APP	CTA-TTCATGCACTAGTTT	3499	TCACTACTTC CT
	GCACTAGTTT		
	CGTGATCAAA		
	AAGTA__ CT		
GAM360 APP	CTA-TTCATGCACTAGTTT	3499	ACTACTTC CTC
	GCACTAGTTT		
	CGTGATCAAA		
	ATAAGTA_ CII		
GAM360 APP	CTA-TTCATGCACTAGTTT	3499	CACTACTTC CT
	GCACTAGTTT		
	CGTGATCAAA		
	TAAGTA__ CT		
GAM360 APP	CTA-TTCATGCACTAGTTT	3499	CTACTTC_ II
	GCACTAGTT		
	CGTGATCAA		
	GATAAGTA AI		
GAM360 APP	CTA-TTCATGCACTAGTTT	3499	TCACTACTTC CT
	GCACTAGTTT		
	CGTGATCAAA		
	AAGTA__ CT		
GAM360 FPGS	TAGCATTGAAGAGCAAGACTCG	5564	____ IIC
	TAGCATTGAAG GACTC		
	ATCGTAACTTC CTGAG		
	TCGTT CIII		
GAM360 FPGS	TAGCATTGAAGAGCAAGACTCG	5564	AA T_ TTGAA
	TGA AGCA GGA		
	ACT TCGT TCTGAGCTT		
	A_ TC ____		
GAM360 FPGS	TAGCATTGAAGAGCAAGACTCG	5564	____ IIC
	TAGCATTGAAG GACTC		
	ATCGTAACTTC CTGAG		
	TCGTT CIII		
GAM360 FPGS	TAGCATTGAAGAGCAAGACTCG	5564	AA T_ TTGAA
	TGA AGCA GGA		

	ACT TCGT TCTGAGCTT	
	A_ TC _____	
GAM360 FUT6	GAT-GC-TAGAGGGACTCGGG 5563 AATGATA ATT A	
	GC GA GGA CTCTGAGCC	
	CG CT CCTGAGCC	
	_____ AT_ C	
GAM360 FUT6	GAT-GC-TAGAGGGACTCGGG 5563 ATA ATT A I	
	GC GA GGA CTCTGAGCC	
	CG CT CCTGAGCC	
	CTA AT_ C I	
GAM360 FUT6	GAT-GC-TAGAGGGACTCGGG 5563 AATGATA ATT A	
	GC GA GGA CTCTGAGCC	
	CG CT CCTGAGCC	
	_____ AT_ C	
GAM360 FUT6	GAT-GC-TAGAGGGACTCGGG 5563 ATA ATT A I	
	GC GA GGA CTCTGAGCC	
	CG CT CCTGAGCC	
	CTA AT_ C I	
GAM360 GPC3	GAGAGCAGTCCCAGGACTCGG 5562 AATGAT _ GA G	
	AGCA TT AGGACTCGG	
	TCGT AG TCCTGAGCC	
	_____ C GG G	
GAM360 GPC3	GAGAGCAGTCCCAGGACTCGG 5562 AT _ GA I	
	AGCA TT AGGACTCG	
	TCGT AG TCCTGAGC	
	C_ C GG I	
GAM360 GPC3	GAGAGCAGTCCCAGGACTCGG 5562 AATGAT _ GA G	
	AGCA TT AGGACTCGG	
	TCGT AG TCCTGAGCC	
	_____ C GG G	
GAM360 GPC3	GAGAGCAGTCCCAGGACTCGG 5562 AT _ GA I	
	AGCA TT AGGACTCG	
	TCGT AG TCCTGAGC	
	C_ C GG I	
GAM360 IL10RA	CACATACCCTGCACTAGTT 3498 _ TC TCTC	
	CAC TACT GCACTAGTT	
	GTG ATGG CGTGATCAA	
	T GA IIIC	
GAM360 IL10RA	CACATACCCTGCACTAGTT 3498 _ TC II	
	CAC TACT GCACTAGT	

	GTG ATGG CGTGATCA	
	T GA AI	
GAM360 IL10RA	CACATACCCTGCACTAGTT 3498 TC _ TC CT	
	AC TACT GCACTAGTTT	
	TG ATGG CGTGATCAAG	
	_ T GA II	
GAM360 IL10RA	CACATACCCTGCACTAGTT 3498 _ TC TCTC	
	CAC TACT GCACTAGTT	
	GTG ATGG CGTGATCAA	
	T GA IIIC	
GAM360 IL10RA	CACATACCCTGCACTAGTT 3498 _ TC II	
	CAC TACT GCACTAGT	
	GTG ATGG CGTGATCA	
	T GA AI	
GAM360 IL10RA	CACATACCCTGCACTAGTT 3498 TC _ TC CT	
	AC TACT GCACTAGTTT	
	TG ATGG CGTGATCAAG	
	_ T GA II	
GAM360 TBL1X	ATGTCAGCTCTGCAAGGACTCG 5559 AA A A _ GG	
	TG TAGC TTG AAGGACTCG	
	AC GTCG GAC TTCCTGAGC	
	_ A A G GI	
GAM360 TBL1X	ATGTCAGCTCTGCAAGGACTCG 5559 TGA A _ I	
	TAGC TTG AAGGACTC	
	GTCG GAC TTCCTGAG	
	CA_ A G I	
GAM360 TBL1X	ATGTCAGCTCTGCAAGGACTCG 5559 TGA A _ I	
	TAGC TTG AAGGACTC	
	GTCG GAC TTCCTGAG	
	CA_ A G I	
GAM360 TBL1X	ATGTCAGCTCTGCAAGGACTCG 5559 AA A A _ GG	
	TG TAGC TTG AAGGACTCG	
	AC GTCG GAC TTCCTGAGC	
	_ A A G GI	
GAM360 WBSCR5	CACTACTT--CTCTAGACTCTC 5560 GCA T	
	CACTACTTC CTAG TTCTC	
	GTGATGAAG GATC GAGAG	
	A_ T	
GAM360 WBSCR5	CACTACTT--CTCTAGACTCTC 5560 GCA T I	
	CACTACTTC CTAG TTC	

	GTGATGAAG GATC GAG	
	A__ T A	
GAM360 WBSR5	TCACTACTT--CTCTAGACTCTC 3505	GCA T
	TCACTACTTC CTAG TTCTC	
	AGTGATGAAG GATC GAGAG	
	A__ T	
GAM360 WBSR5	TCACTACTT--CTCTAGACTCTC 3505_	GCA T I
	CACTACTTC CTAG TTCT	
	GTGATGAAG GATC GAGA	
	A A__ T I	
GAM360 WBSR5	CACTACTT--CTCTAGACTCTC 5560	GCA T
	CACTACTTC CTAG TTCTC	
	GTGATGAAG GATC GAGAG	
	A__ T	
GAM360 WBSR5	CACTACTT--CTCTAGACTCTC 5560	GCA T I
	CACTACTTC CTAG TTC	
	GTGATGAAG GATC GAG	
	A__ T A	
GAM360 WBSR5	TCACTACTT--CTCTAGACTCTC 3505	GCA T
	TCACTACTTC CTAG TTCTC	
	AGTGATGAAG GATC GAGAG	
	A__ T	
GAM360 WBSR5	TCACTACTT--CTCTAGACTCTC 3505_	GCA T I
	CACTACTTC CTAG TTCT	
	GTGATGAAG GATC GAGA	
	A A__ T I	
GAM360 ZNF146	CTACCTT-CACTAGTTTCTC 3500_ CG	I
	TACTT CACTAGTTTCT	
	ATGGA GTGATCAAAGA	
	G A_ I	
GAM360 ZNF146	CTACCTT-CACTAGTTTCTC 3500 AC CG	
	TACTT CACTAGTTTCTC	
	ATGGA GTGATCAAAGAG	
	_ A_	
GAM360 ZNF146	CTACCTT-CACTAGTTTCTC 3500 CACT CG	
	ACTT CACTAGTTTCTC	
	TGGA GTGATCAAAGAG	
	___ A_	
GAM360 ZNF146	CTACCTT-CACTAGTTTCTC 3500 TACTA GC	
	CTTC ACTAGTTTCT	

		GAAG TGATCAAAGA	
		G_____	
GAM360 ZNF146		CTACCTT-CACTAGTTTCTC 3500_ CG I	
		TACTT CACTAGTTTCT	
		ATGGA GTGATCAAAGA	
		G A_ I	
GAM360 ZNF146		CTACCTT-CACTAGTTTCTC 3500 AC CG	
		TACTT CACTAGTTTCTC	
		ATGGA GTGATCAAAGAG	
		_ A_	
GAM360 ZNF146		CTACCTT-CACTAGTTTCTC 3500 CACT CG	
		ACTT CACTAGTTTCTC	
		TGGA GTGATCAAAGAG	
		_ A_	
GAM360 ZNF146		CTACCTT-CACTAGTTTCTC 3500 TCACTA GC	
		CTTC ACTAGTTTCT	
		GAAG TGATCAAAGA	
		G_____	
GAM361 ARSA		CCTGAAGCTCCAGAGGGCCGGGG 5571 TCCCCT _ CA I	
		AAGCTCCA GGGCC GGG	
		TTCGAGGT CCCGG CCC	
		C_____ CT C_ G	
GAM361 ATP6V1C1		CCTAAGCTCC-GGCCTCACGG 5573 TCCCCT AG _ G	
		AAGCTCC GGCC CA G	
		TTCGAGG CCGG GT C	
		_ A G	
GAM361 AXL		TCCCCCAGCTCCAGGCTCCCCGG 5576 A G_ A GI	
		TCCCCT AGCTCCAGG CCC GG	
		AGGGGG TCGAGGTCC GGG CC	
		G GA G	
GAM361 EGLN1		CCTAAGCTCC--GGCGCAG 5572 TCCCCT AG C	
		AAGCTCC GGC CAG	
		TTCGAGG CCG GTC	
		_ C	
GAM361 FMNL		CCTTCAGCTCCAGGGCCGAGGG 5570 TCCCCTA C	
		AGCTCCAGGGCC AGGG	
		TCGAGGTCCCGG TCCC	
		AAG_____ C	
GAM361 MGAT4B		AACCTCCAGCTGGGCCCAGG 5568 TCCCCTA CCA	
		AGCT GGGCCCAGG	

	TCGA CCCGGGTCC		
	G_____		
GAM361 MYOG	CCCCCAAGCTCCAGCAGCCC	5569 TC	_ AGG
	CCCTAAGCTCCAG GGCCC		
	GGGGTTCGAGGTC TCGGG		
	_____ G GII		
GAM361 PITX2	CTCAGCTCCAGGCACCCAGG	5574 TCCCCTAA	_
	GCTCCAGG GCCCAGG		
	CGAGGTCC TGGGTCC		
	_____ G		
GAM361 SART2	TCCTCCTCA-CTCCAGGGCGCCCGGG	5575 _ AA	_ A II
	TCC CCT GCTCCAGGGC CC GGG		
	AGG GGA TGAGGTCCCG GG CCC		
	A G_ C G II		
GAM362 ARSF	TCACTTGAGGTCGGGAGTT	5604	CCCA ATII
	TCACTTGAG GGA		
	AGTGAAGTC CCT		
	CAGC CAAI		
GAM362 ARSF	TCACTTGAGGTCGGGAGTT	5604	CCCA ATTGTGA
	TCACTTGAG GGA		
	AGTGAAGTC CCT		
	CAGC CAAIIG		
GAM362 ATP8A2	ACTGGGCATTAAATGAAGATC	5581 TCAACT	ATAG_ C
	GGGCAT GGAGATC		
	CCCGTA CTTCTAG		
	_____ ATTTA T		
GAM362 CNGA1	TCACTTGAGATCAGGAGTT	5601	CC ATII
	TCACTTGAG CAGGA		
	AGTGAAGTC GTCCT		
	TA CAAI		
GAM362 CNGA1	TCACTTGAGATCAGGAGTT	5601	CC ATTGTGA
	TCACTTGAG CAGGA		
	AGTGAAGTC GTCCT		
	TA CAAIIG		
GAM362 CORO2B	TCAACTGGGCAGTGT-GGCACATC	5596	TATAG AG_ CI
	TCAACTGGGCA GG ATC		
	AGTTGACCCGT CC TAG		
	CACA_ GTG II		
GAM362 DIAPH2	CAACTGGGCCTAAAGGGA	5583 TC	ATAT_ GATC
	AACTGGGC AGGGA		

	TTGACCCG TCCCT		
	— GATTT GIII		
GAM362 DSCR3	CTGGGCAACATAGGGAGACCC 5589 TCAACTGG _		
	GCA TATAGGGAGATCC		
	III		
	CGT GTATCCCTCTGGG		
	_____ T		
GAM362 DYRK1A	CTTAAGCCCAGGAATCTGAGA 5591 T GTGI		
	TGAGCCCAGGAATT		
	ATTCGGGTCCTTAG		
	— ACTC		
GAM362 DYRK1A	CTTAAGCCCAGGAATCTGAGA 5591 TCACTT G		
	GAGCCCAGGAATT TGAG		
	TTCGGGTCCTTAG ACTC		
	_____ —		
GAM362 GLTSCR1	TCACTGGAGCCCAGGAGTT-TGAG 5606 T ATTG I		
	TCACT GAGCCCAGGA TGAG		
	AGTGA CTCGGGTCCT ACTC		
	C CAA_ I		
GAM362 GLTSCR1	TCACTGGAGCCCAGGAGTT-TGAG 5606_ T ATTG I		
	CACT GAGCCCAGGA TGA		
	GTGA CTCGGGTCCT ACT		
	A C CAA_ I		
GAM362 HDAC6	CAA-TGGGCAGG--GGGAGATCC 5584 TCAAC TATA		
	TGGGCA GGGAGATC		
	ACCCGT CCCTCTAG		
	TT__ CC__		
GAM362 HNRPD	AACTGGGCATTTGGGAAAAT 5580 TCAA ATA TC		
	CTGGGCAT GGGAGA		
	GACCCGTA CCCTTT		
	_____ AA_ TA		
GAM362 LILRB4	CAGCTGGGCATAT-GACACATCC 5585 TCAA A GAG		
	CTGGGCATAT GG ATCC		
	GACCCGTATA CT TAGG		
	TC__ _ GTG		
GAM362 MAPK7	CTTCCGCCCAGGGAATTGTG 5590 GA _ II		
	CTT GCCCAGG AATTGT		
	GAA CGGGTCC TTAACA		
	GG C CI		
GAM362 MAPK7	CTTCCGCCCAGGGAATTGTG 5590 TCACTTGA _ A		
	GCCCAGG AATTGTG		

	CGGGTCC TTAACAC		
	GG_____ C A		
GAM362 MTL5	TCAACTGGG-ATCATGCGGA 5597	CA AG GATC	
	TCAACTGGG TAT GGA		
	AGTTGACCC GTA CCT		
	TA CG IIIC		
GAM362 MUC3B	AACTGGGCA-ACAGGGTGA 5579 TCAA	T A	
	CTGGGCA ATAGGG GAT		
	GACCCGT TGTCCC CTG		
	_____ A		
GAM362 NAGA	CTGAGGAGTAT-GGGAGATCC 5588 TCAACTG	CA A	
	GG TAT GGGAGATC		
	CC ATA CCCTCTAG		
	_____ TC _		
GAM362 NCOA6	CTTGAGCCCAGGAGGT-TGAG 5593 _	ATTG I	
	TTGAGCCCAGGA TGA		
	AACTCGGGTCCT ACT		
	G CCA_ I		
GAM362 NCOA6	CTTGAGCCCAGGAGGT-TGAG 5593 TCACTT	ATTG	
	GAGCCCAGGA TGA		
	CTCGGGTCCT ACT		
	_____ CCA_		
GAM362 NCOA6	TCACTTGAGGTCAGGAGTT-TGAG 5607	CC ATTG I	
	TCACTTGAG CAGGA TGAG		
	AGTGA ACTC GTCCT ACTC		
	CA CAA_ I		
GAM362 NCOA6	TCACTTGAGGTCAGGAGTT-TGAG 5607 _	CC ATTG I	
	CACTTGAG CAGGA TGA		
	GTGA ACTC GTCCT ACT		
	A CA CAA_ I		
GAM362 NEU3	CTTGAGCCCAGGAGTTG-GAG 5594 _	A T I	
	TTGAGCCCAGGA TTG GA		
	AACTCGGGTCCT AAC CT		
	G C _ I		
GAM362 NEU3	CTTGAGCCCAGGAGTTG-GAG 5594 TCACTT	A T	
	GAGCCCAGGA TTG GA		
	CTCGGGTCCT AAC CT		
	_____ C _		
GAM362 PPP2R2B	TCAACTGGGGA-AAAGGATGAACC 5600	CATAT _ T I	
	TCAACTGGG AGGGA GA CC		

	AGTTGACCC	TTCCT CT GG	
	CTT__	A T I	
GAM362 PRIM2A	CTGGGCAACATAGGGAGACCC	5589 TCAACTGG _	
	GCA TATAGGGAGATCC		
	CGT GTATCCCTCTGGG		
	_____ T		
GAM362 PRKY	TCAACTGGGACTTTAATAGGTAG	5595 _AT__ G ATCCI	
	TCAACTGGG C ATAGG AG		
	I II		
	AGTTGACCC G TATCC TC		
	T AAAT A IIICC		
GAM362 RAD1	CACTTGAGCCCAGGTGTTG-GAG	5586 _ AA T I	
	ACTTGAGCCCAGG TTG GA		
	II		
	TGAACTCGGGTCC AAC CT		
	G AC _ I		
GAM362 RAD1	CACTTGAGCCCAGGTGTTG-GAG	5586 TC AA T	
	ACTTGAGCCCAGG TTG GAG		
	III		
	TGAACTCGGGTCC AAC CTC		
	_____ AC _		
GAM362 RERE	ACTGT-CATGCAGGGAGATCC	5582 TCAACTGGG A	
	CAT TAGGGAGATC		
	GTA GTCCCTCTAG		
	CA_____ C		
GAM362 RGS9	TCGCTTGAGCCCAGGAGTT-TGAG	5608 A ATTG I	
	TC CTTGAGCCCAGGA TGAG		
	II		
	AG GAACTCGGGTCCT ACTC		
	C CAA_ I		
GAM362 RGS9	TCGCTTGAGCCCAGGAGTT-TGAG	5608 _A ATTG I	
	C CTTGAGCCCAGGA TGA		
	I		
	G GAACTCGGGTCCT ACT		
	A C CAA_ I		
GAM362 SGT	CTTGAGCCCAGAAGAGGTGA	5592 ATT I	
	TTGAGCCCAGGA GTG		
	AACTCGGGTCTT CAC		
	CTC I		
GAM362 SGT	CTTGAGCCCAGAAGAGGTGA	5592 TCACTT ATT	
	GAGCCCAGGA GTGA		
	CTCGGGTCTT CACT		
	_____ CTC		
GAM362 SLC3A2	TCACTTGAGGCCAAGAGTTG	5605 C A TGA	
	TCACTTGAG CCAGGA TTG		

		AGTGAAGTC GGTTC AAC		
		C C III		
GAM362 SLC3A2		TCACTTGAGGCCAAGAGTTG 5605	C	ATTI
		CACTTGAG CCAGGA		
		GTGAAGTC GGTTC		
		C CAAI		
GAM362 SMAC		TCACTTGAGCCCAGGAGTT 5602		ATII
		TCACTTGAGCCCAGGA		
		AGTGAAGTCGGGTCCT		
		CAAI		
GAM362 SMAC		TCACTTGAGCCCAGGAGTT 5602		ATTGTGA
		TCACTTGAGCCCAGGA		
		AGTGAAGTCGGGTCCT		
		CAAIIG		
GAM362 SMAC		TCACTTGAGGTCAGGAATT 5603	CC	GTGA
		TCACTTGAG CAGGAATT		
		AGTGAAGTC GTCCTTA		
		CA IIIIG		
GAM362 SMAC		TCACTTGAGGTCAGGAATT 5603	CC	II
		TCACTTGAG CAGGAAT		
		AGTGAAGTC GTCCTTA		
		CA AI		
GAM362 SMARCD1		TCAACTGGGCAGACAAGGGA 5598	T	A TC
		TCAACTGGGCA ATAGGG GA		
		II		
		AGTTGACCCGT TGTTC CT		
		C _ II		
GAM362 STMN1		TCAACTGGG-ATA-AGGAAAGTCC 5599	CAT	_
		TCAACTGGG ATAGGGAGA TCC		
		AGTTGACCC TATTCCTTT AGG		
		_ C		
GAM362 SUOX		CTGGGATCAAGATAGGGAGACCC 5587	TCAACTGGG T_	I
		CA ATAGGGAGATCC		
		II		
		GT TATCCCTCTGGG		
		CTA_____ TC A		
GAM363 ASTN		ATTACAGTGTTTCATGTACATTC 5613	AT_ AGG G	CI
		CAG GGTT GTGTACATTC		
		GTC CCAA TACATGTAAG		
		TAAT A_ G II		
GAM363 CLASP1		CAGAGGGGTCTGTGGAAT 5614	ATCA G	TACATTC
		GAGGGGTT GTG		

	CTCCCCAG CAC		
	_____ A CTTTACT		
GAM363 IL10RA	CAGAGGGGTGGGGGT-CAT	5615 ATCA	T T A T
	GAGGGGT GG GT CAT		
	CTCCCCA CC CA GTA		
	_____ C C _ C		
GAM363 MN1	ATCAGAGGGGTTCATGGAGT	5612	___ T ACATTC
	ATCAGAGGGGT TGG GT		
	TAGTCTCCCCA ACC CA		
	GT T IIICCT		
GAM363 MYO3A	AGAGGGGTTGGCG-AGATCCC	5611 ATCAGA	TAC
	GGGGTTGGTG ATTC		
	CCCCAACCGC TAGG		
	_____ TC_		
GAM363 NCOA6	TCAGAGGTCT--GTGTACATT	5616 ATCAG	G C
	AGGGGT GTGTACATT		
	TCTCCAG CACATGTAA		
	G_____ A A		
GAM364 ATP11A	GGCAGGATGCAGTGCAGGA	5623	___ T III
	GGCAGGATG GTGC GG		
	CCGTCCTAC CACG CC		
	GT T TII		
GAM364 ATP11A	GGCAGGATGCAGTGCAGGA	5623 TG	___ T GAGCG
	GCAGGATG GTGC GGA		
	CGTCCTAC CACG CCT		
	_____ GT T GIIT		
GAM364 CCND1	CATGTTGGTGCTGGGAAGCG	5620 AGGA	AG I
	TGGTGCTGG AGC		
	ACCACGACC TCG		
	TACA CT I		
GAM364 CCND1	CATGTTGGTGCTGGGAAGCG	5620 TGGCAGGA	AG
	TGGTGCTGG AGCG		
	ACCACGACC TCGC		
	CA_____ CT		
GAM364 CCND1	CAGGATGGTTGAGGTAAGCGT	5621	GCT A I
	AGGATGGT GG GAGCG		
	TCCTACCA CC TTCGC		
	ACT A I		
GAM364 CCND1	CAGGATGGTTGAGGTAAGCGT	5621 TGGCAG	GCT A
	GATGGT GG GAGCGT		

	CTACCA CC TTCGCA		
	_____ ACT A		
GAM364 CDH6	TGGCAGGATGGT-CATGAAAGC 5630	GCTG	GT
	TGGCAGGATGGT GAGAGC		
	ACCGTCCTACCA CTTTCG		
	GTA_ II		
GAM364 CDH6	TGGCAGGATGGT-CATGAAAGC 5630 _	GC	AGI
	GGCAGGATGGT TGGAG		
	CCGTCCTACCA ACTTT		
	A GT CII		
GAM364 CSPG2	GCGGGACGGTGCTGGAAGATGCG 5622 CA	_ _	I
	GGATGGTGCTGGA GA GC		
	CCTGCCACGACCT CT CG		
	_____ T A I		
GAM364 CSPG2	GCGGGACGGTGCTGGAAGATGCG 5622 TGGCA	_ _	TI
	GGATGGTGCTGGA GA GCG		
	CCTGCCACGACCT CT CGC		
	C_____ T A CC		
GAM364 DDX11	GGCAGGATGTTGTCTGGAG 5625	G _	II
	GGCAGGATG TG CTGGA		
	CCGTCCTAC AC GACCT		
	A A CI		
GAM364 DDX11	GGCAGGATGTTGTCTGGAG 5625 TG	G _	AGCG
	GCAGGATG TG CTGGAG		
	CGTCCTAC AC GACCTC		
	_____ A A CIII		
GAM364 G6PD	CAGGATGGT-CTCGAGTGC 5619	G G	AGI
	CAGGATGGT CT GAG		
	GTCCTACCA GA CTC		
	_ G ACG		
GAM364 G6PD	CAGGATGGT-CTCGAGTGC 5619 TGGCAG	G G	A
	GATGGT CT GAG GC		
	CTACCA GA CTC CG		
	_____ _ G A		
GAM364 HCK	TGGC-GGATGGTGCTGGAG 5628	A	AGC
	TGGC GGATGGTGCTGGAG		
	ACCG CCTACCACGACCTC		

GAM364 HCK	TGGC-GGATGGTGCTGGAG 5628	A	I
	TGGC GGATGGTGCTGGA		

	ACCG CCTACCACGACCT			
	— C			
GAM364 IDH3G	TGGCTGG--GGTGCTGGAG 5629	A AT	AGC	
	TGGC GG GGTGCTGGAG			
	ACCG CC CCACGACCTC			
	A — III			
GAM364 IDH3G	TGGCTGG--GGTGCTGGAG 5629	A AT	I	
	TGGC GG GGTGCTGGA			
	ACCG CC CCACGACCT			
	A — C			
GAM364 INHBB	TGGCAGGATGCGT-CTGGCTGTGCGT 5627	_ G	AGA_ II	
	TGGCAGGATG GT CTGG GCGT			
	ACCGTCCTAC CA GACC CGCA			
	G _ GACA II			
GAM364 INHBB	TGGCAGGATGCGT-CTGGCTGTGCGT 5627 G	_ G	AGA_ I	
	GCAGGATG GT CTGG GCG			
	CGTCCTAC CA GACC CGC			
	_ G _ GACA I			
GAM364 LLGL1	GGAAGGATGGTGTGTGGAG 5624 C	C_ II		
	GG AGGATGGTG TGA			
	CC TCCTACCAC ACCT			
	T AC CI			
GAM364 LLGL1	GGAAGGATGGTGTGTGGAG 5624 TGGC	C_ AGCG		
	AGGATGGTG TGGAG			
	TCCTACCAC ACCTC			
	CT_ AC CIII			
GAM364 RASAL1	GGCAGGAT-GCGCTGAAGAG 5626	_ G	I	
	GCAGGATG TGCTGGAGA			
	CGTCCTAC GCGACTTCT			
	C _ I			
GAM364 RASAL1	GGCAGGAT-GCGCTGAAGAG 5626 TG	G CG		
	GCAGGATG TGCTGGAGAG			
	CGTCCTAC GCGACTTCTC			
	— — CI			
GAM365 CD59	GCACTGCTCAGGATGTCTT 5637	T _ ATII		
	GCACTGCTC GGA GT			
	CGTGACGAG CCT CA			
	T A GAAI			
GAM365 DTNB	ACCCGAGCTCCGTCTGGAGTA 5634	CCC_ A C	I	
	GC CTG TCTGGAGT			

	CG GGC AGACCTCA	
	GGCT A _ I	
GAM365 DTNB	ACCCGAGCTCCGTCTGGAGTA 5634 TA _ A C TTG	
	CCC GC CTG TCTGGAGTA	
	GGG CG GGC AGACCTCAT	
	_ CT A _ CII	
GAM365 GPR17	TACCTTGCGCTGCAAAGGAGTATTG 5638 C_ A TCT II	
	TACC GC CTGC GGAGTATTG	
	ATGG CG GACG CCTCATAAC	
	AA C TTT II	
GAM365 GPR17	TACCTTGCGCTGCAAAGGAGTATTG 5638 ACCC A TCT I	
	GC CTGC GGAGTATT	
	CG GACG CCTCATAA	
	GGAA C TTT I	
GAM365 HNRPA2B1	GCATCTGCTCTGGTGTCTT 5636 _ A ATII	
	GCA CTGCTCTGG GT	
	CGT GACGAGACC CA	
	A A GAAI	
GAM365 HNRPA2B1	GCATCTGCTCTGGTGTCTT 5636 TACCCGCAC A ATT	
	TGCTCTGG GT	
	ACGAGACC CA	
	_____ A GAA	
GAM365 MECP2	ACCCGCACTGGCGCTCACGAGTA 5633 CCC _ TG I	
	GCACT GCTC GAGT	
	CGTGA CGAG CTCA	
	_ CCG TG I	
GAM365 MECP2	ACCCGCACTGGCGCTCACGAGTA 5633 TA _ TG TTGI	
	CCCGCACT GCTC GAGTA	
	GGGCGTGA CGAG CTCAT	
	_ CCG TG CIII	
GAM365 PVR	CTGCTCTGGTTGGCAGTATTG 5635 _ IIIC	
	CTGCTCTGG AGTATT	
	GACGAGACC TCATAA	
	AACCG CIII	
GAM366 ATOX1	ACACGCG--G-GTCACCGTGC 5642 _ G TTGA	
	CA GCG GTCACCGTG	
	GT CGC CAGTGGCAC	
	T G C_	
GAM366 ATOX1	ACACGCG--G-GTCACCGTGC 5642 TTACAG T A	
	GCGT G GTCACCGTG	

		TGCG C CAGTGGCAC		
		_____ _C		
GAM366 BRCA1	TTACAGGCG-TGAGCCACCATGCC	5652	T	I
	TTACAGGCGT GAGTCACCGTGCC			
	AATGTCCGCA CTCGGTGGTACGG			
		I		
GAM366 BRCA1	TTACAGGCG-TGAGCCACCATGCC	5652 _	T	I
	TACAGGCGT GAGTCACCGTGC			
	ATGTCCGCA CTCGGTGGTACG			
	A _ I			
GAM366 CHRNA5	TTACAGGTGT-GAGCCACCGTGCC	5657	C T	I
	TTACAGG GT GAGTCACCGTGCC			
	AATGTCC CA CTCGGTGGCACGG			
	A _ I			
GAM366 CHRNA5	TTACAGGTGT-GAGCCACCGTGCC	5657 _	C T	I
	TACAGG GT GAGTCACCGTGC			
	ATGTCC CA CTCGGTGGCACG			
	A A _ I			
GAM366 COG7	TTACAGGCG-TGAGCCACCGTG	5648	T	CC
	TTACAGGCGT GAGTCACCGTG			
	AATGTCCGCA CTCGGTGGCAC			
		II		
GAM366 COG7	TTACAGGCG-TGAGCCACCGTG	5648 _	T	I
	TACAGGCGT GAGTCACCGT			
	ATGTCCGCA CTCGGTGGCA			
	A _ I			
GAM366 CTSS	TTACAGGCGT-GAGCCACCGTGCC	5656	T	I
	TTACAGGCGT GAGTCACCGTGCC			
	AATGTCCGCA CTCGGTGGCACGG			
		I		
GAM366 CTSS	TTACAGGCGT-GAGCCACCGTGCC	5656 _	T	I
	TACAGGCGT GAGTCACCGTGC			
	ATGTCCGCA CTCGGTGGCACG			
	A _ I			
GAM366 CYP3A4	TTACAGGCG-TGAGCCACTGTGCC	5654	T	C I
	TTACAGGCGT GAGTCAC GTGCC			
	AATGTCCGCA CTCGGTG CACGG			
		A I		
GAM366 CYP3A4	TTACAGGCG-TGAGCCACTGTGCC	5654 _	T	C I
	TACAGGCGT GAGTCAC GTGC			

	ATGTCCGCA CTCGGTG CACG		
	A _ A I		
GAM366 CYP3A4	TTACAGGC---GAGTCCACCATGCC 5646	GTT _	
	TTACAGGC GAGTC ACCGTGCC		
	AATGTCCG CTCAG TGGTACGG		
	_ G		
GAM366 CYP3A4	TTACAGGC---GAGTCCACCATGCC 5646 _	GTT _ I	
	TACAGGC GAGTC ACCGTGC		
	ATGTCCG CTCAG TGGTACG		
	A _ G I		
GAM366 CYP7B1	ACAGGAAT---GTCACCGTG 5641 _ C TGA		
	CAGG GT GTCACCGT		
	GTCC TA CAGTGGCA		
	T T _		
GAM366 CYP7B1	ACAGGAAT---GTCACCGTG 5641 TTACAGGCGTTGA		
	GTCACCGTG		
	CAGTGGCAC		
	TCCTTA_____		
GAM366 DCLRE1C	TTACAGGCAT-GAGCCACCGTGCC 5650	T I	
	TTACAGGCGT GAGTCACCGTGCC		
	AATGTCCGTA CTCGGTGGCACGG		
	_ I		
GAM366 DCLRE1C	TTACAGGCAT-GAGCCACCGTGCC 5650 _	T I	
	TACAGGCGT GAGTCACCGTGC		
	ATGTCCGTA CTCGGTGGCACG		
	A _ I		
GAM366 DDOST	TTACAGGCAT-GAGCCACCGTGCC 5650	T I	
	TTACAGGCGT GAGTCACCGTGCC		
	AATGTCCGTA CTCGGTGGCACGG		
	_ I		
GAM366 DDOST	TTACAGGCAT-GAGCCACCGTGCC 5650 _	T I	
	TACAGGCGT GAGTCACCGTGC		
	ATGTCCGTA CTCGGTGGCACG		
	A _ I		
GAM366 EFG2	TTACAGGCG-TGAGCCACCATGCC 5652	T I	
	TTACAGGCGT GAGTCACCGTGCC		
	AATGTCCGCA CTCGGTGGTACGG		
	_ I		
GAM366 EFG2	TTACAGGCG-TGAGCCACCATGCC 5652 _	T I	
	TACAGGCGT GAGTCACCGTGC		

		ATGTCCGCA CTCGGTGGTACG			
		A _ I			
GAM366 F2R		TTACAGGCG-TGAGCCACCGCGCC 5653	T		I
		TTACAGGCGT GAGTCACCGTGCC			
		AATGTCCGCA CTCGGTGGCGCGG			
		_ I			
GAM366 F2R		TTACAGGCG-TGAGCCACCGCGCC 5653 _	T		I
		TACAGGCGT GAGTCACCGTGC			
		ATGTCCGCA CTCGGTGGCGCG			
		A _ I			
GAM366 GAS7		TTACAGGCGT-GAGCCACCGTGCC 5656	T		I
		TTACAGGCGT GAGTCACCGTGCC			
		AATGTCCGCA CTCGGTGGCACGG			
		_ I			
GAM366 GAS7		TTACAGGCGT-GAGCCACCGTGCC 5656 _	T		I
		TACAGGCGT GAGTCACCGTGC			
		ATGTCCGCA CTCGGTGGCACG			
		A _ I			
GAM366 HFE		TTACAGGCGT-GAGCCACCGTGCC 5656	T		I
		TTACAGGCGT GAGTCACCGTGCC			
		AATGTCCGCA CTCGGTGGCACGG			
		_ I			
GAM366 HFE		TTACAGGCGT-GAGCCACCGTGCC 5656 _	T		I
		TACAGGCGT GAGTCACCGTGC			
		ATGTCCGCA CTCGGTGGCACG			
		A _ I			
GAM366 HIP1		TTACAGGCG-TGAGCCACTGTGCC 5654	T	C	I
		TTACAGGCGT GAGTCAC GTGCC			
		AATGTCCGCA CTCGGTG CACGG			
		_ A I			
GAM366 HIP1		TTACAGGCG-TGAGCCACTGTGCC 5654 _	T	C	I
		TACAGGCGT GAGTCAC GTGC			
		ATGTCCGCA CTCGGTG CACG			
		A _ A I			
GAM366 IFNAR1		TTACAGGTGT-GAGCCACCGTGCC 5657	C T		I
		TTACAGG GT GAGTCACCGTGCC			
		AATGTCC CA CTCGGTGGCACGG			
		A _ I			
GAM366 IFNAR1		TTACAGGTGT-GAGCCACCGTGCC 5657 _	C T		I
		TACAGG GT GAGTCACCGTGC			

		ATGTCC CA CTCGGTGGCACG		
		A A _ I		
GAM366 IL11		TTACAGGCG-TGAGCCACCATGCC 5652	T	I
		TTACAGGCGT GAGTCACCGTGCC		
		AATGTCCGCA CTCGGTGGTACGG		
		_ I		
GAM366 IL11		TTACAGGCG-TGAGCCACCATGCC 5652 _	T	I
		TACAGGCGT GAGTCACCGTGC		
		ATGTCCGCA CTCGGTGGTACG		
		A _ I		
GAM366 IL17R		TTACAGGCGT-GAGCCACCGTGCC 5656	T	I
		TTACAGGCGT GAGTCACCGTGCC		
		AATGTCCGCA CTCGGTGGCACGG		
		_ I		
GAM366 IL17R		TTACAGGCGT-GAGCCACCGTGCC 5656 _	T	I
		TACAGGCGT GAGTCACCGTGC		
		ATGTCCGCA CTCGGTGGCACG		
		A _ I		
GAM366 KERA		TACAC-CGTTGAGTC-CTGTG 5643 GG		ACCGI
		TACA CGTTGAGTC		
		ATGT GCAACTCAG		
		G_ GACAC		
GAM366 KERA		TACAC-CGTTGAGTC-CTGTG 5643 TTACAGG		ACC C
		CGTTGAGTC GTG		
		GCAACTCAG CAC		
		TGTG__ GA_ A		
GAM366 LILRB1		TTACAGGCGT-GAGCCACCGTGCC 5656	T	I
		TTACAGGCGT GAGTCACCGTGCC		
		AATGTCCGCA CTCGGTGGCACGG		
		_ I		
GAM366 LILRB1		TTACAGGCGT-GAGCCACCGTGCC 5656 _	T	I
		TACAGGCGT GAGTCACCGTGC		
		ATGTCCGCA CTCGGTGGCACG		
		A _ I		
GAM366 LRRC2		TTATAGGCGT-GAGTCACCGCGCC 5658 TAC_	T	I
		AGGCGT GAGTCACCGTGC		
		TCCGCA CTCAGTGGCGCG		
		AATA _ I		
GAM366 LRRC2		TTATAGGCGT-GAGTCACCGCGCC 5658 TTAC	T	I
		AGGCGT GAGTCACCGTGCC		

	TCCGCA CTCAGTGGCGCGG			
	AATA _ I			
GAM366 LRRC2	TTATAGGTGT-GAGCCACCGTGCC	5659	TAC_ C T	I
	AGG GT GAGTCACCGTGC			
	TCC CA CTCGGTGGCACG			
	AATA A _ I			
GAM366 LRRC2	TTATAGGTGT-GAGCCACCGTGCC	5659	TTAC C T	I
	AGG GT GAGTCACCGTGCC			
	TCC CA CTCGGTGGCACGG			
	AATA A _ I			
GAM366 MUC3B	TTACAGGTGTGGGAGTCACCG	5645	C T_ TGCC	
	TTACAGG GT GAGTCACCG			
	AATGTCC CA CTCAGTGGC			
	A CC IIIC			
GAM366 MUC3B	TTACAGGTGTGGGAGTCACCG	5645	T C T_ I	
	ACAGG GT GAGTCACC			
	TGTCC CA CTCAGTGG			
	_ A CC I			
GAM366 MYO1C	TTACAGGCG-TGAGCCACCATGCC	5652	T	I
	TTACAGGCGT GAGTCACCGTGCC			
	AATGTCCGCA CTCGGTGGTACGG			
	_ I			
GAM366 MYO1C	TTACAGGCG-TGAGCCACCATGCC	5652	_ T	I
	TACAGGCGT GAGTCACCGTGC			
	ATGTCCGCA CTCGGTGGTACG			
	A _ I			
GAM366 NFKBIL2	TTACAGGCG-TGAGCCACCGCGCC	5653	T	I
	TTACAGGCGT GAGTCACCGTGCC			
	AATGTCCGCA CTCGGTGGCGCGG			
	_ I			
GAM366 NFKBIL2	TTACAGGCG-TGAGCCACCGCGCC	5653	_ T	I
	TACAGGCGT GAGTCACCGTGC			
	ATGTCCGCA CTCGGTGGCGCG			
	A _ I			
GAM366 NT5C2	TTACAGGCG-TGAGCCGCGTGCC	5655	T A	I
	TTACAGGCGT GAGTC CCGTGCC			
	AATGTCCGCA CTCGG GGCACGG			
	_ C I			
GAM366 NT5C2	TTACAGGCG-TGAGCCGCGTGCC	5655	_ T A	I
	TACAGGCGT GAGTC CCGTGC			

		ATGTCCGCA CTCGG GGCACG		
		A _ C I		
GAM366 PA2G4		TTACAGGCG-TGAGCCACCGCGCC 5653	T	I
		TTACAGGCGT GAGTCACCGTGCC		
		AATGTCCGCA CTCGGTGGCGCGG		
		_ I		
GAM366 PA2G4		TTACAGGCG-TGAGCCACCGCGCC 5653 _	T	I
		TACAGGCGT GAGTCACCGTGC		
		ATGTCCGCA CTCGGTGGCGCG		
		A _ I		
GAM366 PCDH11Y		TTACAGGCG-TGAGCCACCGCGCC 5653	T	I
		TTACAGGCGT GAGTCACCGTGCC		
		AATGTCCGCA CTCGGTGGCGCGG		
		_ I		
GAM366 PCDH11Y		TTACAGGCG-TGAGCCACCGCGCC 5653 _	T	I
		TACAGGCGT GAGTCACCGTGC		
		ATGTCCGCA CTCGGTGGCGCG		
		A _ I		
GAM366 PIK3R2		TTACAGGCAT-GAGCCACCGTGCC 5650	T	I
		TTACAGGCGT GAGTCACCGTGCC		
		AATGTCCGTA CTCGGTGGCACGG		
		_ I		
GAM366 PIK3R2		TTACAGGCAT-GAGCCACCGTGCC 5650 _	T	I
		TACAGGCGT GAGTCACCGTGC		
		ATGTCCGTA CTCGGTGGCACG		
		A _ I		
GAM366 PSMB9		TTACAGGCGT-GAGCCACCGTGCC 5656	T	I
		TTACAGGCGT GAGTCACCGTGCC		
		AATGTCCGCA CTCGGTGGCACGG		
		_ I		
GAM366 PSMB9		TTACAGGCGT-GAGCCACCGTGCC 5656 _	T	I
		TACAGGCGT GAGTCACCGTGC		
		ATGTCCGCA CTCGGTGGCACG		
		A _ I		
GAM366 RAB3B		TTACAGGCG-TGAGCCACCGCGCC 5653	T	I
		TTACAGGCGT GAGTCACCGTGCC		
		AATGTCCGCA CTCGGTGGCGCGG		
		_ I		
GAM366 RAB3B		TTACAGGCG-TGAGCCACCGCGCC 5653 _	T	I
		TACAGGCGT GAGTCACCGTGC		

	ATGTCCGCA CTCGGTGGCGCG		
	A _ I		
GAM366 RAD51L1	TTACAGGCG-TGATCCACCG 5647	T GT	TGC
	TTACAGGCGT GA CACCG		
	AATGTCCGCA CT GTGGC		
	_ AG III		
GAM366 RAD51L1	TTACAGGCG-TGATCCACCG 5647 _	T GT	I
	TACAGGCGT GA CACC		
	ATGTCCGCA CT GTGG		
	A _ AG I		
GAM366 SFRS2IP	TACAGGCG-TGAGCTACTGTGCC 5644 _	T TC C	I
	ACAGGCGT GAG AC GTGC		
	TGTCCGCA CTC TG CACG		
	A _ GA A I		
GAM366 SFRS2IP	TACAGGCG-TGAGCTACTGTGCC 5644 TT	T TC C	
	ACAGGCGT GAG AC GTGCC		
	TGTCCGCA CTC TG CACGG		
	_ _ GA A		
GAM366 SLC14A2	TTACAGGCGT-GAGCCACCGTGCC 5656	T	I
	TTACAGGCGT GAGTCACCGTGCC		
	AATGTCCGCA CTCGGTGGCACGG		
	_ I		
GAM366 SLC14A2	TTACAGGCGT-GAGCCACCGTGCC 5656 _	T	I
	TACAGGCGT GAGTCACCGTGCC		
	ATGTCCGCA CTCGGTGGCACG		
	A _ I		
GAM366 SMG1	TTACAGGCG-TGAGCCACTGTGCC 5654	T C	I
	TTACAGGCGT GAGTCAC GTGCC		
	AATGTCCGCA CTCGGTG CACGG		
	_ A I		
GAM366 SMG1	TTACAGGCG-TGAGCCACTGTGCC 5654 _	T C	I
	TACAGGCGT GAGTCAC GTGC		
	ATGTCCGCA CTCGGTG CACG		
	A _ A I		
GAM366 SRGAP1	TTACAGGCG-TGAGTCACTGTG 5649	T C CC	
	TTACAGGCGT GAGTCAC GTG		
	AATGTCCGCA CTCAGTG CAC		
	_ A II		
GAM366 SRGAP1	TTACAGGCG-TGAGTCACTGTG 5649 _	T C I	
	TACAGGCGT GAGTCAC GT		

	ATGTCCGCA CTCAGTG CA		
	A _ A I		
GAM366 TCTA	TTACAGGCG-TGAGCCACCATGCC 5652	T	I
	TTACAGGCGT GAGTCACCGTGCC		
	AATGTCCGCA CTCGGTGGTACGG		
	_ I		
GAM366 TCTA	TTACAGGCG-TGAGCCACCATGCC 5652 _	T	I
	TACAGGCGT GAGTCACCGTGC		
	ATGTCCGCA CTCGGTGGTACG		
	A _ I		
GAM366 TRIM14	TTACAGGCG-TGAGCCACCGCGCC 5653	T	I
	TTACAGGCGT GAGTCACCGTGCC		
	AATGTCCGCA CTCGGTGGCGCGG		
	_ I		
GAM366 TRIM14	TTACAGGCG-TGAGCCACCGCGCC 5653 _	T	I
	TACAGGCGT GAGTCACCGTGC		
	ATGTCCGCA CTCGGTGGCGCG		
	A _ I		
GAM366 TRIM9	TTACAGGCATGG-GCCACCGTGCC 5651	T A	I
	TTACAGGCGT G GTCACCGTGCC		
	AATGTCCGTA C CGGTGGCACGG		
	_ C I		
GAM366 TRIM9	TTACAGGCATGG-GCCACCGTGCC 5651 _	T A	I
	TACAGGCGT G GTCACCGTGC		
	ATGTCCGTA C CGGTGGCACG		
	A _ C I		
GAM366 UC28	TTACAGGCGT-GAGCCACCGTGCC 5656	T	I
	TTACAGGCGT GAGTCACCGTGCC		
	AATGTCCGCA CTCGGTGGCACGG		
	_ I		
GAM366 UC28	TTACAGGCGT-GAGCCACCGTGCC 5656 _	T	I
	TACAGGCGT GAGTCACCGTGC		
	ATGTCCGCA CTCGGTGGCACG		
	A _ I		
GAM366 USP14	TTACAGGCGT-GAGCCACCGTGCC 5656	T	I
	TTACAGGCGT GAGTCACCGTGCC		
	AATGTCCGCA CTCGGTGGCACGG		
	_ I		
GAM366 USP14	TTACAGGCGT-GAGCCACCGTGCC 5656 _	T	I
	TACAGGCGT GAGTCACCGTGC		

	ATGTCCGCA CTCGGTGGCACG		
	A _ I		
GAM366 VDR	TTACAGGCG-TGAGCCACCGCGCC 5653	T	I
	TTACAGGCGT GAGTCACCGTGCC		
	AATGTCCGCA CTCGGTGGCGCGG		
	_ I		
GAM366 VDR	TTACAGGCG-TGAGCCACCGCGCC 5653 _	T	I
	TACAGGCGT GAGTCACCGTGC		
	ATGTCCGCA CTCGGTGGCGCG		
	A _ I		
GAM366 WIG1	TTACAGGCG-TGAGCCACCGCGCC 5653	T	I
	TTACAGGCGT GAGTCACCGTGCC		
	AATGTCCGCA CTCGGTGGCGCGG		
	_ I		
GAM366 WIG1	TTACAGGCG-TGAGCCACCGCGCC 5653 _	T	I
	TACAGGCGT GAGTCACCGTGC		
	ATGTCCGCA CTCGGTGGCGCG		
	A _ I		
GAM366 XT3	TTACAGGCGT-GAGCCACCGTGCC 5656	T	I
	TTACAGGCGT GAGTCACCGTGCC		
	AATGTCCGCA CTCGGTGGCACGG		
	_ I		
GAM366 XT3	TTACAGGCGT-GAGCCACCGTGCC 5656 _	T	I
	TACAGGCGT GAGTCACCGTGC		
	ATGTCCGCA CTCGGTGGCACG		
	A _ I		
GAM367 APBA2	CAGCCATCATCACCCGGAGGC 5663 TGGCAG	_	TG CT
	CCATCA ACCCG GGC		
	GGTAGT TGGGC CCG		
	_ AG CT TC		
GAM367 CHRNE	TGGCAGCCACCAGAGTCCCGTGGGGCT5671	A__	C III
	TGGCAGCCATCA CCCGTGGG CT		
	ACCGTCGGTGGT GGGCACCC GA		
	CTCA C III		
GAM367 DPYSL3	TGGGTGCCCTCACCACGTGGGCCT 5675	CA A A _	I
	TGG GCC TCA CC CGTGGGCCT		
	ACC CGG AGT GG GCACCCGGA		
	CA G _ T I		
GAM367 ECEL1	TGGCCGCCGCGCCTCCTCGTGGGCCT 5673	A ATCAA _	II
	TGGC GCC CC CGTGGGCCT		

	ACCG CGG GG GCACCCGGA	
	G CCGGA A II	
GAM367 FZD1	TGCCAGCGCCACACCCGTGGGCC 5672 G CA _ TI	
	TG CAGC TCA ACCCGTGGGCC	
	II IIII III IIIIIIIII	
	AC GTCG GGT TGGGCACCCGG	
	G CG G II	
GAM367 HRASLS	CAGCCATC-ACTCG-GGGCC 5664 TGGCAG A C T	
	CCATCA C CG GGGC	
	IIIIII I II IIII	
	GGTAGT G GC CCCG	
	_____ _A _	
GAM367 JTB	GCAGCCATCTAGCCCGTGG 5666 TGGC AA__ CC	
	AGCCATC CCCGTGGG	
	IIIIII IIIIIII	
	TCGGTAG GGGCACCT	
	_____ ATCG CI	
GAM367 LGR6	GCAGCCATCATTCACCGAGGG 5665 TGGC AC__ T CCT	
	AGCCATCA CCG GGG	
	IIIIII III III	
	TCGGTAGT GGC CCC	
	_____ AAGT T CCI	
GAM367 LYL1	GGCCGCGCCTC--CTCGTGGGCCT 5667 TG_ A A AACC	
	GC GCC TC CGTGGGCCT	
	II III II IIIIIII	
	CG CGG AG GCACCCGGA	
	CGG _ _ GA__	
GAM367 PRKY	TGTCATGCCATCAACACCCAGGG 5670 G _ _ GT CCTI	
	TG CA GCCATCAAC CC GGG	
	II II IIIIIII II III	
	AC GT CGGTAGTTG GG CCC	
	A A T GT IIIT	
GAM367 RFX5	TGGCAGCCATTAA---GTGGCCC 5674 C CCC G	
	TGGCAGCCAT AA GTGG CC	
	IIIIIIII II IIII II	
	ACCGTCGGTA TT CACC GG	
	A _ _ G	
GAM367 SUV39H1	GGCAGCCATCAGAACC-TTCGCCT 5668 TG AC_ GTGG I	
	GCAGCCATCA CC GCCT	
	IIIIIIII II IIII	
	CGTCGGTAGT GG CGGA	
	_____ CTT AAG_ A	
GAM367 TEM5	GGCGCCCATCAACCCATCGCCC 5669 TG AG GG	
	GC CCATCAACCCGT GCCT	
	II IIIIIIIII IIII	
	CG GGTAGTTGGGTA CGGG	
	CG _ _ G_	
GAM367 VIPR2	AGCCCCGAACC-GTGGGCCT 5662 TGGCAGCCATCAAC	
	CCGTGGGCC	
	IIIIIIII	

		GGCACCCGG		
		GGCTT_____		
GAM368 ABCB9	GCTGGGTGCCGGGCTGGGC	5692	C_ CA	CC
	GCTGGGTGCT GC GGGC			
	CGACCCACGG CG CCCG			
	CC A_ II			
GAM368 ABCB9	GCTGGGTGCCGGGCTGGGC	5692	C_ CA	II
	GCTGGGTGCT GC GGG			
	CGACCCACGG CG CCC			
	CC A_ GI			
GAM368 CAPN2	GCTGGG-GCGCGGCCAGGGCCC	5689	_ TC	I
	GCTGGG TGC GCCAGGGCCC			
	CGACCC GCG CGGTCCCGGG			
	C C_ I			
GAM368 CAPN2	GCTGGG-GCGCGGCCAGGGCCC	5689	CT_ TC	I
	GGGTGC GCCAGGGCC			
	CCCGCG CGGTCCCGG			
	GAC C_ I			
GAM368 CLCN7	GCAGGGTGCTCGCCATTGCC	5694	T	GG CI
	GC GGGTGCTCGCCA GCC			
	CG CCCACGAGCGGT CGG			
	T AA II			
GAM368 CLCN7	GCAGGGTGCTCGCCATTGCC	5694	CT	GG I
	GGGTGCTCGCCA GC			
	CCCACGAGCGGT CG			
	GT AA I			
GAM368 COL9A3	GGGTGCTCGCTGGCAAGGCC	5699	___	III
	GGGTGCTCGC CAGGGCC			
	CCCACGAGCG GTTCCGG			
	ACC GII			
GAM368 COL9A3	GGGTGCTCGCTGGCAAGGCC	5699	GCTGGG	___ I
	TGCTCGC CAGGGCCC			
	ACGAGCG GTTCCGGG			
	___ ACC C			
GAM368 COX15	GCTGGGGCACCTGCTCGCCAG	5685	___	GGCCCI
	GCTGGG TGCTCGCCAG			
	CGACCC ACGAGCGGTC			
	CGTGG IIICC			
GAM368 COX15	GCTGGGGCACCTGCTCGCCAG	5685	___	IIIC
	GCTGGG TGCTCGCCA			

	CGACCC ACGAGCGGT			
	CGTGG CIII			
GAM368 FBLN5	CTTGGGGCGTCTGCCAGGGCCC	5678 GC	T _ _	II
	TGGG GC TC GCCAGGGCCC			
	ACCC CG AG CGGTCCCGGG			
	A_ _ C A TI			
GAM368 FBLN5	CTTGGGGCGTCTGCCAGGGCCC	5678 T	_ C	I
	GGGTG CT GCCAGGGCC			
	CCCGC GA CGGTCCCGG			
	C A _ I			
GAM368 FBXL7	CTGGGTGCTCTATGCCAAGG	5679	___	III
	CTGGGTGCTC GCCAGG			
	GACCCACGAG CGGTTC			
	ATA CII			
GAM368 FBXL7	CTGGGTGCTCTATGCCAAGG	5679 GC	___	CCCI
	TGGGTGCTC GCCAGGG			
	ACCCACGAG CGGTTCC			
	___ ATA AIII			
GAM368 FLOT2	GCTGAGCTCTGGCCAGGGCC	5695	G C	CI
	GCTGGGT CT GCCAGGGCC			
	CGACTCG GA CGGTCCCGG			
	A C II			
GAM368 FLOT2	GCTGAGCTCTGGCCAGGGCC	5695	G C	I
	CTGGGT CT GCCAGGGC			
	GACTCG GA CGGTCCCG			
	A C I			
GAM368 LLGL1	GCTGG-TGCTGCTCCAGGGCCC	5686	G CG_	I
	GCTGG TGCT CCAGGGCCC			
	CGACC ACGA GGTCCCGGG			
	_ CGA I			
GAM368 LLGL1	GCTGG-TGCTGCTCCAGGGCCC	5686 CTG	CG_	I
	GGTGCT CCAGGGCC			
	CCACGA GGTCCCGG			
	GA_ CGA I			
GAM368 MDFI	GGGTGCTCGCCTGGCGCCC	5700	A _	II
	GGGTGCTCGCC GG GCC			
	CCCACGAGCGG CC CGG			
	A G GI			
GAM368 MDFI	GGGTGCTCGCCTGGCGCCC	5700 GCTGGG	A _	
	TGCTCGCC GG GCCC			

	ACGAGCGG CC CGGG		
	_____ A G		
GAM368 MECP2	CTGGGTGCT-GCCTGGAGCC 5681	C A _ II	
	CTGGGTGCT GCC GG GC		
	III II II		
	GACCCACGA CGG CC CG		
	_____ A T GI		
GAM368 MECP2	CTGGGTGCT-GCCTGGAGCC 5681 GC	C A _ C	
	TGGGTGCT GCC GG GCC		
	III II III		
	ACCCACGA CGG CC CGG		
	_____ A T A		
GAM368 NDST1	CTGGGTGCTCCCCAGCCCC 5684	G AG I	
	TGGGTGCTC CC GGCC		
	II IIII		
	ACCCACGAG GG TCGG		
	G G_ G		
GAM368 NDST1	CTGGGTGCTCCCCAGCCCC 5684 GC	G AG I	
	TGGGTGCTC CC GGCCC		
	II IIII		
	ACCCACGAG GG TCGGG		
	_____ G G_ G		
GAM368 NDUFA9	GCTGGGTGCTCAAACCACATGGGCC 5687	_____ CIII	
	GCTGGGTGCTC GCCA GGGCC		
	III IIII		
	CGACCCACGAG TGGT CCCGG		
	TT GTA IIIC		
GAM368 OLFM1	CTGGGTGCTGGCC--GGCC 5682	C AG I	
	CTGGGTGCT GCC GGC		
	III III		
	GACCCACGA CGG CCG		
	C _ G		
GAM368 OLFM1	CTGGGTGCTGGCC--GGCC 5682 GC	C AG	
	TGGGTGCT GCC GGCC		
	III IIII		
	ACCCACGA CGG CCGG		
	_____ C _		
GAM368 PSCD4	GCTGGGTGCCCAGGCCAGGG 5688	_____ CCCI	
	GCTGGGTGCTC GCCAGGG		
	IIII		
	CGACCCACGGG CGGTCCC		
	TC IIIC		
GAM368 PSCD4	GCTGGGTGCCCAGGCCAGGG 5688	_____ III	
	GCTGGGTGCTC GCCAGG		
	IIII		
	CGACCCACGGG CGGTCC		
	TC CII		
GAM368 RAP1GA1	GCTGGGTGCTGGCTGAGGAGCC 5690	C C_ _ CII	
	GCTGGGTGCT GC AGG GCC		
	II III III		

	CGACCCACGA CG TCC CGG		
	C AC T III		
GAM368 RAP1GA1	GCTGGGTGCTGGCTGAGGAGCC 5690 CT	C C_ _ I	
	GGGTGCT GC AGG GC		
	II III II		
	CCCACGA CG TCC CG		
	_ C AC T I		
GAM368 RGS3	CTGGCT--TGGCCAGGGCCC 5683 GCTG GCTC		
	GGT GCCAGGGCCC		
	III		
	CCG CGGTCCCGG		
	A_ AAC_		
GAM368 RGS3	CTGGCT--TGGCCAGGGCCC 5683 TG GCTC	I	
	GGT GCCAGGGCC		
	III		
	CCG CGGTCCCGG		
	GA AAC_ I		
GAM368 RGS3	TGGCTCATCCCCAGGGCCC 5702 TG GC_ G	II	
	GGT TC CCAGGGCC		
	III II		
	CCG AG GGTCCCGG		
	A_ AGT G GI		
GAM368 ROR2	TGGGTGCTCCTAGGCAGGGC 5701	GC_ III	
	TGGGTGCTC CAGGG		
	III		
	ACCCACGAG GTCCC		
	GATCC GII		
GAM368 ROR2	TGGGTGCTCCTAGGCAGGGC 5701 GCTG	GC_ CCI	
	GGTGCTC CAGGGC		
	III		
	CCACGAG GTCCCG		
	_ GATCC TCI		
GAM368 SET7	CTGGGTGCTC-CCGGCGGC 5680	G A GII	
	CTGGGTGCTC CC GG		
	II II		
	GACCCACGAG GG CC		
	_ _ GCC		
GAM368 SET7	CTGGGTGCTC-CCGGCGGC 5680 GC	G AG_ CC	
	TGGGTGCTC CC GGC		
	II III		
	ACCCACGAG GG CCG		
	_ _ CCG AI		
GAM368 SFRP1	GCTGGGTGCGCCCCGGCTCCC 5698	TC AG_ I	
	GCTGGGTGC GCC GGC CC		
	III III II		
	CGACCCACG CGG CCG GG		
	_ GG A G		
GAM368 SFRP1	GCTGGGTGCGCCCCGGCTCCC 5698	TC AG CI	
	CTGGGTGC GCC GGC		
	III III		

	GACCCACG CGG CCG		
	__ GG AG		
GAM368 SFRP2	GCTGGGTGCGACTCGGGGCC 5697	__ CCA	I
	GCTGGGTGC TCG GGGCCC		
	CGACCCACG AGC CCCGGG		
	CTG __ I		
GAM368 SFRP2	GCTGGGTGCGACTCGGGGCC 5697	__ CCA	I
	CTGGGTGC TCG GGGCC		
	GACCCACG AGC CCCGG		
	CTG __ I		
GAM368 TESK1	GCAGGGTCC---CCAGGGGCC 5696	T TGC	G
	GC GGG TC CCAGGGGCC		
	CG CCC AG GGTCCCGG		
	T __ G		
GAM368 TESK1	GCAGGGTCC---CCAGGGGCC 5696	CT_ TGC	G
	GGG TC CCAGGGCC		
	CCC AG GGTCCCG		
	CGT __ G		
GAM368 TM7SF3	GCTGGGCCACGCCAGGGC 5691	GCT	CC
	GCTGGGT CGCCAGGGC		
	CGACCCG GCGGTCCG		
	GGT II		
GAM368 TM7SF3	GCTGGGCCACGCCAGGGC 5691	GCT	II
	GCTGGGT CGCCAGGG		
	CGACCCG GCGGTCCC		
	GGT GI		
GAM368 TNC	GCTGGGTGCT-GCTGGGGC 5693	C CA	CC
	GCTGGGTGCT GC GGGC		
	CGACCCACGA CG CCCG		
	_ AC II		
GAM368 TNC	GCTGGGTGCT-GCTGGGGC 5693	C CA	I
	GCTGGGTGCT GC GGG		
	CGACCCACGA CG CCC		
	_ AC G		
GAM369 ACVR1B	GAGATGGGGTCTCCCCACA 5707	GA TCII	
	GAGATGGGGTCT CC		
	CTCTACCCAGG GG		
	GG TGTI		
GAM369 ACVR1B	GAGATGGGGTCTCCCCACA 5707	TG GA T GTT	
	AGATGGGGTCT CC CA		

	TCTACCCCAGA GG GT			
	___ GG T AII			
GAM369 CRY2	GAGATGGG-TCTGACCCAG 5709 _ G I			
	AGATGGG TCTGACCTCA			
	TCTACCC AGACTGGGGT			
	C _ I			
GAM369 CRY2	GAGATGGG-TCTGACCCAG 5709 TG G TT			
	AGATGGG TCTGACCTCAG			
	TCTACCC AGACTGGGGTC			
	___ _ CI			
GAM369 DNMT3L	TGGGGTTTGGGGACCTCAGT 5717 CT___ III			
	TGGGGT GACCTCAG			
	ACCCCA CTGGAGTC			
	AACCC AII			
GAM369 DNMT3L	TGGGGTTTGGGGACCTCAGT 5717 TGAGA TCTG T			
	TGGGG ACCTCAGT			
	ACCC TGGAGTCA			
	AA___ _ C			
GAM369 ELF3	AGATGCT-TCTGACCTCAGT 5706 _ GGG I			
	GATG TCTGACCTCAG			
	CTAC AGACTGGAGTC			
	T GA_ I			
GAM369 ELF3	AGATGCT-TCTGACCTCAGT 5706 TGAG GGG T			
	ATG TCTGACCTCAGT			
	TAC AGACTGGAGTCA			
	___ GA_ C			
GAM369 HOXB5	GAGATGGG-TCTGACC-CAG 5708 G CI			
	GAGATGGG TCTGACCT			
	CTCTACCC AGACTGGG			
	_ TC			
GAM369 HOXB5	GAGATGGG-TCTGACC-CAG 5708 TG G T T			
	AGATGGG TCTGACC CAG			
	TCTACCC AGACTGG GTC			
	___ _ _ T			
GAM369 IFNA1	TGAGATGGGTGACTCTGAACCT 5714 G___ _ CAGTTC			
	TGAGATGGG TCTGA CCT			
	ACTCTACCC AGACT GGA			
	ACTG T IICTT			
GAM369 IFNA1	TGAGATGGGTGACTCTGAACCT 5714 G___ _ IIIA			
	TGAGATGGG TCTGA CC			

	ACTCTACCC AGACT GG		
	ACTG T AIII		
GAM369 IFNA13	TGAGATGGGTGACTCTGAACCT 5714	G__ _ CAGTTC	
	TGAGATGGG TCTGA CCT		
	ACTCTACCC AGACT GGA		
	ACTG T IIICTT		
GAM369 IFNA13	TGAGATGGGTGACTCTGAACCT 5714	G__ _ IIIA	
	TGAGATGGG TCTGA CC		
	ACTCTACCC AGACT GG		
	ACTG T AIII		
GAM369 IFNAR1	GAGATGGGGTTTCACCAC-GTT 5711 _	CTG TCA I	
	AGATGGGGT ACC GT		
	TCTACCCCA TGG CA		
	C AAG TG_ I		
GAM369 IFNAR1	GAGATGGGGTTTCACCAC-GTT 5711 TG	CTG TCA C	
	AGATGGGGT ACC GTT		
	TCTACCCCA TGG CAA		
	_ AAG TG_ C		
GAM369 MAT1A	TGAGATGTG--CTGACCTCA 5715	GG T GT	
	TGAGATG G CTGACCTCA		
	ACTCTAC C GACTGGAGT		
	A_ _ II		
GAM369 MAT1A	TGAGATGTG--CTGACCTCA 5715 _	GG T I	
	GAGATG G CTGACCTC		
	CTCTAC C GACTGGAG		
	A A_ _ I		
GAM369 NHLH1	TGGGGTCTGCCACTGAGCTC 5718	A TC_ _ II	
	TGGGGTCTG CC AGTT		
	ACCCAGAC GG TCGA		
	_ TGAC GI		
GAM369 NHLH1	TGGGGTCTGCCACTGAGCTC 5718 _	AGA_ G ACCTCAGTT	
	TG TGGG TCTG		
	AC ACTC AGAT		
	AG GGTG G CTTIIICTT		
GAM369 POLL	GAGATGGGGCACGCCGCAG 5710	C A T I	
	AGATGGGGT TG CC CA		
	TCTACCCCG GC GG GT		
	T C C I		
GAM369 POLL	GAGATGGGGCACGCCGCAG 5710 TG	C A T T	
	AGATGGGGT TG CC CAGT		

	TCTACCCCG GC GG GTCG		
	___ T C C I		
GAM369 SCN4A	TGAGG-GGGGTCTGAGCCCACTTC 5716 AT C G I		
	TGAG GGGGTCTGA CTCA TTC		
	ACTC CCCCAGACT GGGT AAG		
	C_ C G I		
GAM369 SCN4A	TGAGG-GGGGTCTGAGCCCACTTC 5716_ AT C G I		
	GAG GGGGTCTGA CTCA TT		
	CTC CCCCAGACT GGGT AA		
	A C_ C G I		
GAM369 SMURF1	AGGTGGGGCCTCTGACCTCA 5705 A _		
	AG TGGGGT CTGACCTC		
	TC ACCCCG GACTGGAG		
	C GA TII		
GAM369 SMURF1	AGGTGGGGCCTCTGACCTCA 5705 TGAGA _ GTT		
	TGGGGT CTGACCTCA		
	ACCCCG GACTGGAGT		
	C_ GA AGI		
GAM369 TNFSF15	TGAGACTGAGTGGTCTGACCT 5712 _ _ CAGTTC		
	TGAGAT GG GGTCTGACCT		
	ACTCTG TC CCAGACTGGA		
	AC A CTT		
GAM369 TNFSF15	TGAGACTGAGTGGTCTGACCT 5712 _ _		
	TGAGAT GG GGTCTGACC		
	ACTCTG TC CCAGACTGG		
	AC A AII		
GAM369 VDR	TGAGAGTGGGGGTCTGAGCTCA 5713 T_ C GTTC		
	TGAGA GGGGTCTGA CTCA		
	ACTCT CCCCAGACT GAGT		
	CAC C IIIC		
GAM369 VDR	TGAGAGTGGGGGTCTGAGCTCA 5713 AT C I		
	GAG GGGGTCTGA CTC		
	CTC CCCCAGACT GAG		
	AC C I		
GAM370 ARVCF	CGG-GCCTTCTGTCACTCGC 5723 T AG _ GTCT		
	CGG GC TC GTCACTCGC		
	GCC CG AG CAGTGAGCG		
	_ GA A IIIG		
GAM370 COL5A3	CGGTGCA---GTCACTCGC 5725 GTC GT		
	CGGTGCAGTC ACTCGC		

	GCCACGTCAG TGAGCG	
	_____ II	
GAM370 COLQ	CGGATGCAGTCGTACCCACATC 5722 _	TGI
	CGG TGCAGTCGTCACTCGCGTC	
	GCC ACGTCAGCAGTGGGTGTAG	
	T III	
GAM370 GRB10	GCAGTCGTCAAGGCAGGCGTTTG 5726 ____	T T CACTCGCGTCTG
	CGG GCAG CGT	
	GTC CGTC GCA	
	AGCA _ C AACCTCTIIIGT	
GAM370 HSF4	GGTGCAGTC-TCGGCCCGGCTCTG 5727 CG	G A_ CG I
	GTGCAGTC TC CTCG TCTG	
	CACGTCAG AG GGGC AGAC	
	____ _ CC CG G	
GAM370 IFNAR2	AGTCGTCACTGTCCTCGTC 5721 CGGTGCAGTC A _ T	
	GTC CTCG CGTC	
	CAG GAGC GTAG	
	GTGA_____ _ A T	
GAM370 KCNK4	GGAGCTGTCGTCACT-GCG 5728 CGGT A	C TC
	GC GTCGTCACT GCG	
	CG CAGCAGTGA CGC	
	CT_ A _ CI	
GAM370 PCDH7	CGGTGCAGGGGAGACTACTCGCGTC 5724	TC_ TC TGII
	CGGTGCAG G ACTCGCGTC	
	GCCACGTC T TGAGCGCAG	
	CCCTC GA IIIG	
GAM371 ATRN	ACACACACACCGCACGGCCGGCTC 5735	____ _ IIIG
	ACACACACA ACGGC GCT A	
	TGTGTGTGT TGCCG CGA T	
	GGCG GC GIII	
GAM371 ATRN	ACACACACACCGCACGGCCGGCTC 5735 TA	A_ _ GGI
	ACACACAC ACGGC GCTCTG	
	TGTGTGTG TGCCG CGAGGC	
	_ GCG GC III	
GAM371 BAZ2A	ACACACACACACGGCGCTCT 5737	_ II
	ACACACACA ACGGCGCTC	
	TGTGTGTGT TGCCGCGAG	
	G AI	
GAM371 BAZ2A	ACACACACACACGGCGCTCT 5737 TA	A GG
	ACACACACA CGGCGCTCT	

		TGTGTGTGT GCCGCGAGA			
		— — GA			
GAM371 BAZ2A		ACACACACAGC-GCGTTGTG 5742 C A TCTI			
		ACACACA CGGCGC			
		TGTGTGT GTCGCG			
		— — CAAC			
GAM371 BAZ2A		ACACACACAGC-GCGTTGTG 5742 TAACAC A TC G			
		ACACA CGGCGC TG			
		TGTGT GTCGCG AC			
		— — CA A			
GAM371 BAZ2A		ACACACACACACTGCGCGCTG 5739 _ ACG T I			
		CACACACA GCGC CT			
		GTGTGTGT CGCG GA			
		T GA_ C I			
GAM371 BAZ2A		ACACACACACACTGCGCGCTG 5739 TA ACG T GG			
		ACACACACA GCGC CTG			
		TGTGTGTGT CGCG GAC			
		— GA_ C AC			
GAM371 CLCN7		ACACACACAGCTGATCCCTGG 5744 CA A G_ I			
		CACACA CGGC CTCTG			
		GTGTGT GTCG GGGAC			
		— — ACTA I			
GAM371 CLCN7		ACACACACAGCTGATCCCTGG 5744 TAAC ACGGCG			
		ACACACA CTCTGGG			
		TGTGTGT GGGACCT			
		— CGACTA			
GAM371 CRY2		ACACACACATGCTCGCTCT 5741 ACGG II			
		ACACACACA CGCTC			
		TGTGTGTGT GCGAG			
		ACGA AI			
GAM371 CRY2		ACACACACATGCTCGCTCT 5741 TAAC ACGG G			
		ACACACA CGCTCTG			
		TGTGTGT GCGAGAT			
		— ACGA A			
GAM371 GRB10		AACAAACCCATCT-CGCTCTGGG 5734 _ C A ACGG I			
		ACA AC CA CGCTCTGG			
		TGT TG GT GCGAGACC			
		T T G AGA_ I			
GAM371 GRB10		AACAAACCCATCT-CGCTCTGGG 5734 TA C A ACGG			
		ACA AC CA CGCTCTGGG			

	TGT TG GT GCGAGACCC		
	___ T G AGA_		
GAM371 HLCS	ACACACACATCCTCCCTCTG	5743 TAAC	ACGGCG
	ACACACA CTCTGG		
	TGTGTGT GAGACT		
	_____ AGGAGG		
GAM371 HLCS	ACACACACATCCTCCCTCTG	5743	ACGGCG I
	CACACACA CTCT		
	GTGTGTGT GAGA		
	AGGAGG I		
GAM371 IL18RAP	AACACACACACACAGAGCTGTG	5732_	A C CTI
	ACACACACA CGG GCT		
	TGTGTGTGT GTC CGA		
	G _ T CAI		
GAM371 IL18RAP	AACACACACACACAGAGCTGTG	5732 TA	_ C C G
	ACACACACA ACGG GCT TGG		
	TGTGTGTGT TGTC CGA ACT		
	___ G T C I		
GAM371 KCNK10	ACACACACACACAACGCTC	5736	_ II
	ACACACACA ACGGCGCT		
	TGTGTGTGT TGTTGCGA		
	G GI		
GAM371 KCNK10	ACACACACACACAACGCTC	5736 TA	A TGG
	ACACACACA CGGCGCTC		
	TGTGTGTGT GTTGCGAG		
	___ _ TCI		
GAM371 KCNN4	CACACACAATGG---TCTG	5746	C CGCTCT
	CACACACAA GG		
	GTGTGTGTT CC		
	A AGACII		
GAM371 KCNN4	CACACACAATGG---TCTG	5746 TAACAC	C CGC
	ACACAA GG TCT		
	TGTGTT CC AGA		
	_____ A _____		
GAM371 RDX	ACACACACACAGTCTCTCT	5740	A CG_ II
	ACACACACA CGG CTC		
	TGTGTGTGT GTC GAG		
	_ AGA AI		
GAM371 RDX	ACACACACACAGTCTCTCT	5740 TA	ACGGCG GG
	ACACACACA CTCT		

		TGTGTGTGT	GAGA			
		___	CAGA___	GA		
GAM371	SLC25A13	AACACACACGAA	CACTGCTCTG	5731	AC GC	I
		ACACAC	AACG GCTCT			
		TGTGTG	TTGT CGAGA			
		CT	GA I			
GAM371	SLC25A13	AACACACACGAA	CACTGCTCTG	5731	TA ___ GC	GI
		ACACACAC	AACG GCTCTGG			
		TGTGTGTG	TTGT CGAGACT			
		___	CT GA II			
GAM371	SLC26A4	ACACACACAGG	TGCGGTCT	5738	AC _ TCII	
		ACACACACA	GGC GC			
		TGTGTGTGT	CCG CG			
		___	A CCAG			
GAM371	SLC26A4	ACACACACAGG	TGCGGTCT	5738	TAAC ACG_ C	GG
		ACACACA	GCG TCT			
		TGTGTGT	CGC AGA			
		___	CCGA C AA			
GAM371	VPS26	AAAACACACA	ACGGTACTACTGG	5733	AC CG _	I
		ACACACA	ACGG CT CTG			
		TGTGTGTTGCC	GA GAC			
		T_	AT T I			
GAM371	VPS26	AAAACACACA	ACGGTACTACTGG	5733	TAAC CG _	I
		ACACACA	ACGG CT CTGGG			
		TGTGTGTTGCC	GA GACCT			
		TT_	AT T I			
GAM371	ZNF277	CACAC-CTACG	CCGCGCTCTGG	5745	A ACA _	I
		CAC	ACG GCGCTCTG			
		GTG	TGC CGCGAGAC			
		_	GA_ GG I			
GAM371	ZNF277	CACAC-CTACG	CCGCGCTCTGG	5745	TAACACACACA _	
		ACG	GCGCTCTGG			
		TGC	CGCGAGACC			
		TGGA_	GG			
GAM372	AF3P21	GGGTAGGAGTGA	AAGGGCAGCGA	5756	TCCGGG ACA	AG
		TAGGAG	AAGGGCG			
		ATCCTC	TTCCCGT			
		___	AC_ CG			
GAM372	CAPZA1	GGGAAGGAGACA	AATGAGAGA	5757	TCCGGGT A C	
		AGGAGACAA	GGG GA			

	TCCTCTGTT CTC CT	
	T_____ A T	
GAM372 CHGA	TCAGGAGTAGGAGACAAGGCGCG 5761 C _ A _ AGI	
	TC GG GTAGGAGACAA GG GCG	
	AG CC CATCCTCTGTT CC CGC	
	T T _ G	
GAM372 CSPG4	TCTGGGGCAGAGACAAAGGG 5763 TCC TA CGA	
	GGG GGAGACAAAGGG	
	CCC TCTCTGTTTCCC	
	AGA CG	
GAM372 DDEF2	TCCGGCCCGCGGACAAAGGG-GAG 5764 GTAGGA C I	
	TCCGG GACAAAGGG GAG	
	AGGCC CTGTTTCCC CTC	
	GGGCGC _ I	
GAM372 HNF3A	GGGTAGAGAGGACAAAGGG 5753 TCCG T GA CGA	
	GG AG GACAAAGGG	
	TC TC CTGTTTCCC	
	A__ _ TC CAA	
GAM372 HR	CCGGGAAGTGGAG-CAAAGGGCG 5749 TC TA__ A AG	
	CGGG GGAG CAAAGGGCG	
	GCCC CCTC GTTTCCCGC	
	_ TTGA _ CI	
GAM372 IRS1	GGGGAGGGGACAA-GGGCGAG 5758 TCCGGGT A A	
	AGG GACAA GGGCGA	
	TCC CTGTT CCCGCT	
	C_____ C _	
GAM372 MDFI	GGGTAGGAGAGGACCAGGGAGAG 5755 TCC T GA AA C I	
	GGG AG GAC AGGG GAG	
	TCC TC CTG TCCC CTC	
	A__ _ TC G_ T C	
GAM372 OFD1	CGGTTCTGAGGCA-AGGGCGAG 5752 TCCGGGTAG ACA	
	GAG AAGGGCGAG	
	CTC TTCCCGCTC	
	CAAGA_____ CG_	
GAM372 PON1	TCGGGGGAT-AGACAAAGGG 5762 TC TAGG CGA	
	CGGG AGACAAAGGG	
	GCCC TCTGTTTCCC	
	A_ CCTA	
GAM372 SLC2A3	GGGT-GGAGCCTGAAAGGGCGA 5754 TCCGGGTA AC__ G	
	GGAG AAAGGGCGA	

	CCTC TTTCCCGCT			
	A_____ GGAC G			
GAM372 SNCB	CGGGTAGGACAGACAGATGG	5751 TCCG	___ AA_ GA	
	GGTAGGA GACA GGGC			
	CCATCCT CTGT CCTG			
	_____ GT CTA II			
GAM372 SPHK2	CCGGGTAGGAG-CAGGTGGCAAG	5750 TC	A AAG	
	CGGGTAGGAG CA GGCGAG			
	GCCCATCCTC GT CCGTTC			
	_____ _ CCA			
GAM372 TAZ	GGGTAGGAGCC--AGGCCGAG	5760 TCCGGG	ACAA G	
	TAGGAG AGG CGA			
	ATCCTC TCC GCT			
	_____ GG_ G			
GAM372 VGF	GGGTAGGAG-CGACGGTCGAG	5759 TCCGGG	ACAAA G	
	TAGGAG GG CGA			
	ATCCTC CC GCT			
	_____ GCTG_ A			
GAM373 ADRA2A	GGCGTCCGCCTGG--TGGGCGC	5784 TG	GGTGG	
	GCGTCTG GGTGGGCGC			
	CGCAGGC CCACCCGCG			
	_____ GGA_			
GAM373 ATSV	TGG-GTGTGGGTGGGGAGGGC	5794 C C	T GC	
	TGG GT TGGGTGGGG GGGC			
	ACC CA ACCCAGCCC CCCG			
	_____ C T II			
GAM373 CAPS	TGGCGT--GGGTGGGGAGAGCG	5798 CT	T C	
	TGGCGT GGGTGGGG GGGCG			
	ACCGCA CCCACCCC CTCGC			
	_____ T I			
GAM373 CBFA2T3	TGGAG-CTGGGTGGGGTTGGCACG	5799 C T	G I	
	TGG G CTGGGTGGGGT GGCGCG			
	ACC C GACCCACCCCA CCGTGC			
	T_ A I			
GAM373 CDH5	TGGCGTCTGACTGGCCTGGGC	5795	G GG GCG	
	TGGCGTCTGG TGG TGGGC			
	ACCGCAGACT ACC ACCCG			
	G GG			
GAM373 CLDN3	TGGCTTCTGG---GGGTGGGC	5796 G	TGG G	
	TGGC TCTGGG GGTGGGC			

	ACCG AGACCC CCACCCG			
	A _ _ I			
GAM373 DIA1	GGCGT--GGCTGGGGTGGGC 5781 TG CT G G			
	GCGT GG TGGGGTGGGC			
	CGCA CC ACCCCACCCG			
	_ _ G G			
GAM373 FASN	TGGCGG--GGGTGGGGTGGG 5791 TCT CG			
	TGGCG GGGTGGGGTGGG			
	ACCGC CCCACCCACCC			
	C _ II			
GAM373 FASN	TGGGGTG--GGGTGGGGTGGG 5793 C CT CGC			
	TGG GT GGGTGGGGTGGG			
	ACC CA CCCACCCACCC			
	C C_ III			
GAM373 FSTL3	GGCCCCAGGGTGGGGTGGGC 5780 TG G T GC			
	GC TC GGGTGGGGTGGGC			
	CG GG CCCACCCACCCG			
	_ G T AI			
GAM373 FXYD1	GGCGGCGGAGGGGGCGGTGGGCGCG 5771 T_ TCT T _ II			
	GGCG GGG GG GGTGGGCGCG			
	CCGC CCC CC CCACCCGCGC			
	CG CT_ _ G GI			
GAM373 GNAO1	TGGCGTCTGTGGT-GTCTGGGCG 5789 _ GGG CG			
	TGGCGTCTG GGTG TGGGCG			
	ACCGCAGAC CCAC ACCCGC			
	A AG_ II			
GAM373 GRP58	GGCGGCGAGGTGGGGTGGG 5779 T_ TCT CGC			
	GGCG GGGTGGGGTGGG			
	CCGC TCCACCCACCC			
	CG _ CII			
GAM373 HCRT	TGGCGCTCAGGGTGGGGTAGCCG 5788 _ T G CGI			
	TGGCG TC GGGTGGGGTGG CG			
	ACCGC AG CCCACCCCATC GC			
	G T G III			
GAM373 HNRPM	GCGTCTGGGCTTTGTGTGAGCG 5770 TGGC GGG_ CG			
	GTCTGGGT GTGGGCG			
	CAGACCCG CACTCGC			
	_ AAACA TT			
GAM373 HPD	TGGCCTCCG--TGGGGTGGGCG 5797 G GG C			
	TGGC TCT GTGGGGTGGGCG			

	ACCG AGG CACCCACCCGC	
	G _ I	
GAM373 HSF4	TGGAGTG-GGGTGGGGTGGG 5790 C CT CGC	
	TGG GT GGGTGGGGTGGG	
	ACC CA CCCACCCACCC	
	T C_ III	
GAM373 IGLL1	GGCCTTTGGGTGGGGTCGGGGC 5783 TGGC _ _ C G	
	GTCT GGGTGGGGT GGG GC	
	CGGA CCCACCCCA CCC CG	
	_ _ AA G _ A	
GAM373 ITGA4	GGCCGCTGGGTGGGGTCCCGGGCG 5777 T G T _ CGI	
	G CG CTGGGTGGGGT GGGCG	
	C GC GACCCACCCCA CCCGC	
	_ G _ GGG A	
GAM373 MAP3K1	CGACTCGGTAAGGTGGGCGC 5767 TGGCGT G	
	CT GGTGGGGTGGGCGC	
	GA CCATTCCACCCGCG	
	_ _ G	
GAM373 NTSR1	GTCCGGGCAGGAGTGGGCGCG 5786 TGGCGTCT TG _	
	GGG GG GTGGGCGCG	
	CCC CC CACCCGCGC	
	_ _ _ GT T	
GAM373 PRX2	GGCGTCTGGGTCCTGGTGGG 5774 TG GG_ CGC	
	GCGTCTGGGT GGTGGG	
	CGCAGACCCA CCACCC	
	_ GGA T	
GAM373 RANBP3	TGGACG-CTGCCGGTGGGGTGGGGGCG5787 _ T _ C	
	TGG CG CTG GGTGGGGTGGG GCG	
	ACC GC GAC CCACCCACCC CGC	
	T _ GG C	
GAM373 RNF26	GGCATCTGGGTGGGCCCTGGGC 5776 TG G_ CG	
	GCGTCTGGGTGGG TGGGCG	
	CGTAGACCCACCC ACCCGT	
	_ GGG	
GAM373 RRAS2	GGCGTCTGGAGGGCCGGTCAGCGCG 5775 TG T G _	
	GCGTCTGGG GGG TGG GCGCG	
	CGCAGACCT CCC GCC CGCGC	
	_ _ G AGT CI	
GAM373 S100A1	GGGGTGGGGGTGGGGTGGGC 5782 T C CT C	
	GG GT GGGTGGGGTGGGCG	

	CC CA CCCACCCCACCCGT			
	_ _ CC I			
GAM373 SCN8A	GGCGGGCGGGACTGCGGTGGGCGC	5772	TG TC _ G GI	
	GCG TGGG TG GGTGGGCGC			
	CGC GCCC AC CCACCCGCG			
	_ CC TG G GI			
GAM373 SLC12A7	TGGGGTG-GGGTGGGGTGGG	5793	C CT CGC	
	TGG GT GGGTGGGGTGGG			
	ACC CA CCCACCCCACCC			
	C C_ III			
GAM373 SSPN	CTGGGTGGGTGGGTGGGTGCG	5768	TGGCGTCT G C	
	GGGTGGG TGGG GCG			
	CCCACCC ACCC CGC			
	_____ _ A			
GAM373 TACSTD2	GGCGTCTGGGATGGTCTGCAGGCG	5773	TG _ G_ TG CGI	
	GCGTCTGGG TGG G GGCG			
	CGCAGACCC ACC C CCGC			
	_ T AGA GT AII			
GAM373 TCF3	TGGGGACATGGTGGGGTGGG	5792	T_ CTG CGC	
	GGCGT GGTGGGGTGGG			
	CTGTA CCACCCCACCC			
	ACCC _ III			
GAM373 WDR1	GCCTCTTGTGGTGGGGTGGGGGC	5769	TGGCG _ _ C I	
	TCT G GGTGGGGTGGG GCG			
	AGA C CCACCCCACCC CGT			
	G_ A A C A			
GAM373 WSX1	GGCGTCTG---GGGGTGGGGGC	5785	TG T _ T GC	
	GCGTCTGGG GG GG GGCG			
	CGCAGACCC CC CC CCCG			
	_ _ A _ GI			
GAM373 WT1	GGC-TCTGGGT-GGGTGGG	5778	TG G G CG	
	GC TCTGGGTGGG TGGG			
	CG AGACCCACCC ACCC			
	_ _ _ AI			
GAM374 ABCD1	GGCA---GGGGCCGGGGACG	5808	TCC TI	
	GGCA GGGGCCGGGG			
	CCGT CCCC GGCCCC			
	_ TG			
GAM374 ABCD1	GGCA---GGGGCCGGGGACG	5808	TG TCC TC	
	GCA GGGGCCGGGG GC			

CGT CCCC GGCCCC TG

GAM374	AES	GCATACCTGGGACCCGGGGTCGGGG 5804	_____ C	C	TCGCGGII
		TGG ATCCGGGG CGGGG			
		ACC TGGGCCCC GCCCC			
		TATGG C A CTIIIGGC			
GAM374	AES	GCATACCTGGGACCCGGGGTCGGGG 5804 AT	_ _	CGI	
		CC GGGGCC GGGGTCG			
		GG CCCTGG CCCCAGC			
		T_ A G CII			
GAM374	FLNA	GGCGGCCTGGGCGGGGTTGAGG 5811	_ ATCCG	CGCI	
		GGC GGGCCGGGGT			
		CCG CCGGCCCCA			
		G GA_____ ACTC			
GAM374	FLNA	GGCGGCCTGGGCGGGGTTGAGG 5811 T_	ATCCG	CGC I	
		GGC GGGCCGGGGT GG			
		CCG CCGGCCCCA CC			
		CG GA_____ ACT C			
GAM374	GALNT2	GGGATGCCGGGGCCGAGGCCG 5805 GCAT		I	
		CCGGGGCCGGGGTC			
		GGCCCCGGCTCCGG			
		CTAC I			
GAM374	GALNT2	GGGATGCCGGGGCCGAGGCCG 5805 T C	_	CGG	
		GG AT CCGGGGCCGGGGTCG			
		CC TA GGCCCCGGCTCCGGC			
		_ _ C CII			
GAM374	INSM1	TCGGGGGCCGGGGTGGAGG 5812 C	CGCGII		
		TC GGGGCCGGGGT			
		AG CCCC GGCCCCA			
		C CCTCCI			
GAM374	INSM1	TCGGGGGCCGGGGTGGAGG 5812 TGGCAT	CC_ T		
		CCGGGG GGGG CGCG			
		GGCCCC TCCC GCGC			
		CC_____ ACC _			
GAM374	NGB	GGCTGCCGGG--CGGGGTCGC 5810 AT	GC I		
		GGC CCGGG CGGGTC			
		CCG GGCCC GCCCCAG			
		AC _ C			
GAM374	NGB	GGCTGCCGGG--CGGGGTCGC 5810 TG AT	GC G		
		GC CCGGG CGGGGTCGC			

	CG GGCCC GCCCAGCG		
	— AC — G		
GAM374 PTPRS	GGCATCCGGGGCCAGTGGTGTCTCGG 5806 G	— CG I	
	CATCCGGGGCCCGG GGT CG		
	III II		
	GTAGGCCCCCGGTC CCA GC		
	— A CA I		
GAM374 PTPRS	GGCATCCGGGGCCAGTGGTGTCTCGG 5806 TG	— CG I	
	GCATCCGGGGCCCGG GGT CGG		
	III III		
	CGTAGGCCCCCGGTC CCA GCC		
	— A CA C		
GAM374 RPS6KA2	GGC-TCCGAGGCCGGGGTC 5807 A	I	
	GGC TCCGGGGCCCGGGT		
	III		
	CCG AGGCTCCGGCCCCA		
	— G		
GAM374 RPS6KA2	GGC-TCCGAGGCCGGGGTC 5807 TG A	GC	
	GC TCCGGGGCCCGGGTC		
	II		
	CG AGGCTCCGGCCCCAG		
	— — AI		
GAM374 RUNX3	ATCCCGGGCCGGGGTG GGGG 5802 G	CGCGI	
	TCC GGGCCGGGGT		
	III		
	AGG CCCGGCCCCA		
	G CCCI		
GAM374 RUNX3	ATCCCGGGCCGGGGTG GGGG 5802 TGGCATCCG	CGC	
	GGGCCGGGGT G		
	I		
	CCCGGCCCCA C		
	G — CCC		
GAM374 SGT	GGCA--CAGGGCCGGGGTG GGC 5809 TC	CI	
	GGCA CGGGGCCGGGGT		
	III		
	CCGT GTCCCGGCCCCA		
	— CC		
GAM374 SGT	GGCA--CAGGGCCGGGGTG GGC 5809 TG TC	C G	
	GCA CGGGGCCGGGGT GC		
	III II		
	CGT GTCCCGGCCCCA CG		
	— — C G		
GAM374 TRAF1	CATTCGGGGCCGGAGTG GGC 5803 C	CGII	
	CAT CGGGGCCGGGGT		
	III		
	GTA GCCCGGCCTCA		
	A CCGI		
GAM374 TRAF1	CATTCGGGGCCGGAGTG GGC 5803 TGGCATC	C G	
	CGGGGCCGGGGT GC		
	II		

		GCCCGGCCTCA CG			
		A_____C A			
GAM375	ABCD1	GGCA---GGGGCCGGGGACG	5808	TTC	TI
		GGCA GGGGCCGGGG			
		CCGT CCGCGGCCCC			
		_____TG			
GAM375	AES	GCATACCTGGGACCCGGGGTTCGGGG	5804	ATTC	_ CI
		GGGGCC GGGGTCG			
		CCCTGG CCCCAGC			
		GGA_ G CI			
GAM375	ALOX12B	TGCCCTTGGTGGCCGGGGT	5832	TG ATTC _	II
		GC GG GGCCGGGG			
		CG CC CCGGCCCC			
		A_ GGAA A AI			
GAM375	BMPR2	GGGATTTCGAT-CCGGGGTTCGGGG	5827	C GG	CI
		GG ATTCGG CCGGGGTCG			
		CC TAAGCT GGCCCCAGC			
		_ A_ CC			
GAM375	CHGA	TGG-ACTGGCGGCCGGGGTCG	5833	_ C C _	I
		GG ATT GG GGCCGGGGTC			
		CC TGA CC CCGGCCCCAG			
		A _ _ G I			
GAM375	FLOT1	TCGGGAAGGGCGGGGTTCGCG	5828	C___	III
		TCGGGG CGGGGTTCG			
		AGCCCT GCCCCAGCG			
		TCCC CII			
GAM375	GTF2I	GGCAGCTCCGGGGCCGGGG	5820	___	III
		GGCA TTCGGGGGCCGGG			
		CCGT AGGCCCCGGCCC			
		CG CII			
GAM375	GTF2I	GGCAGCTCCGGGGCCGGGGCCTCG	5822	_ A	GCI
		GC TTCGGGGGCCGGGGTC			
		CG AGGCCCCGGCCCCG			
		T _ AGI			
GAM375	HIF1A	GGCAATCG---CCGGGGTTC-CGG	5826	T GGG	GI
		GGCA TC GCCGGGGTC			
		CCGT AG CGGCCCCAG			
		T ___ GC			
GAM375	HIPK2	CGGGGCCGGGGTGTCCGCGG	5816	___	III
		CGGGGCCGGGGT CGCG			

	GCCCCGGCCCCA GCGC		
	CAG CII		
GAM375 INSM1	GGCACAGTTCGGGGGCCGGGTGGAGG5819 A	_	CGCI
	TTCGGGG CCGGGGT		
	AAGCCCC GGCCCCA		
	C C CII		
GAM375 KCNH3	GCAGACCGGGATCCGGGGTCGCG 5817 CAT	_	I
	TCGGGG CCGGGGTCGCG		
	GGCCCT GGCCCCAGCG		
	CT_ A I		
GAM375 LMO2	TGGCACCTTTCGGCCCCGGGTGCGCG5830 GGCA	G G G	I
	TTC GG CC GGGTCGCG		
	AAG CC GG CCCAGCGC		
	TGGA G G G I		
GAM375 MAN2A1	GGCAGCTCCCGGGCCGGGGCCGCG 5821_ A G		I
	GC TTC GGGCCGGGGTCGCG		
	CG AGG CCCGGCCCCGGCG		
	T_ G I		
GAM375 NCOR2	GCATTGCGGGGAGGCAGTGGCG 5818	CC	CGCI
	ATTCGGGG GGGGT		
	TAAGCCCC CTCCG		
	_ TCAC		
GAM375 NFATC2	GGC-TGCGGGGCCGGGGGCGAGG 5825_ ATT		TC I
	GC CGGGGCCGGGG GCG		
	CG GCCCCGGCCCC CGC		
	C AC_ _ T		
GAM375 NGB	GGC-TGCCGGGC-GGGGTGCG 5823 AT	GC	I
	GGC TCGGG CGGGGTC		
	CCG GGCCC GCCCAG		
	AC _ C		
GAM375 NR2F6	GGCAG-CGGGGCCGGGG-CGC 5824 TT		CI
	GGCA CGGGGCCGGGT		
	CCGT GCCCCGGCCCCG		
	C_ CG		
GAM375 RABL2A	ATT-GGGGCCGGG--CGCGG 5815 TTC		GT
	GGGGCCGGG CGCG		
	CCCCGGCCC GCGC		
	TAA _		
GAM375 RABL2B	ATT-GGGGCCGGG--CGCGG 5815 TTC		GT
	GGGGCCGGG CGCG		

	CCCCGGCCC GCGC			
	TAA —			
GAM375 RAD23B	TGGCCTGGCGGGGCCCGGGGTCGC	5831	—	ATTC — I
	GGC GGGGCC GGGGTCG			
	CCG CCCC GG CCCCAGC			
	GA — GG I			
GAM375 ROR2	TTCG-GGCCGGGG-CGCGG	5836	G	T I
	TTCGGG CCGGGG CGCG			
	AAGCCC GGCCCC GCGC			
	— — C			
GAM375 RPS6KA2	GGC-TCCGAGGCCGGGGTC	5807	A	I
	GGC TTCGGGGCCGGGGT			
	CCG AGGCTCCGGCCCCA			
	— G			
GAM375 RUNX3	ATCCCGGGCCGGGGTGGGGG	5802	G	CGCGI
	TTC GGGCCGGGGT			
	AGG CCCGGCCCCA			
	G CCCCI			
GAM375 SGT	GGCA--CAGGGCCGGGGTGGC	5809	TT	CI
	GGCA CGGGGCCGGGGT			
	CCGT GTCCCGCCCCA			
	— CC			
GAM375 SIL	TCTGGGACGTTGGGGTCGCGG	5829	TC_	C_
	GGGGC GGGGTCGCG			
	CCCTG CCCCAGCGC			
	AGA CAA CII			
GAM375 TIMM23	TGACACTCCCAGACGGGGTCGCGG	5834	GG C	I
	GGCATTG GG CGGGGTCGCG			
	CTGTGAG TC GCCCCAGCGC			
	GG T I			
GAM375 TRAF1	CATTCGGGGCCGGAGTGGC	5803		CGII
	CATTCGGGGCCGGGGT			
	GTAAGCCCCGGCCTCA			
	CCGI			
GAM375 ZNF137	TTAGGGGCCGGG--CGCGG	5835	TTC	GT I
	GGGGCCGGG CGCG			
	CCCCGGCCC GCGC			
	AAT — C			
GAM376 CAMLG	TGTAAAC-CAATTTGCCTCC	5848	T	CT
	TGTAAAC CAATTTGCCTCC			

	ACATTTG GTTAAACGGAGG			
	— II			
GAM376 GNA14	GTAAACTCAAATATCTTCC	5842 TG	TTTGCC	CT
	TAAACTCAA TCC			
	ATTTGAGTT AGG			
	— TATAGA TI			
GAM376 MAN1A2	AAACTCAATTTTGCTCTCT	5839 TGTA	AA	— — C
	CTCAATTT GC CTC CT			
	GAGTTAAA CG GAG GA			
	— A A A			
GAM376 MOX2	TGTATGCTCATATTTGCCTCC	5846 AA	—	CTI
	TGTA CTCA ATTTGCCTCC			
	ACAT GAGT TAAACGGAGG			
	AC A			
GAM376 PCDHGA7	GTAAACTCATTTTTACCTC	5841 TG	A—	CCT
	TAAACTCA TTTGCCTC			
	ATTTGAGT AAATGGAG			
	— AA AII			
GAM376 RNMT	TAAACAAAATGATTTGCCTC	5843 TGTA	AACTCA	CCT
	ATTTGCCTC			
	TAAACGGAG			
	TTGTTTTAC— ACI			
GAM376 SLC12A6	TGTTAATTCTAATTTGCCT	5845 A C	—	CCCT
	TGT AA TC AATTTGCCT			
	ACA TT AG TTAAACGGA			
	A A A IIIT			
GAM376 SLC7A8	TGCAACCTCAAAAGCTGCCTCCCT	5847 A T—		II
	TGTAA CTCAA TTGCCTCCCT			
	ACGTT GAGTT GACGGAGGGA			
	G TTC II			
GAM376 TPM4	GTAAATCCTCAATTTGCTGTTCCCT	5840 TGTA	AA	C— III
	CTCAATTTGC TCCCT			
	GAGTTAAACG AGGGA			
	ATTTAG ACA CII			
GAM376 ZNF151	TGTAAACTCCAGCTTGGCTCCC	5844 AA—	C	TI
	TGTAAACTC TTTG CTCCC			
	ACATTTGAG GAAC GAGGG			
	GTC C II			
GAM377 GUCY1A2	AGGCGGTGGCG---GCGAGGACG	5851 AA	A	CCCT
	GGCG TGGC GCGAGGAC			

	CCGC ACCG CGCTCCTG		
	__ C C__		
GAM377 TRC8	GCGATGGCC--GAGAGGGCG 5852 AAGGCG	CCT C A	
	ATGGCC G GAGG		
	TACCGG C CTCC		
	_____ T C		
GAM378 ACHE	GGCGCCCGAGCGAGGCGGGAGGG 5861 TG ATTC _	CA	
	GCGC CG GGCGGGAGGG		
	CGCG GC CCGCCCTCCC		
	__ GGTC T CI		
GAM378 BSN	GCATCTCGGA-GGGAGGGCA 5856 TGGCGCATT C		
	CGGG GGGAGGGC		
	GCCT CCCTCCCG		
	GA_____ -		
GAM378 COL5A1	TGGCGCGCTCGCCACGGGCGGGAGGGC5871	A _____	A
	TGGCGC TTC CGGGCGGGAGGGC		
	ACCGCG GAG GCCCGCCCTCCCG		
	C CGGT A		
GAM378 CRLF1	CGCAGGCCGGGCGCGGGAGGGC 5855 TGGCGCATT _	A	
	CCGGGC GGGAGGGC		
	GGCCCG CCCTCCCG		
	TCC_____ CG C		
GAM378 CYBA	GGTGCA--CCTGGCGGGAGGGCA 5868 TGGC TT G		
	GCA CC GGCGGGAGGGCA		
	CGT GG CCGCCCTCCCGT		
	CA__ _ A		
GAM378 FUT3	TGGCAGGTTTCCTGGGGCGGGAGG 5870	CA_ _	GCAI
	TGGCG TTCC GGGCGGGAGG		
	ACCGT AAGG CCCGCCCTCC		
	CCA AC A		
GAM378 FXD7	GGCTCATTCCG---GGGAGCGC 5866 TG G	CGG G	
	GC CATTCCGGG GAG GC		
	CG GTAAGGCC CTC CG		
	_ A _ G		
GAM378 HRMT1L2	GGCTCGTGAGGGCGGGAGAGC 5867 TGGC_ TTCC	A	
	GCA GGGCGGGAGGGC		
	CGT CCCGCCCTCTCG		
	CGAGCA _ G		
GAM378 HS3ST3A1	TGGCTCGGTCCC--CGGGAGGGCA 5874	GCAT GGG	
	TGGC TCC CGGGAGGGCA		

	ACCG AGG GCCCTCCCGT			
	AGCC G__			
GAM378 ILF1	GGAGCACGCGCGGGCGGGAGG 5860 T	ATTC	CA	
	GGCGC CGGGCGGGAGGG			
	TCGTG GCCCGCCCTCCT			
	C CGC_ II			
GAM378 MAF	GGCGTCTGTCCGGGCGGCGCGGGC 5859 TG	CAT_	GA_ AI	
	GCG TCCGGGCGG GGGC			
	CGC AGGCCCGCC CCG			
	_ AGAC GCG GI			
GAM378 MAN1A1	GGCGCAGCGTGGGCGGGAG 5862 TG	TTCC	GC	
	GCGCA GGGCGGGAGG			
	CGCGT CCCGCCCTCT			
	_ CGCA II			
GAM378 MAPK8IP1	TGGC-CAT-CCGGGC-GGAGCGC 5873	G T	G G	
	TGGC CAT CCGGGCGG AG GC			
	ACCG GTA GGCCCGCC TC CG			
	_ _ _ G			
GAM378 MN1	GCGCACCGTTGCAGGCGCGGGAGGGCA5857 TG	ATTCC_ _		
	GCGC GG GCGGGAGGGCA			
	CGTG CC CGCCCTCCCGT			
	_ GCAACGT G CGI			
GAM378 NFKBIA	GGCGC-TGGCGGGCGGGACGGC 5865 TG	ATTC	G A	
	GCGC CGGGCGGGA GGC			
	CGCG GCCCGCCCT CCG			
	_ ACC_ G C			
GAM378 NRXN2	GGCGCATG--GGGCGGGAGGG 5864 TG	TCC	C	
	GCGCAT GGGCGGGAGGG			
	CGCGTA CCCGCCCTCCC			
	_ C_ C			
GAM378 PODXL	GCGCGT-CCGGGCGGTAGG 5858 TG	CAT	G	
	GCG TCCGGGCGG AGGG			
	CGC AGGCCCGCC TCCT			
	_ _ A			
GAM378 PYGM	TGGCCAGCATT---GGCGGGAGG 5869	_ CCG	GC	
	TGGC GCATT GGCGGGAGG			
	ACCG CGTAA CCGCCCTCC			
	GT _ II			
GAM378 SH3GL2	TGGCGGCTGCTGTGCGGGAGGG 5872	CATTCCGG	CA	
	TGGCG GCGGGAGGG			

	ACCGC CGCCCTCCC			
	CGACGACA II			
GAM378 SMURF1	GGCG---TCCGGGCGGCAGG 5863 TG CAT GA			
	GCG TCCGGGCGG GGG			
	III IIIIIII III			
	CGC AGGCCCGCC TCC			
	___ ___ G_			
GAM379 DYT1	GGGATGCCCTCCTGTTTCAGGAA 2529 A _ GCA			
	GGGATGCCCTC TGTT GGGAA			
	IIIIIIII III IIII			
	CCCTACGGGAG ACAA TCCTT			
	G G III			
GAM379 IL1RAP	GATGCCTT--TCTTGGAAGC 2528 GGGA CTCATG			
	TGCC TTGGGAAGC			
	III IIIIIII			
	ACGG AACCCTTCG			
	___ AAAG_			
GAM379 SLC21A3	GGCATTGCCTCAC-TTGGGAAGC 2530 G GC G A			
	GG AT CCTCAT TTGGGAAGC			
	II II IIIII IIIIIII			
	CC TA GGAGTG AACCCTTCG			
	G AC _ I			
GAM379 SOST	GGGAAGCC---AGGCTGGGAAGCA 2531 T CTCAT			
	GGGA GCC GTTGGGAAGCA			
	III III IIIIIIIII			
	CCCT CGG CGACCCTTCGT			
	T TC___			
GAM380 APG5L	TCC-CCGCACTGGTG--GGGACGC 5891 G C T TC A			
	TCC CC CACT GTG GGGA GC			
	III II III III III II			
	AGG GG GTGA CAC CCCT CG			
	_ C C _ G			
GAM380 APG5L	TCC-CCGCACTGGTG--GGGACGC 5891 G C T TC AI			
	TCC CC CACT GTG GGGA			
	III II III III III			
	AGG GG GTGA CAC CCCT			
	_ C C _ GC			
GAM380 CD1A	CCCACTTGTAAGTCAGGGAAG 5881 _ AAIII			
	CCCACTTGT GTCGGG			
	IIIIII IIIII			
	GGGTGAACA CAGTCC			
	TT CTTCI			
GAM380 CDKN3	CCGCCCCAC---GTCGAGA 5884 _ TTGT			
	CGCCCCAC GTCGGG			
	IIIIII IIIII			
	GCGGGGTG CAGCTC			
	G _			
GAM380 CDKN3	CCGCCCCAC---GTCGAGA 5884 TC TTGT			
	CGCCCCAC GTCGGGA			
	IIIIII IIIII			

GCGGGGTG CAGCTCT

GAM380 CSNK2A2	CCCCATGCTTTCTGGGTCGGGAAG 5882	___ GT___	IIIC
	CCCCA CTT GTCGGGAA		
	GGGGT GAA CAGCCCTT		
	AC AGACC CIII		
GAM380 CSNK2A2	CCCCATGCTTTCTGGGTCGGGAAG 5882	TCC CCCAC T	CI
	GC TTG GTCGGGAAG		
	CG GAC CAGCCCTTC		
	TA_ AAA_ C TT		
GAM380 CYP4A11	TCCCGCCCACTTGTG--GGGA 5890	_ C TC AG	
	TCCGCCC ACTTGTG GGGA		
	GGGCGGG TGAACAC CCCT		
	A _ _ II		
GAM380 CYP4A11	TCCCGCCCACTTGTG--GGGA 5890	_ C TC I	
	CCGCCC ACTTGTG GGG		
	GGGCGGG TGAACAC CCC		
	AG _ _ I		
GAM380 H1F0	TCCTCCCCGGGCTCGGGTGTCTGGGAGAGC5889	G A_ _ _ III	
	TCC CCCC CTT GTGTCGGGA AGC		
	AGG GGGG GAG CACAGCCCT TCG		
	A CC CC C III		
GAM380 H1F0	TCCTCCCCGGGCTCGGGTGTCTGGGAGAGC5889	G CA _ AGI	
	CCC CTT GTGTCGGGA		
	GGG GAG CACAGCCCT		
	_ CC CC CII		
GAM380 HR	CGCCCCACTGGCCTGTGTC 5886	___ IIIG	
	CGCCCCACT TGTGT		
	GCGGGGTGA ACACA		
	CCGG GIII		
GAM380 HR	CGCCCCACTGGCCTGTGTC 5886	TCCG ___ GGGAAG	
	CCCCACT TGTGT		
	GGGGTGA ACACAG		
	___ CCGG ACIIIC		
GAM380 LIF	GCCCTGGCGCTTGTGTCTGGGA 5887	CA___ III	
	GCCC CTTGTGTCTGGG		
	CGGG GAACACAGCCC		
	ACCGC TII		
GAM380 LIF	GCCCTGGCGCTTGTGTCTGGGA 5887	TCC CCCA A	
	GC CTTGTGTCTGGGA GC		

	CG GAACACAGCCCT CG			
	GAC C___ _			
GAM380 MLLT4	GCACCGCT-G-GTCGGAAG	5888	C A T T	I
	GC CC CT G GTCGGA			
	CG GG GA C CAGCCCT			
	T C ___ T			
GAM380 MLLT4	GCACCGCT-G-GTCGGAAG	5888	T CCCACT	T
	CCGC TG GTCGGA			
	GGCG AC CAGCCCTT			
	— — — — —			
GAM380 SLC19A1	CCGCCCCACGCGTGGCTGGCAG	5885	T TCG	AAI
	CGCCCCAC TGTG GG			
	GCGGGGTG GCAC CC			
	C CGA GTI			
GAM380 SLC19A1	CCGCCCCACGCGTGGCTGGCAG	5885	TC T TCG	A C
	CGCCCCAC TGTG GG AG			
	GCGGGGTG GCAC CC TC			
	— C CGA G C			
GAM380 XRCC3	CCGAGCCCCGTGTGTCTGGG	5883	CC__ ACT	II
	GCCCC TGTGTCTGG			
	CGGGG ACACAGCC			
	GGCT C__ CI			
GAM380 XRCC3	CCGAGCCCCGTGTGTCTGGG	5883	TCC ACT	AAG
	GCCCC TGTGTCTGGG			
	CGGGG ACACAGCCC			
	GCT C__ CII			
GAM381 ALPPL2	CAGGGGAAGTCCGGGATGGGGA	5900	TGACAA	__ T
	GGGAAT TGGGATGGGGA			
	CCCTTG GCCCTACCCCT			
	— AG T			
GAM381 C3	GACAGAGGGAGA--GGATGGGGA	5903	TG _ ATT	T
	ACA AGGGA GGGATGGGGA			
	TGT TCCCT TCCTACCCCT			
	_ C C__ C			
GAM381 DLEC1	TGACAAGGGA--GGGCCAGATGGG	5909	ATTG_	GAT
	TGACAAGGGA GGATGGG			
	ACTGTTCCCT TCTACCC			
	CCCGG III			
GAM381 GRIK3	TGCCCAGGCATATGGGATGGGTAT	5912	ACA GAAT	GATI
	TG AGG TGGGATGGG			

	AC TCC ACCCTACCC			
	GGG GTAT ATAI			
GAM381 IRS1	GACAAGGGCGAGAGGGGATGGGG	5904 TG	AATT__	ATI
	ACAAGGG GGGATGGGG			
	TGTTCCC CCCTACCCC			
	__ GCTCTC CII			
GAM381 LIF	GACATGGGTGGGAGTGGGATGGGG	5905 TGACAA__	AT	ATI
	GGGA TGGGATGGGG			
	CCCT ACCCTACCCC			
	TGTACCCA C_ CII			
GAM381 MFAP2	AAGGAACATGGGGATGGGGA	5894 TGACAAGGGAATT		
	GGGATGGGGA			
	CCCTACCCCT			
	TTGTAC_____			
GAM381 MSN	ACAAGG-AATTGGGGTAGG	5898 TGACA	A	
	AGGGAATTGGG TGGGG			
	TTCCTTAACCC ATCCT			
	_____ C			
GAM381 MYO1C	TGCCAAGGGAATCAGGA-GGAGA	5911 TGA	TG T T	
	CAAGGGAAT GGA GGGGA			
	GTTCCCTTA CCT CCTCT			
	ACG GT _ I			
GAM381 NF1	CACGGGGGTGGGGATGGGG	5901 TGACAA	AATT	A
	GGG GGGATGGGG			
	CCC CCCTACCCC			
	C_____ CAC_ C			
GAM381 NOS1	TGAGCAGGGGAAATTGGGAT	5908 _ A _	GGGGA	
	TGA CA GGGAA TTGGGAT			
	ACT GT CCCTT AACCCTA			
	C C T ITA			
GAM381 PAX5	ACAAGGGAAGTTGGGCTAGG	5897 TGAC	_ A GA	
	AAGGGAA TTGGG TGGG			
	TTCCCTT AACCC ATCC			
	_____ C G AG			
GAM381 PPP2R4	ACAGAGGGGAG--GGGATGGGGA	5896 TGACA	ATT	
	AGGGA GGGATGGGGA			
	TCCCT CCCTACCCCT			
	TC__ C__			
GAM381 PTGIR	GACAATGAGAT--GGATGGGGA	5907 TG	_ ATTG	
	ACAA GGGG GGATGGGGA			

	TGTT CTCT CCTACCCCT	
	__ A A__	
GAM381 RUNX3	TGTCAGGGGATGGGGGATGGGG 5910 TGA A ATT AT	
	CA GGA GGGATGGGG	
	GT CCCT CCCTACCCC	
	ACA C ACC II	
GAM381 TRPV4	CAAGGGAAT--GAAAGGGGA 5902 TGACAA T GG T	
	GGGAAT G A GGGG	
	CCCTTA C T CCCC	
	____ _ TT _	
GAM381 UNRIP	AGGAAAGTAGGGGATGGGGA 5899 TGACAAGGGAATT	
	GGGATGGGGA	
	CCCTACCCCT	
	TCATC_____	
GAM381 WBSCR1	ACACAGGCAACAGGGATGGGG 5895 TG A G T AT	
	ACA GG AAT GGGATGGGG	
	TGT CC TTG CCCTACCCC	
	__ _ G T CC	
GAM381 XPNPEP2	GACAAGGGAGAGAGGGAGGG 5906 TG ATT_ T GA	
	ACAAGGGA GGA GGG	
	TGTTCCCT CCCT CCC	
	__ CTCT _ GI	
GAM382 AKAP13	AGCCAAGCCCCGGGTAGATCTC 5916 G ____ CII	
	AG CGAGCC GGTAGATCTC	
	TC GTTCGG CCATCTAGAG	
	G GGC III	
GAM382 AKAP13	AGCCAAGCCCCGGGTAGATCTC 5916 G ____ III	
	AG CGAGCC GGTAGATCT	
	TC GTTCGG CCATCTAGA	
	G GGC GII	
GAM382 BARX2	AGG-GAGACGGGTAGATCTC 5917 C _C CI	
	AGG GAG C GGTAGATCTC	
	TCC CTC G CCATCTAGAG	
	_ T C II	
GAM382 BARX2	AGG-GAGACGGGTAGATCTC 5917 C _C II	
	AGG GAG C GGTAGATCT	
	TCC CTC G CCATCTAGA	
	_ T C GI	
GAM382 CALB2	GGCGAGCCGCTCGGAGACCTC 5921 ____ T III	
	GGCGAGCC GG AGATCT	

	CCGCTCGG	CC TCTGGA		
	CGAG _	GII		
GAM382 CALB2	GGCGAGCCGCTCGGAGACCTC	5921 AG	_____ T	CII
	GCGAGCC	GG AGATCTC		
	CGCTCGG	CC TCTGGAG		
	__ CGAG _	TII		
GAM382 HK1	GGCGAGCC-GTGGTCCTCC	5923	GTAGA	I
	GGCGAGCCG	TCTC		
	CCGCTCGGC	GGAG		
	ACCA_	G		
GAM382 HK1	GGCGAGCC-GTGGTCCTCC	5923 AG	GTAGA	
	GCGAGCCG	TCTCC		
	CGCTCGGC	GGAGG		
	__ ACCA_			
GAM382 IHPK3	AGGTGAGATGGGTAGATCTC	5918	C CC_	CI
	AGG GAG	GGTAGATCTC		
	TCC CTC	CCATCTAGAG		
	A TAC	II		
GAM382 IHPK3	AGGTGAGATGGGTAGATCTC	5918	C CC_	II
	AGG GAG	GGTAGATCT		
	TCC CTC	CCATCTAGA		
	A TAC	GI		
GAM382 KCNK5	AGGGCAGACACTAGATCTCC	5919_	G C G	I
	GGC AG CG	TAGATCTC		
	CCG TC GT	ATCTAGAG		
	C _ T G	I		
GAM382 KCNK5	AGGGCAGACACTAGATCTCC	5919 A_	G C G	I
	GGC AG CG	TAGATCTCC		
	CCG TC GT	ATCTAGAGG		
	TC _ T G	I		
GAM382 SBF1	GGCGAGCCGCTGGTAGCTCC	5922	_____ A	CII
	GGCGAGCC	GGTAG TCT		
	CCGCTCGG	CCATC AGG		
	CGA	G III		
GAM382 SBF1	GGCGAGCCGCTGGTAGCTCC	5922 AG	_____ AT	I
	GCGAGCC	GGTAG CTCC		
	CGCTCGG	CCATC GAGG		
	__ CGA	_ C		
GAM382 SF1	AGGCGAGCCCGAGGGAGCTC	5915	_ TA T	CI
	AGGCGAGCC	GG GA CTC		

	TCCGCTCGG CT CT GAG		
	G CC C II		
GAM382 SF1	AGGCGAGCCCGAGGGAGCTC 5915	GGTAGATIII	
	AGGCGAGCC		
	TCCGCTCGG		
	G _____		
GAM382 TCTE1L	GCGACACGCCGGTAGAGCACC 5920	____ TCTCIII	
	GCGA GCCGGTAGA		
	CGCT CGGCCATCT		
	GTG CGTGGII		
GAM382 TCTE1L	GCGACACGCCGGTAGAGCACC 5920 A A	TCT II	
	GGCG GCCGGTAGA CC		
	II		
	CTGT CGGCCATCT GG		
	_ G CGT CG		
GAM383 ACHE	TGGCAA--GA-GGATCAGGAGAAT 5944	CT T A	
	TGGCAA GA GGA CAGGAGAAT		
	II		
	ACCGTT CT CCT GTCCTCTTA		
	_ _ A		
GAM383 ACTN1	CAGCAGATGGAACAGATAGAA 5928	TGGCAACT _ T	
	GATGGAACAGG AGAA		
	CTACCTTGTCT TCTT		
	GT_____ A C		
GAM383 ATF5	TGGGCACTGATGGCAACAGGAGA 5938 T_ A _	ATI	
	GGCA CTGATGG AACAGGAGA		
	CCGT GACTACC TTGTCCTCT		
	AC _ G III		
GAM383 CANX	TGACAACA-ATGGAACAGG 5941	T AGA	
	TGGCAAC GATGGAACAGG		
	ACTGTTG TTACCTTGTCC		
	_ III		
GAM383 CDH11	TGGTTACGTGGTAGGCACAGGAGAAT 5936	CA _ A A_ II	
	TGG AC TG TGG ACAGGAGAAT		
	ACC TG AC ATC TGTCTCTTA		
	AA C C CG II		
GAM383 ECT2	AACTGATGGCAACTTCAGAAT 5927	____ GAT CAGGAGAAT	
	TGGCAACT GGAA		
	ACCGTTGA TCTT		
	CT AG_ AATAAIIIT		
GAM383 EGR3	GGCAACTTACTGACCACAGGAGAA 5930	TG GA_ A_ TI	
	GCAACT TGG ACAGGAGAA		

	CGTTGA ACT TGTCTCTT		
	___ ATG GG CI		
GAM383 EZH1	GGAAACTGGAGGAACAGGAGTAT 5932 TGGC AT AAT		
	AACTG GGAACAGGAG		
	TTGAC CCTTGTCTC		
	CT___ CT ATAA		
GAM383 FGF1	GGGACCTGATGGAAGTGCAGAA 5931 T CAA AGG T		
	GG CTGATGGAAC AGAA		
	CC GACTACCTTG TCTT		
	_ TG_ ACG T		
GAM383 HFL1	CAACTGATGAAGCTGGAGCAT 5929 TGGCAA ACA AAT		
	CTGATGGA GGAG		
	GACTACTT CTC		
	_____ CGA GTA		
GAM383 MPP2	GGGAAAAGA-GGAGCAGGAGAAT 5933 T C CT T A		
	GG AA GA GGA CAGGAGAAT		
	CC TT CT CCT GTCCTCTTA		
	_ _ TT _ C		
GAM383 MYLK	TGGCAACTGGGCCAGTGGGACAGGA 5937 A_____ A GAATII		
	TGGCAACTG TGG ACAGGA		
	ACCGTTGAC ACC TGTCTT		
	CCGGTC C IIITAA		
GAM383 NOLA2	TGGCA-CTGATGG-ACAGAAGA 5943 A A A		
	TGGCA CTGATGGA CAGGAGA		
	ACCGT GACTACCT GTCTTCT		
	_ _ I		
GAM383 PPID	TGGGAAGCTGA-GG--CAGGAGAAT 5935 C _ T AA		
	TGG AA CTGA GG CAGGAGAAT		
	ACC TT GACT CC GTCCTCTTA		
	C C _ _		
GAM383 RAB13	TGACAAGTGACAGAACAGGAG 5942 C AAT		
	TGGCAA TGATGGAACAGGAG		
	ACTGTT ACTGTCTTGTCTC		
	C III		
GAM383 RET	TGGTCACTGATGGACACAG 5939 CA _ GAGAA		
	TGG ACTGATGGA ACAG		
	ACC TGACTACCT TGTC		
	AG G IIITA		
GAM383 SLC24A1	TGACCACTGATGGAGACAACACGAAT 5940 A _ GA_ II		
	TGGC ACTGATGGA ACAG GAAT		

	ACTG TGA	CTACCT	TGTT	CTTA	
	G	C	GTG	II	
GAM383 SMOH	AACTGAAAT	TGGAACAGGAGAA	5926	TGGCAA T	T
	C	GATGGAACAGGAGAA			
	I				
	C	TTACCTT	GTCTCTT		
	_____	T	C		
GAM383 ZNF157	TGGGAGACTGA	GG--CAGGAGAAT	5934	T_ CA	T AA
	GG	ACTGA GG CAGGAGAAT			
	II				
	CC	TGACT CC	GTCTCTTA		
	AC	TC	_____		
GAM384 ABCD4	GAGAAGACAGAAAGCTGTAA	5963	TG	C C	CAAAG
	AGAAGACA	AAA	CTG		
	TCTTCTGT	TTT	GAC		
	_____	C C	ATTAI		
GAM384 ALDH3A2	GAAGACCTACTAACCTGCAA	5957	TGAGAA	_____	A AG
	GAC	AC AACCTGCAA			
	CTG	TG TTGGACGTT			
	_____	GA A	GA		
GAM384 BSND	GAGAAGACACTGAAATCGCTGCAA	5960	TG	AAAC_____	AGAI
	AGAAGACAC	CTGCAA			
	TCTTCTGTG	GACGTT			
	_____	ACTTTAGC	GII		
GAM384 CARD10	GAGAAGACACAGACACACATAAGA	5962	TG	A C	_____
	AGAAGACACA	AC TGCA	AAGA		
	TCTTCTGTGT	TG GTGT	TTCT		
	_____	C T	A G		
GAM384 CCR9	AAGACACAAAAGATGCAAAG	5947	TGAGAAGA	CC_	
	CACAAA	TGCAAAG			
	GTGTTT	ACGTTTC			
	_____	TCT			
GAM384 CPNE3	AGGCACAGCAACCTGCAAA	5954	TGAGAAGACACA		G
	AACCTGCAAA				
	TTGGACGTTT				
	GTCG_____	G			
GAM384 DHCR24	AGATGACAACAACCTGCAA	5952	TGAGAA	CA	AG
	GACA	AACCTGCAA			
	CTGT	TTGGACGTT			
	TA_____	TG	CA		
GAM384 EHF	AAGAATTAATACCTGCAAAGA	5948	TGAGAAGACACAA		
	ACCTGCAAAGA				

		TGGACGTTTCT		
		TAATTA_____		
GAM384 FLOT2	GAGATGAGACACAAACCTG	5959 T GA	CAAAG	
	GA AGACACAAACCTG			
	CT TCTGTGTTTGGAC			
	T AC TIIIA			
GAM384 KPNA1	AAGACACAAAAGACCAAAGA	5949 TG_	A CCTGCAAAG	
	AGAAGAC CAAA			
	TTTTCTG GTTT			
	GTG _ CTCTTCIII			
GAM384 KRT19	AGAAGACAC---CCTCCAAAG	5953 TGAG	AAA G	
	AAGACAC CCT CAAA			
	TTCTGTG GGA GTTT			
	_____ G			
GAM384 MTAP	TGTGAAGACACAGAAAGATTCAAAGA	5966 TGA	AACCTG__	
	GAAGACACA CAAAGA			
	CTTCTGTGT GTTTCT			
	ACA CTTTCTAA			
GAM384 OTP	GAGAAGACAGAAA-CAGAAAAG	5965 TG	C CTGC A	
	AGAAGACA AAAC AAAG			
	TCTTCTGT TTTG TTTC			
	__ C TCT_ C			
GAM384 PCDH11Y	AGAGAGACACAAACAAGCA	5950 TG A	CT AAG	
	AGA GACACAAAC GCA			
	TCT CTGTGTTTG CGT			
	__ _ TT CAI			
GAM384 PCSK2	GAGAAGACAGAAATCCATGCCAA	5961 TG	C _ _ AAAGAI	
	AGAAGACA AAA CC TGC			
	TCTTCTGT TTT GG ACG			
	__ C A T GTTII			
GAM384 PIK3CG	TGAGAAAAAACCAAACCTGCAAA	5967 T__	A GAI	
	GAGAAGAC CAAACCTGCAAA			
	CTTTTTTG GTTTGGACGTTT			
	ACT _ III			
GAM384 PLN	GAAGACA---ACCTGCAAA	5958 TGAGAA	CAA	
	GACA ACCTGCAA			
	CTGT TGGACGTT			

GAM384 PNN	GACAAGACACAAA-CT-CAAA	5964 TGAG	CTG	
	AAGACACAAAC CAAAG			

		TTCTGTGTTTG	GTTTT			
		TG__	A__			
GAM384	RAD23B	AGAAGAAATAAAGACCTGCAAA	5951 T	ACACAA		A
		GAGAAG	ACCTGCAAAG			
		TTCTTT	TGGACGTTTT			
		_	ATTTC_	C		
GAM384	SHMT2	TGTGAAGAGTCCAACCTGCAAGGA	5968 TGA	CACA		A I
		GAAGA	AACCTGCAA GA			
		CTTCT	TTGGACGTT CT			
		ACA	CAGG	C I		
GAM384	TNFRSF11A	GAACGACACAAACTTAAAAAGA	5956 TGAGAA		C C	
		GACACAAAC	TG AAAGA			
		CTGTGTTTG	AT TTTCT			
		G_____	A T			
GAM384	TRIM14	AGACACAAATCCCTGGAAAGA	5955 TGAGAAGACACAAA		C	
		CCTG	AAAGA			
		GGAC	TTTCT			
		GTTTAG_____	C			
GAM385	EPB41L2	TATCATTTAATACAACTTGA	5974	TTCC	ACC	
		TATCATTTAAT	CTTGA			
		ATAGTAAATTA	GAAC			
		TGTT				
GAM385	OGG1	ATTATTTAATTTCTTCCCTT	5971 TATC	___	GAACC	
		ATTTAATT	TCCCTT			
		TAAATTAA	AGGGAA			
		AA__	AGA	GIIT		
GAM385	PPP1R2	TATCATTTAATT---CTTG	5973	TCC	AA	
		TATCATTTAATT	CTTG			
		ATAGTAAATTAA	GAAC			

GAM385	ZNF175	TATCATTGATATAATTTCCC	5972	___	TTGAACC	
		TATCATT	TAATTTCCC			
		ATAGTAA	ATTAAAGGG			
		CTAT	ITCCA			
GAM386	BLK	GCGGCACAGAGAGGCCGCGTAACT	5979 CG	CC	_	I
		GCAG	GAGGCCGCG AAC			
		TGTC	CTCCGGCGC TTG			
		CG	T_	A I		
GAM386	BLK	GCGGCACAGAGAGGCCGCGTAACT	5979 T	G	CC	_ I
		GGCG	CAG GAGGCCGCG AAC			

	CCGT GTC CTCCGGCGC TTGA		
	— _ T_ A G		
GAM386 DLX2	TGGCGGCAG-CG-GGCCGGA 5983	C A	C AC
	TGGCGGCAGC G GGCCG GA		
	ACCGCCGTCG C CCGGC CT		
	— _ C II		
GAM386 DLX2	TGGCGGCAG-CG-GGCCGGA 5983	C A	CI
	TGGCGGCAGC G GGCCG		
	ACCGCCGTCG C CCGGC		
	— _ CC		
GAM386 MMP25	TGGCGGCAGCCG-GG-AGGGAAC 5984	A CCGC	T
	TGGCGGCAGCCG GG GAAC		
	ACCGCCGTCGGC CC CTTG		
	_ TCC_ I		
GAM386 MMP25	TGGCGGCAGCCG-GG-AGGGAAC 5984	_ CC	GAI
	TGGCGGCAGCC GAGG GC		
	ACCGCCGTCGG CTCC TG		
	CC CT III		
GAM386 MUC4	GCCGAGGCCCCAGCGACCT 5978	_ ACIII	
	GCCGAGGCC GCGA		
	CGGCTCCGG CGCT		
	GGT GGAI		
GAM386 NDRG1	GGCGGCAGCTGGGCAGGCCGC 5980	CG_	III
	GGCGGCAGC AGGCCG		
	CCGCCGTCG TCCGGC		
	ACCCG GII		
GAM386 NDRG1	GGCGGCAGCTGGGCAGGCCGC 5980 TG	CG_	GAAC
	GCGGCAGC AGGCCG		
	CGCCGTCG TCCGGCG		
	_ ACCCG IIIT		
GAM386 P23	GGCGGCAGCGGCGGGCTCGACCT 5981	_ A CG	ACI
	GCGGCAGC CG GGC CGA		
	CGCCGTCG GC CCG GCT		
	CC _ A_ GGI		
GAM386 P23	GGCGGCAGCGGCGGGCTCGACCT 5981 TG	_ A CG	A I
	GCGGCAGC CG GGC CGA CT		
	CGCCGTCG GC CCG GCT GA		
	_ CC _ A_ G G		
GAM386 POLS	TGCCGGTGGCCGAGGCCGCG 5982 G CA		AAC
	TG CGG GCCGAGGCCGCG		

		AC GCC CGGCTCCGGCGC			
		G AC III			
GAM386	POLS	TGCCGGTGGCCGAGGCCGCG	5982	G CA I	
		G CGG GCCGAGGCCGC			
		I III I			
		C GCC CGGCTCCGGCG			
		G AC I			
GAM386	STIP1	GCAGCCGAGACAGC-AACT	5977	C ACI	
		GCAGCCGAGGC GCGA			
		I I I I I I I I I I			
		CGTCGGCTCTG CGTT			
		T GAI			
GAM386	STIP1	GCAGCCGAGACAGC-AACT	5977	T__ CG CCGCGAA	
		GGCGGCAGC AGG			
		I I I I I I I I I I			
		CTGTCTGTG TCC			
		GCT A_ CCIIITC			
GAM387	AGXT	GAGGCTGCCTGGTTCTGCCTCCCG	5997	TGAGAGG GG I	
		CTGGT TTGCCTCCCG			
		I I I I I I I I I I			
		GACCA GACGGAGGGC			
		CGACG__ A_ C			
GAM387	ASPH	TGAG-GGCTGGTGG--ACCTCC	6004	A TT C	
		TGAG GGCTGGTGG GCCTCC			
		I I I I I I I I I I			
		ACTC CCGACCACC TGGAGG			
		_ _ I			
GAM387	ATF7	GAGCGGCTGGTAGCTCCGTTGCCTCCCG	5994	TG A _____ III	
		AG GGCTGGTGGT TGCCTCCCG			
		I I I I I I I I I I			
		TC CCGACCATCG ACGGAGGGC			
		_ G AGGCA GII			
GAM387	ATP6V0A4	AGCCTGGCCTTTGCCTCCC	5991	TGAGAGGC GG	
		TGGT TTGCCTCCC			
		I I I I I I I I I I			
		ACCG AACGGAGGG			
		_____ GA			
GAM387	CASP3	GAGGCCTGGAGCCTGCCTCCCG	5996	TGAGA G T _	
		G CTGG GGT TGCCTCCCG			
		I I I I I I I I I I			
		C GACC TCG ACGGAGGGC			
		_____ G _ G			
GAM387	CLK2	AGAG-CTGGTGGTGTTCCTC	5988	TGAGA TG_ CC	
		GGCTGGTGGT CCTC			
		I I I I I I I I I I			
		TCGACCACCA GGAG			
		_____ CAA AC			
GAM387	COL1A1	TGAGGGGCTGGTGGCT-CC-CCCG	6006	A G T	
		TGAG GGCTGGTGGTT CC CCCG			
		I I I I I I I I I I			

	ACTC CCGACCACCGA GG GGGC	
	C _ _	
GAM387 FHL2	GGCTGGTGGCTGCGGCTCC 6001 TGAGA G G TCCC	
	GGCTG TGGTT CC	
	CCGAC GCCGA GG	
	CA_ _ _ CGAC	
GAM387 KCNJ6	GAGAGGCTGTTAGGAGACTCC 5995 TG GT_ TTGC CG	
	AGAGGCTG GG CTCC	
	TCTCCGAC CC GAGG	
	_ AAT TCT_ TI	
GAM387 LFG	AGACTCGTGTGTGCCTCCCG 5992 TGAGAGGCTG GT	
	GTG TGCCTCCC	
	CAC ACGGAGGG	
	AG_ _ _ AC	
GAM387 MEN1	AGAGGCTGGCAGTGGCTTCC 5989 TGAG TG T C C	
	AGGCTGG GT GC TCC	
	TCCGACC CA CG AGG	
	_ GT C A T	
GAM387 MYO1C	GAGGCCCTTGTTGCCTTCCG 5998 TGAGAG GG C	
	GCT TGGTTGCCT CCG	
	CGG ACCAACGGA GGC	
	_ GA A	
GAM387 PROK1	AGGTTGGTGTGTAGTTGCCTCCC 5990 TGAGA C _ GI	
	GG TG GTGGTTGCCTCCC	
	CC AC CATCAACGGAGGG	
	A_ _ A AC	
GAM387 RNH	TGAGAGGCTCCTGGTGCCT 6003 GG T CCC	
	TGAGAGGCT TGGT GCCT	
	ACTCTCCGA ACCA CGGG	
	GG _ A	
GAM387 SET7	GGCTGCGCGGCTGCCTCCCG 6000 TGAGAGGCTG	
	GTGGTTGCCTCCC	
	CGCCGACGGAGGG	
	G_ _ _	
GAM387 SLC13A4	AGAGGCTGGGCTCCTGGCCTCC 5987 TGAG _ GG _ CG	
	AGGCTGG T TTG CCTCC	
	TCCGACC G GAC GGAGG	
	_ C AG C AC	
GAM387 SLC7A1	GAGGGTGG-GGT-GCCTCCCG 5999 TGAGA C T T	
	GG TGG GGT GCCTCCC	

CC ACC CCA CGGAGGG

GAM387 SNL TGAAAGGCAAGGGGGCTTGCCTCCCG 6002 T_ T _ II
TGAGAGGC GG GGTT GCCTCCCG
||||||| || ||| |||||||
ACTTTCCG CC CCGA CGGAGGGC
TT C A II

GAM387 SUFU GAGAGGCTGGTCATGGTGGC 5993 TG ____ T CTCCC
AGAGGCTGGT GGT GC
||||||| ||| ||
TCTCCGACCA CCA CG
____ GTA C TIIIG

GAM387 XK TGGGAGGCTGGTGGCT-ACTCCC 6005 A C G
TG GAGGCTGGTGGTTGC TCCC
|| ||||||||||| ||||
AC CTCCGACCACCGATG AGGG
C _ I

GAM388 BBS4 GGGACTAATAAACCTCACAACCTG 6014 _ _ IIIC
GGGACT TAAAC ACAACCT
||||| ||||| |||||||
CCCTGA ATTTG TGTTGGA
TT GAG CIII

GAM388 BBS4 GGGACTAATAAACCTCACAACCTG 6014 TGCG__ AAA AI
GGACTT CACAACCTGG
||||| |||||||
TTTGGA GTGTTGGACT
TGATTA _ CC

GAM388 CDH5 TGCAGCAGTTAAACACAGTCTG 6018 GAC AC GA
TGCGG TTAAACACA CTG
||||| ||||||| |||
ACGTC AATTTGTGT GAC
GTC CA II

GAM388 CDH5 TGCAGCAGTTAAACACAGTCTG 6018 _ GAC ACI
GCGG TTAAACACA
||| |||||||
CGTC AATTTGTGT
T _ CAG

GAM388 EXTL2 GCTGGA-TTAA---CAACCTGGA 6012 CG_ C AAC
GGA TTA ACAACCTGG
||| ||| |||||||
CCT AAT TGTTGGACC
CGA _ _

GAM388 EXTL2 GCTGGA-TTAA---CAACCTGGA 6012 TGCG C AAC
GGA TTA ACAACCTGG
||| ||| |||||||
CCT AAT TGTTGGACC
GA_ _ _

GAM388 GJA1 GGGACTTAAGGACAATCCT 6016 AC _ II
GGGACTTAA ACAA CC
||||||| ||| ||

	CCCTGAATT TGTT GG	
	CC A AI	
GAM388 GJA1	GGGACTTAAGGACAATCCT 6016 TGCGGG AC _ GG	
	ACTTAA ACAA CCT	
	TGAATT TGTT GGA	
	_____ CC A GA	
GAM388 HYAL1	CGGGACTGGTCGAGGACAACCTGG 6009 ____ GACTTAAAC I	
	GG ACAACCTG	
	CC TGTTGGAC	
	TGA AGCTCC____ I	
GAM388 HYAL1	CGGGACTGGTCGAGGACAACCTGG 6009 TGCG TAAAC____ AI	
	GGACT ACAACCTGG	
	CCTGA TGTTGGACC	
	_____ CCAGCTCC GG	
GAM388 MAP3K12	GGGACTTAAACAGCACCCCGG 6015 G _ A I	
	GACTTAAACA CA CCTG	
	CTGAATTTGT GT GGGC	
	_ C G I	
GAM388 MAP3K12	GGGACTTAAACAGCACCCCGG 6015 TGCGGG _ A A	
	ACTTAAACA CA CCTGG	
	TGAATTTGT GT GGGCC	
	_____ C G A	
GAM388 NONO	GGAGTTCAAGATCAACCTGGA 6013 GACTTAAACA I	
	CAACCTGG	
	GTTGGACC	
	TCAAGTTCTA I	
GAM388 NONO	GGAGTTCAAGATCAACCTGGA 6013 TG CTTAAACA	
	CGGGA CAACCTGGA	
	GTTCT GTTGGACCT	
	AA A_____	
GAM388 PTHLH	CGGGACTTATTTAGCAACC 6010 AACA_ II	
	CGGGACTTA CAAC	
	GCCCTGAAT GTTG	
	AAATC GI	
GAM388 PTHLH	CGGGACTTATTTAGCAACC 6010 TGCG AACA_ T	
	GGACTTA CAACC GG	
	CCTGAAT GTTGG CC	
	_____ AAATC _	
GAM388 RRM2	GAATTAACTCACACAACCT 6011 _____ AA III	
	GACTT ACACAACC	

	TTGAG TGTGTTGG		
	CTTAA AII		
GAM388 RRM2	GAATTAACACACAACCT 6011 TCGGG AA G		
	GACTT ACACAACCTG		
	TTGAG TGTGTTGGAT		
	_____ G		
GAM388 SCA2	TGCGGGACTCTGAAACAGCATATGGA 6017 _ _ ACC II		
	TGCGGGACTT AAACA CA TGG		
	II		
	ACGCCCTGAG TTTGT GT ACCT		
	AC C AT_ II		
GAM388 SCA2	TGCGGGACTCTGAAACAGCATATGGA 6017 GC _ _ ACC I		
	GGGACTT AAACA CA TGG		
	II		
	CCCTGAG TTTGT GT ACC		
	_ AC C AT_ I		
GAM389 ANXA8	TGGTCAGCCACCAGGGGAGCCCACGCCT6029 _ _ _ A GIII		
	TGG CAGC ACCAGGGGA CAC CCT		
	ACC GTCG TGGTCCCCT GTG GGA		
	A G CGG C IIIG		
GAM389 ARF3	GGCAGCACCAAGGCAACCTCCT 6027 TG _ ACA		
	GCAGCACCAGGG GAC CCTG		
	CGTCGTGGTTCC TTG GGAT		
	_____ G GA_		
GAM389 BCAT2	GGCAGCACCAGGGGTCTGGCCTG 6028 TG ACACA I		
	GCAGCACCAGGGG CCTG		
	CGTCGTGGTCCCC GGAC		
	_____ AGACC T		
GAM389 COL16A1	GCAGCACCAGAGGAACCCAC 6022 TGGC CA_ CT		
	AGCACCAGGGGA CAC		
	TCGTGGTCTCCT GTG		
	_____ TGG AC		
GAM389 DOCK1	GCAG-ACTCAGGGGACACA 6021 TGGC C _ CC		
	AG AC CAGGGGACACA		
	TC TG GTCCCCTGTGT		
	_____ _ A CT		
GAM389 JAG1	GGCTGCA--AGGGGACACAC 6026 TG A CC C		
	GC GCA AGGGGACACAC		
	CG CGT TCCCCTGTGTG		
	_ A _ T		
GAM389 LIF	GGCAGCAT--GGGGACACA 6025 TG CCA CC		
	GCAGCA GGGGACACA		

	CGTCGT CCCCTGTGT			
	___ A___ CI			
GAM389 PRKCM	TGACAACACCAATGGGACACACC 6031	___	TGI	
	TGGCAGCACCAG GGGACACACC			
	ACTGTTGTGGTT CCCTGTGTGG			
	A III			
GAM389 SCD	TGACAGCATCTG-GGACACAC 6032	CCAG	CT	
	TGGCAGCA GGGACACAC			
	ACTGTCGT CCCTGTGTG			
	AGA_ II			
GAM389 TNFRSF8	GGCAGCACCAGGAGGGTCCCAC 6023	TG	ACA___ CTG	
	GCAGCACCAGGGG CAC			
	III			
	CGTCGTGGTCCTC GTG			
	___ CCAGG TII			
GAM389 TRPV4	GGCAGAGCCAGGGGACCACA 6024	TG CA	A CT	
	GCAG CCAGGGGAC CAC			
	CGTC GGTCCCCTG GTG			
	___ TC ___ TC			
GAM389 WHSC1	TGGCAGAACTCGCCCGCGGGACACACCTG6030	CA_____ AG	III	
	TGGCAG CC GGGACACACCTG C			
	II I			
	ACCGTC GG CCCTGTGTGGAC G			
	TTGAGCG CG III			
GAM390 APOBEC2	GAGGGGCTGTGGCTCAGGAGTC 6040	TGAGAG	___ A C C	
	GGGCT GGTT AGG GTC			
	CCCGA CCGA TCC CAG			
	___ CA G T T			
GAM390 HR	AGGGGCTGG-AGAGGCGCCC 6037	TGAGAGGG	TTA	
	GCTGG AGGCGTC			
	CGACC TCCGCGG			
	___ TC_			
GAM390 KCNK7	TGGGAGGGGCTGGGCAGGGCG 6043	A	T A TCC	
	TG GAGGGGCTGG TA GGCG			
	AC CTCCCCGACC GT CCGC			
	C C C III			
GAM390 MYLK	AGTGGGACAGGA-AAGGCGTCC 6036	TGAGA	T TT	
	GGGGC GG AAGGCGTCC			
	CCCTG CC TTCCGCAGG			
	A___ T T_			
GAM390 PLA2G10	GGGGCGGCGCAAAGGCGTCC 6041	TGAGAGG	TG T	
	GGC GT AAGGCGTC			

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          CCG CG TTCCGCAG
          _____ T
GAM390 PTPRN    AGAGGGGCTG---AGGCG      6035 TGAG      GTTA
                  AGGGGCTG AGGCG
                  ||||| ||||
                  TCCCCGAC TCCGC

          _____
GAM390 REV3L    TGACAGGGGCCTGGGTGAGG      6042 G _ TTA CGTC
                  TGA AGGGGC TGG AGG
                  ||| ||||| ||| |||
                  ACT TCCCCG ACC TCC
                  G G CAC IIIC
GAM390 SLC9A1    GAGAGGGGCGAGGGGTCCAGGCG      6038 TG T__ A CC
                  AGAGGGGC GGT AGGCGT
                  ||||| ||| |||||
                  TCTCCCCG CCAG TCCGCG
                  _ TCC G II
GAM390 TAF6      GAGGCGGCAGG--AAGGCGTCC      6039 TGAGA G T TT
                  G GGC GG AAGGCGTC
                  | ||| || |||||
                  C CCG CC TTCCGCAG
                  _____ G T _
GAM391 CEP2      GGTGCACAGCGAGTGCAAAAA      6050 TGGG TC__ GTG
                  TGCACAGT CAAAAAT
                  ||||| |||||
                  ACGTGTCTG GTTTTTG
                  _____ CTCAC GII
GAM391 CEP2      GGTGCACAGCGAGTGCAAAAA      6050 TCCAAAAIII
                  GGTGCACAGT
                  |||||
                  CCACGTGTCTG
                  CTCACGTTTT
GAM391 CHC1L     TGGGATTGGAAAGTTCCAAA      6061 TGCAC__ AATGT
                  TGGG AGTTCCAAA
                  ||| |||||
                  ACCC TCAAGGTTT
                  TAACCTT IIIGT
GAM391 CHC1L     TGGGATTGGAAAGTTCCAAA      6061 TGCAC__ III
                  TGGG AGTTCCAA
                  ||| |||||
                  ACCC TCAAGGTT
                  TAACCTT TII
GAM391 CYP1B1    GGTACAAAGATTCCAAAAA      6051 C _ II
                  GGTGCA AG TTCCAAAA
                  ||||| || |||||
                  CCATGT TC AAGGTTTT
                  T T TI
GAM391 CYP1B1    GGTACAAAGATTCCAAAAA      6051 TGGG C _ T
                  TGCA AG TTCCAAAAA GT
                  ||| || ||||| ||| ||

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		ATGT TC AAGGTTTTT CG		
		____ T T ____		
GAM391 ETV5	TGCACACTTC-AAAAATGT	6058	G C I	
	TGCACA TTC AAAAATG			
	ACGTGT AAG TTTTAC			
	G _ A			
GAM391 FGFR2	GTGCACTCTGACAAAAATGT	6054	AGTTC I	
	TGCAC CAAAAATG			
	ACGTG GTTTTAC			
	AGACT I			
GAM391 FUT9	TGGACAACACTACAAAAATGTG	6060	GC GT C I	
	ACA T CAAAAATGT			
	TGT A GTTTTAC			
	CC TG T I			
GAM391 GABRP	TGGGTGCACACTTGGCCTAAAAT	6063	G _ A GTGI	
	TGGGTGCACA TT CC AAAAT			
	ACCCACGTGT AA GG TTTTA			
	G CC A G			
GAM391 GABRP	TGGGTGCACACTTGGCCTAAAAT	6063	GG G _ A I	
	GTGCACA TT CC AAAA			
	CACGTGT AA GG TTTT			
	_ G CC A I			
GAM391 HDGF	ACATTCCTAAAAAATGTG	6047	G _	
	ACA TTCC AAAAATGT			
	TGT AAGG TTTTAC			
	A AT CII			
GAM391 IL13RA1	TGGTTGAAGACTACCAAAAATGT	6065	G GCAC TT_ I	
	GGT AG CCAAAAATG			
	CCA TC GGTTTTTAC			
	_ ACT_ TGAT I			
GAM391 IL13RA1	TGGTTGAAGACTACCAAAAATGT	6065	TG GCAC TT_ GI	
	GGT AG CCAAAAATGT			
	CCA TC GGTTTTTAC			
	A_ ACT_ TGAT II			
GAM391 LCP1	GCATGGTTCCAAAAGTGTG	6049	CA A II	
	GCA GTTCCAAAA TGT			
	CGT CAAGGTTTT ACA			
	AC C CI			
GAM391 MYO6	TGGAAATTTCCAAAATGT	6059	TGCACAG II	
	TTCCAAAATG			

			AAGGTTTTTAC			
			ACCTTTA AI			
GAM391 NDN	GTACACTTTTCCAAAAATG	6053	AG	II		
	GTGCAC TTCCAAAAAT					
	CATGTG AAGGTTTTTA					
	AA CI					
GAM391 NDN	GTACACTTTTCCAAAAATG	6053	TGGGTG AG	T		
	CAC TTCCAAAAATG					
	GTG AAGGTTTTTAC					
	_____ AA T					
GAM391 NR1I2	GCACAGTTCTCGAGAATGTG	6048	CAAA_	II		
	GCACAGTTC AATGT					
	CGTGTCAAG TTACA					
	AGCTC CI					
GAM391 REV3L	TGCACAGTTCCTCACAATG	6055	AAAAATII			
	TGCACAGTTCC					
	ACGTGTCAAGG					
	AGTGTTAC					
GAM391 REV3L	TGCACAGTTCCTCACAATG	6055	TGGGTGCA	AAA_		
	CAGTTCC AATGT					
	GTCAAGG TTACG					
	_____ AGTG					
GAM391 REV3L	TGCACAGTTTGATCAAAAT	6056	C_	AIII		
	TGCACAGTT CAAAA					
	ACGTGTCAA GTTTT					
	ACTA AIII					
GAM391 SCN1A	ACAGATTCCATAAAAATGTG	6046	_ _	III		
	ACAG TTCCA AAAATGT					
	TGTC AAGGT TTTTACA					
	T AT CII					
GAM391 SLC9A1	TGGGAGCACAGTTCGAAAA	6064	T C	ATGT		
	TGGG GCACAGTTC AAAA					
	ACCC CGTGTCAAG TTTT					
	T C IIIG					
GAM391 SLC9A1	TGGGAGCACAGTTCGAAAA	6064	T	CAAII		
	TGGG GCACAGTTC					
	ACCC CGTGTCAAG					
	T CTTTTI					
GAM391 TFCEP2	TGGCTGCCCCAGGTTCCAAAA	6062	G A_ _	ATGTG		
	TGG TGC CAG TTCCAAAA					

	ACC ACG GTC AAGGTTTT			
	G GG C III GT			
GAM391 TFCP2	TGGCTGCCCCAGGTTCCAAAA	6062	G A_ _	III
	TGG TGC CAG TTCCAAA			
	III III III IIIIIII			
	ACC ACG GTC AAGGTTTT			
	G GG C TII			
GAM391 TJP1	GGTGCA---TTTAAAAAATGTG	6052	CAGTTCC	I
	GGTGCA AAAAATG			
	IIIIII IIIIIII			
	CCACGT TTTTAC			
	AAAT_ A			
GAM391 TRAP240	TGCACAGTTCCATCAAATG	6057	AAAATII	
	TGCACAGTTCCA			
	IIIIIIIIII			
	ACGTGTCAAGGT			
	AGTTTAC			
GAM391 TRAP240	TGCACAGTTCCATCAAATG	6057	TGGGTGCA	A_ T
	CAGTTCCA AAATG			
	IIIIII IIIII			
	GTCAAGGT TTTAC			
	_____ AG T			
GAM392 ATP1A2	GAACAGCCCTGCCACCTAA	6071	TGAAA G	AGG
	GGCCC GCCACCTAA			
	IIII IIIIIII			
	TCGGG CGGTGGATT			
	TTG_ A CII			
GAM392 CORO2B	GAAAGGCCCAGCTCACCTGGAGG	6070	TG _	AA CI
	AAAGGCCCGGC CACCT AGG			
	IIIIIIII IIIII III			
	TTTCCGGGTCG GTGGA TCC			
	_____ A CC CI			
GAM392 IL16	AAGGAGAGGCCACCTATAAGC	6069	TGAAAGGCCC	A
	GGCCACCTA AGGC			
	IIIIIIII IIIII			
	CCGGTGGAT TTCG			
	CTCT_____ A			
GAM392 PML	AAGACCAGGGCCACCTAGAG	6068	TGAAAG C_	A _
	GCC GGCCACCTA AG G			
	III IIIIIII III			
	TGG CCGGTGGAT TC C			
	_____ TC C T			
GAM393 ACCN2	TGGGGGTGAACCTATAGGTATCAG	6085	A _ C_	CTTI
	TGGG GTG CTT AGGTATCAG			
	IIII III III IIIIIII			
	ACCC CAC GAA TCCATAGTC			
	C TT TA IIIT			
GAM393 ACCN2	TGGGGGTGAACCTATAGGTATCAG	6085	GAGT C_	I
	GG GCTT AGGTATCA			
	II III IIIIIII			

	CC TGAA TCCATAGT		
	ACT_ TA I		
GAM393 ADD1	GAGTGCTTCTGAAGGTTTCATCAG 6076	___ A IIIC	
	GAGTGCTTC AGGT TCA		
	CTCACGAAG TCCA AGT		
	ACT _ AGTC		
GAM393 ARSB	GGAGTGTTGCAGATTTTATCAGCTT 6077 GAG TTCAGG I		
	TGC TATCAGCT		
	ACG ATAGTCGA		
	ACA TCTAAA I		
GAM393 ARSB	GGAGTGTTGCAGATTTTATCAGCTT 6077 TGGG CTT ___ II		
	AGTG CAGGT ATCAGCTT		
	TCAC GTCTA TAGTCGAA		
	___ AAC AAA GA		
GAM393 CARD10	GGGAGAAGGTGCAGGTATCAG 6079 ___ _ TTC I		
	GGAG TGC AGGTATCA		
	CTTC ACG TCCATAGT		
	CT C ___ I		
GAM393 CARD10	GGGAGAAGGTGCAGGTATCAG 6079 T ___ TTC CTT		
	GGGA GTGC AGGTATCAG		
	CTCT CACG TCCATAGTC		
	C TC ___ TII		
GAM393 CDK10	TGGGAACCTTGTGCTTCAGGT 6084 ___ ATCAGCT		
	TGGGA GTGCTTCAGGT		
	ACCCT CACGAAGTCCA		
	TGAA IIITTCG		
GAM393 CDK10	TGGGAACCTTGTGCTTCAGGT 6084 ___ IIIA		
	TGGGA GTGCTTCAGG		
	ACCCT CACGAAGTCC		
	TGAA AIII		
GAM393 CPD	AGTGCTTCACAGATATAAGC 6074 ___ C III		
	AGTGCTTCA GGTAT AG		
	TCACGAAGT CTATA TC		
	GT T GII		
GAM393 CPD	AGTGCTTCACAGATATAAGC 6074 TGGGAGTGCTT ___ T		
	CAGGTAT CAGC		
	GTCTATA GTCG		
	GAAGT___ TTC T		
GAM393 DDX11	TGCTTCAGGTACATCAGGTT 6083 ___ CTIII		
	TGCTTCAGGTA TCAG		

	ACGAAGTCCAT AGTC		
	GT CAAII		
GAM393 DDX11	TGCTTCAGGTACATCAGGTT 6083	TG A T A A__ T	
	GG GTGC TCAGGT TC GC		
	II IIII IIIII II II		
	TC CATG AGTCCA AG CG		
	__ _ T _ AAC I		
GAM393 FOLR1	GGGATTTC--CAGGTATCAG 6080	GTGC I	
	GGGA TTCAGGTATC		
	IIII IIIIIIIII		
	CCCT AGGTCCATAG		
	AA__ T		
GAM393 FOLR1	GGGATTTC--CAGGTATCAG 6080	TG GTGC C	
	GGA TTCAGGTATCAG		
	III IIIIIIIII		
	CCT AGGTCCATAGTC		
	__ AA__ T		
GAM393 PCDHA11	TGGGAGTGCCTCACTGT-TCAG 6087	G_ A CTT	
	TGGGAGTGCTTCA GT TCAG		
	IIIIIIIIII II IIII		
	ACCCTCACGGAGT CA AGTC		
	GA _ III		
GAM393 PCDHA11	TGGGAGTGCCTCACTGT-TCAG 6087	G_ A I	
	GGGAGTGCTTCA GT TCA		
	IIIIIIIIII II IIII		
	CCCTCACGGAGT CA AGT		
	GA _ I		
GAM393 PLD2	TGGGAGTGCCCTTTTCAGCTAT 6086	CAGGTA T	
	TGGGAGTGCTT TCAGCT		
	IIIIIIIIII IIIII		
	ACCCTCACGGG AGTCGA		
	AAA__ T		
GAM393 PLD2	TGGGAGTGCCCTTTTCAGCTAT 6086	___ G IIIA	
	TGGGAGTGCT TCAG TA		
	IIIIIIIIII IIII II		
	ACCCTCACGG AGTC AT		
	GAAA G AIII		
GAM393 PPOX	AGTGCTTCA--AATCCGCT 6075	ATCA I	
	AGTGCTTCAGGT GC		
	IIIIIIIIII II		
	TCACGAAGTTTA CG		
	GG__ A		
GAM393 TCTA	GTCCTTCAGGTAATCAGCTT 6082	G _ II	
	GT CTTCAAGGTA TCAGCT		
	II IIIIIIIII IIIII		
	CA GAAGTCCAT AGTCGA		
	G T AI		
GAM393 TH1L	TGGGAGTGC-TCA-GTCTCA 6088	T GTA GC	
	TGGGAGTGCT CAG TCA		
	IIIIIIIIII III III		

	ACCCTCACGA GTC AGT		
	_ AG_ II		
GAM393 TH1L	TGGGAGTGC-TCA-GTCTCA 6088	T	GTATI
	TGGGAGTGCT CAG		
	ACCCTCACGA GTC		
	_ AGAGT		
GAM393 UBE2V1	GTGACTTCAGGTAAGACGCTT 6081	_	TCA_ III
	GTG CTT CAGGTA GCT		
	CAC GAAGTCCAT CGA		
	T TCTG AII		
GAM393 ULBP2	GGAGC-CTTTTGGTATCAGCTT 6078	_	G CA I
	GAGT CTT GGTATCAGCT		
	CTCG GAA CCATAGTCGA		
	C _ AA I		
GAM393 ULBP2	GGAGC-CTTTTGGTATCAGCTT 6078	TGGGAGT	CA_
	GCTT GGTATCAGCTT		
	CGGA CCATAGTCGAA		
	T_____ AAA		
GAM394 FETUB	CAACATGCTGAGA-CCAAG 6095	GA	II
	CAACATGCTG GCCAA		
	GTTGTACGAC TGGTT		
	TC CI		
GAM394 GUK1	ACATGCTG--GCCAAGGGC 6094	GA	TGI
	ACATGCTG GCCAAG		
	TGTACGAC CGGTTC		
	_ CCG		
GAM394 HFE	ACCACATTTATGCAGCCAAGTGC 6091	CA	GC_ G I
	ACAT TG AGCCAAGTG		
	TGTA AC TCGGTTAC		
	G_ AAT G I		
GAM394 HOXA3	CATGCTGGAGCCAGAGGGC 6097		AGTGII
	CATGCTGGAGCCA		
	GTACGACCTCGGT		
	CTCCCG		
GAM394 KEL	ACAAGCGGAAGCCAAGTGC 6093	T T	II
	ACA GC GGAGCCAAGTG		
	TGT CG CTT CGGTTAC		
	T C GI		
GAM394 KRT3	GACAATCACAGGCTGGAGCC 6098	_ _	III
	GACAA CAT GCTGGAGC		

	CTGTT GTG CGACCTCG		
	A TC GII		
GAM394 LBR	GACTACCGGATGCTGGAGCAAA 6099 A ____ CAIII		
	GAC AC ATGCTGGAGC		
	CTG TG TACGACCTCG		
	A GCC TTTII		
GAM394 PPP1R7	GACCACATGA-GGAGCCAAG 6101 _ A CT I		
	AC ACATG GGAGCCAA		
	TG TGTAC CCTCGGTT		
	C G T_ I		
GAM394 SIRT3	CAACATGCT--AG--AAGTGC 6096 CCAAGI		
	CAACATGCTGGAG		
	GTTGTACGATCTT		
	CACGII		
GAM394 SNX6	GACAACATGCGGCTGAG-GAAGTG 6100 A TG__ CC I		
	CAACATGC GAG AAGT		
	GTTGTACG CTC TTCA		
	_ CCGA C_ I		
GAM394 UBE2I	ACAGCCAGCTGAGGCCAAGTGC 6092 CAA_ T GA I		
	CA GCTG GCCAAGTG		
	GT CGAC CGGTTTAC		
	GTCG _ TC I		
GAM394 XPC	TGACAAGG-GCTGGAGCCA 6102 CAT I		
	TGACAA GCTGGAGCC		
	ACTGTT CGACCTCGG		
	CC_ T		
GAM395 CRMP1	TCAGGCCACGCAGGGGCGAGCCATC 6115 T T__ AT I		
	TCAG CC CGGG GGCAGCCATC		
	AGTC GG GTCC CCGTCGGTAG		
	C TGC _ I		
GAM395 DIA1	CAGT--TCAGGATGGCAGACCA 6108 TCAGTCC _ T		
	TCGGGATGGCAG CCA		
	AGTCCTACCGTC GGT		
	TCA__ T T		
GAM395 EN2	TCAGTCCTCAGGGAGACCAGC 6111 AT _ CATC		
	TCAGTCCTCGGG GGC AGC		
	AGTCAGGAGTCC CTG TCG		
	CT G IIIC		
GAM395 FUT1	CATTCCT-GGG--GGCAGCCATC 6110 TCAG C AT		
	TCCT GGG GGCAGCCAT		

	AGGA CCC CCGTCGGTA		
	TA__ _ _		
GAM395 ITGA6	TCAGTCCTCAGGGATTG-AGC 6112	_	GGC CAT
	TCAGTCCTC GGGAT AGC		
	AGTCAGGAG CCCTA TCG		
	T AC_		
GAM395 LGTN	TCAGCCGT-GGG--GGCAGCCAT 6114	CTC	AT
	TCAGTC GGG GGCAGCCAT		
	AGTCGG CCC CCGTCGGTA		
	CA_ _		
GAM395 OXTR	CAGTTCCTCGGGATGTTTCAGC 6106	TCAG	G_ CATC
	TCCTCGGGATG CAGC		
	AGGAGCCCTAC GTCG		
	TCA_ AA C		
GAM395 PCLO	AGTCCTGGAAACTGGCAGCCA 6105	TCAG C _ C	
	TCCT GGGA TGGCAGCCAT		
	AGGA CCTT ACCGTCGGTG		
	_ _ TTG A		
GAM395 PCSK1N	CAGTCCTGGTGGCGGGATGGC 6107	TC _ _	AGCCATC
	AGTCCT CGGGATGGC		
	TCAGGA GCCCTACCG		
	_ CCACC C CTA		
GAM395 PFKFB4	CAGTCCTCGTAAT-GCATCCA 6109	TC GG G G T	
	AGTCCTCG ATG CA CCA		
	TCAGGAGC TAC GT GGT		
	_ AT _ A C		
GAM395 SMAC	TCAGTCCTCCCGACCGGAGC 6113	GG _ C CAT	
	TCAGTCCTC GAT GG AGC		
	AGTCAGGAG CTG CC TCG		
	GG G _		
GAM395 TIMM23	TCCTAGACGGGATGGCAGCC 6116	TCAGTCCT	AT
	CGGGATGGCAGCC		
	GCCCTACCGTCGG		
	TCT_ _ CC		
GAM396 ACE2	TGA-ACAGAGTCA-TAGTTTT 6133	C CC CC	
	TGA ACAGAGTCA AGTTTT		
	ACT TGTCTCAGT TCAAAA		
	_ A_		
GAM396 ATP5B	TGATACC-AGTCACCAGAATTTCC 6132	C AG T_ GI	
	TGA AC AGTCACCAG TTTCC		

		ACT TG TCAGTGGTC AAAGG		
		A G_ TT II		
GAM396 BACH2		ACACAGAGTCA--GGTTTTCC 6126 TGAC CCA		
		ACAGAGTCA GTTTTTCC		
		TGTCTCAGT CAAAAGG		
		_____ C_		
GAM396 DEFA5		ACACAGAGTAAAATGTTTT 6122 TGAC CACCA CC		
		ACAGAGT GTTTT		
		TGTCTCA CAAAA		
		_____ TTTTA AG		
GAM396 DMXL1		ACACATGAAAAACCAGTTTTTC 6119 TGAC _ TC CG		
		ACA GAG ACCAGTTTTTC		
		TGT CTT TGGTCAAAAG		
		_____ A TT CG		
GAM396 DNMT3B		ACACAGAG-CAGTAGCCAGTTTTTC 6121 TGAC CA___ CGI		
		ACAGAGT CCAGTTTTTC		
		TGTCTCG GGTCAAAAG		
		_____ TCATC TTI		
GAM396 DNMT3B		CACCGAGCTTTGCAGTTTTTC 6127 TGACACA CAC_ G		
		GAGT CAGTTTTTC		
		CTCG GTCAAAAGG		
		G_____ AAAC G		
GAM396 DPYSL3		ACACCCACACACCAGTTTTTC 6123 TGA GAGT C		
		CACA CACCAGTTTTTC		
		GTGT GTGGTCAAAAG		
		TGG _____ T		
GAM396 FIGF		GA CTCAGAGACTACAGTTTTTC 6129 TG A TCAC G		
		AC CAGAG CAGTTTTTC		
		TG GTCTC GTCAAAAGG		
		_____ A TGAT A		
GAM396 GPX1		TGGCACAG-G---CAGTTTTCCG 6134 A A TCAC		
		TG CACAG G CAGTTTTTC		
		AC GTGTC C GTCAAAAGG		
		C _____		
GAM396 KCNJ15		ACACAGAGT---CAGTTTTTC 6125 TGAC CCA		
		ACAGAGTCA GTTTTC		
		TGTCTCAGT CAAAAG		
		_____ _____		
GAM396 LMO7		ACAGAAAGGCTCACCAGTTT 6120 TGACAC AG CC		
		AG TCACCAGTTTT		

	TC AGTGGTCAAAG		
	TCTT__ CG AI		
GAM396 PPP2R2B	ACCCAGA---ACCAGTTTTTC 6124 TGACA GTC		
	CAGA ACCAGTTTTTC		
	GTCT TGGTCAAAAG		
	G____ _		
GAM396 RALB	CACAGAGTCACAAATATTTTTTC 6128 TGACAC CAG__ GI		
	AGAGTCAC TTTTCC		
	TCTCAGTG AAAAGG		
	____ TTTATA GG		
GAM396 TGFB1	TGACACAGAGATCCGCAGT 6131 _ AC TTTCC		
	TGACACAGAG TC CAGT		
	ACTGTGTCTC AG GTCA		
	T GC IGC		
GAM396 TULP1	GACACAG-G--AGCAGTTTTCCG 6130 TG _ TCAC		
	ACACAG AG CAGTTTTTC		
	TGTGTC TC GTCAAAAGG		
	_ C _		
GAM397 AK1	GGGGCCCCGCACGCTTCGGG 6150 G TCCG		
	GGGGCCCCG AT		
	CCCCGGGGC TG		
	G CGAAGCC		
GAM397 ARHGAP6	GGGGGCCCTGGATCCAGG 6156 _ CG		
	GGGGGCCCC GGATTC		
	CCCCCGGGG CCTAGG		
	A TCCI		
GAM397 ATBF1	AGGGGG-CCCGGAGACAGGG 6146 _ C TTCCGGI		
	GGGGGCCCC GGA		
	CCCCCGGG CCT		
	T _ CTGTCCI		
GAM397 BCAR1	GGGGCCCCGGCTCTCGCGGG 6151 A_ _		
	GGGGCCCCGG TTC CGG		
	CCCCGGGGCC GAG GCC		
	GA C C		
GAM397 BLK	GCCCACTGGATTCCGGGTC 6149 C__		
	GCCC GGATTCCGGGT		
	CGGG CCTAAGGCCCA		
	TGA G		
GAM397 CDK4	GGGGCCCCGGA-GCCGGTTC 6153 _ TT GTI		
	GGGCCCCGGA CCGG		

	CCCCGGGGCCT GGCC		
	C C_ AAI		
GAM397 CPNE7	GGGGGCCCCAGA-GCCGGG 6158	TT I	
	GGGGGCCCCCGGA CCGG		
	CCCCCGGGGTCT GGCC		
	C_ C		
GAM397 CPT2	AAGGGGGCCCCAGCCTCCGCGT 6139	A GGI	
	AGGGGGCCCCCGG TTCCG		
	TCCCCCGGGGTC GAGGC		
	G GCI		
GAM397 DLG4	AGGGGGCCCTGACTTCTGG 6144	C GA CGI	
	AGGGGGCCC G TTC		
	TCCCCCGGG C AAG		
	A TG ACCI		
GAM397 GNA15	GGGGGCCCCAGGGAGGGCGGG 6155	__ TTC III	
	GGGGGCCCC GGA CGG		
	CCCCCGGGG CCT GCC		
	TC CCC CII		
GAM397 IFNGR2	GGGGCCCCG--CTCGGGGTC 6152	GA C I	
	GGGGCCCCG TTC GGG		
	CCCCGGGGC GAG CCC		
	__ C A		
GAM397 INHBB	GGGGGCCCCGCAGCCCCGGT 6159	GA_ GI	
	GGGGCCCCG TTCCGG		
	CCCCGGGGC GGGGCC		
	GTC II		
GAM397 JPH3	AGTGGGCCCCGCTTCCCTGGGGTC 6143	GGG A __ I	
	GGCCCCG TTCC GGGT		
	CCGGGGCC AAGG CCCA		
	__ G GAC I		
GAM397 MAGEA3	TAAGGGATGCGGCCCGGA 6160	__ IIIT	
	TAAGGG GGCCCCG		
	ATTCCC CCGGGGCC		
	TACG TIII		
GAM397 MAP4	AAGGGGGCCAAGGA-CCCGGG 6138	_ CC T I	
	AGGGGGCC GGAT CCGG		
	TCCCCCGG CCTG GGCC		
	T TT _ I		
GAM397 MAPK1	AAGTGCTCCCCAAGGATTCCGG 6137	AGGGGG _ I	
	CCCC GGATTCCG		

	GGGG CCTAAGGC		
	ACGA__ TT I		
GAM397 PTBP1	AGGAGCGCCCGCCTTCCGGGTC	6147 G	_ GA I
	GGGGC CCCG TTCCGGGT		
	CCTCG GGGC AAGGCCCA		
	_ C GG I		
GAM397 RDBP	GGGGGCCCCACGGTCTCCGG	6154	_ A
	GGGGGCCCC GG TTCCG		
	CCCCCGGGG CC GAGGC		
	TG A CII		
GAM397 RFX1	AGGAGGGCCCCGGTCTTCCCTGTC	6140 G	A_ GG I
	GGGGCCCCGG TTCC GT		
	TCCCGGGGCC AAGG CA		
	_ AG GA I		
GAM397 SLC12A7	GGGGGCCCC---TTCCCGG	6157	GGA
	GGGGGCCCC TTCCGG		
	CCCCCGGGG AGGGCC		
	A_		
GAM397 SMARCD1	AGGAGGCCCGGAGTTCCG	6142	_
	AGGGGGCCCCCGGA TTCC		
	TCCTCCGGGGCCT AAGG		
	C CI		
GAM397 ST14	AGGCGGCG--GGATTCCGGG	6145_ G	CCC I
	GG GGC GGATTCCGG		
	CC CCG CCTAAGGCC		
	T G C_ I		
GAM397 TBX1	AGGGGGCCCCCATGGCTTC	6141	GGATT
	AGGGGGCCCC		
	TCCCCCGGGG		
	GTACCGAA		
GAM397 ZFP36L1	AGGGGGCTGCTGGTTCCGGGTC	6148	CCC_ A I
	GGGGGC GG TTCCGGGT		
	CCCCCG CC AAGGCCCA		
	ACGA _ I		
GAM398 ANXA1	AAAAATG---ATTTAAAGGC	6169	TGAAAAGATGGG
	GATTTAAAGG		
	CTAAATTTCC		
	TTA_____		
GAM398 CEP1	TGAATGAGATGGGGAAAAAATGC	6181	A_ TTT G CI
	TGAA AGATGGGGA AAA GC		

	ACTT TCTACCCCT TTT CG		
	AC TTT A II		
GAM398 DBY	TGAAAAGATTTGTTTTTAAAG 6185	GGGGA	GCC
	TGAAAAGAT TTAAAG		
	ACTTTTCTA AAATTTC		
	AACAA III		
GAM398 DTNA	TGAAAAG---GGATTTAATTGCC 6188	AGAT	AG
	TGAAA GGGGATTTA GC		
	ACTTT TCCCTAAATT CG		
	AA		
GAM398 EDNRA	TGAAAAGATGTAG---TAAAGG 6187	GG ATT	C
	TGAAAAGATG G TAAAGG		
	ACTTTTCTAC C ATTTCC		
	AT ___ I		
GAM398 EIF1A	GAAAAGAT-GGAATGTAAA 6175 TG	G T	G
	AAAAGATGGG AT TAAAG		
	TTTTCTACCT TA ATTTT		
	___ _ C I		
GAM398 EIF2B1	TGAAAAGATGCTGAATTTA 6183	G_	AAGGC
	TGAAAAGATG GGATTTA		
	ACTTTTCTAC CTAAAT		
	GA IIICC		
GAM398 FGD1	TGAAAAGAT---GAATTAAA 6184	GATTTAAAGG	
	TGAAAAGATGGG		
	ACTTTTCTACTT		
	AATTTIIICC		
GAM398 FY	GAAAAGATGAGGAGGAAAAGG 6178 TG	TTT	CC
	AAAAGATGGGGA AAAGG		
	TTTTCTACTCCT TTTCC		
	___ CCT TI		
GAM398 GPR86	TGAATAGATCTATGTGGATTAAA 6182	A GG___	GGCCI
	TGAA AGAT GGATTAAA		
	ACTT TCTA CCTAAATTT		
	A GATACA IIICC		
GAM398 JTB	GAAGAAGATGGGGA---AAAGG 6171 TGAA	TTT	C
	AAGATGGGGA AAAGG		
	TTCTACCCCT TTTCC		
	TTC_ ___ C		
GAM398 KLRC1	AAAAGGTGAA-ATTTAAAGGC 6167 TGAAAAGATG GG		
	G ATTTAAAGGC		

		C TAAATTTCCG		
		TTCCA_____TT		
GAM398 MAML1		GAAGAATATGGGGATTAATAGG	6172 TGAAAAG	TAA CC
		ATGGGGATT AGG		
		TACCCCTAA TCC		
		TTCTTA_ TTA TI		
GAM398 MUC3B		GAGAAGATGGGG--TTACAGG	6180 TGAA	A TAA C
		AAGATGGGG TT AGG		
		TTCTACCCC AA TCC		
		TC_ _ TG_ A		
GAM398 MYO1B		AAATGATGCAATATTTAAAGG	6164 TGAAAA	G _ CC
		GATG GG ATTTAAAGG		
		CTAC TT TAAATTTCC		
		TA_ G A TA		
GAM398 PRSS16		GAAAAGATGGTGAGTGAAGGG	6179 TG	G TTTA CC
		AAAAGATGG GA AAGG		
		TTTTCTACC CT TTCC		
		_ A CAC_ CA		
GAM398 RPL24		AAAAGATGGCGA---AAAG	6166 TGAA	G TTT
		AAGATGG GA AAAG		
		TTCTACC CT TTTC		
		_ G _		
GAM398 STS		TGGAAAAC TGGGGATT TATAG	6186 T_ GA	A GCC
		GAAAA TGGGGATT TA AG		
		CTTTT ACCCCTAAAT TC		
		AC G_ A		
GAM398 SULT1C1		GAATA-ATGGGGATTAAAA	6177 TGAAAA	TA
		GATGGGGATT AAGG		
		TTACCCCTAA TTTT		
		TTA_ _		
GAM398 TAC3		GAAAAGATGGAGAAGGAGTCAAAG	6174 TG	TTTA_ CI
		AAAAGATGGGGA AAGGC		
		TTTTCTACCTCT TTTCG		
		_ TCCTCAG		
GAM398 TNFRSF9		AAAAG-TGGTGCATTTTAAAGGCC	6163 TGAA	A GGA_ I
		AAG TGG TTAAAGGCC		
		TTC ACC AAATTTCCGG		
		_ _ ACGTAA T		
GAM398 TOP1		AAAAGATGGATATCTTAAAGG	6165 TGAA	GA_ CC
		AAGATGGG TTAAAGG		

	TTCTACCT GAATTTCC	
	____ ATA CA	
GAM398 TYK2	AAGCTGGGGGATTTAAGGGC 6170 TGAAAAGAT A	
	GGGGATTTAA GGC	
	CCCCTAAATT CCG	
	AC_____ C	
GAM398 WASF3	GAAAAGATCTGGATTTAAA 6176 TG GG GGC	
	AAAAGAT GGATTTAAA	
	TTTTCTA CCTAAATTT	
	___ GA All	
GAM398 YWHAZ	AAAGAGGAAGGATTTTAAAGGC 6168 TGAAA AT A C	
	AG GGGG TTAAAGGC	
	TC TCCT AAATTTCCG	
	C___ CT A T	
GAM398 ZNF141	GAAAAGACTGAGGAAGATTTAAAG 6173 TG ____ CCI	
	AAAAGAT GGGGATTTAAAGG	
	TTTTCTG CTTCTAAATTTCT	
	___ ACTC III	
GAM399 CNTN3	ATATGTAAATTCCTTTGGTT 6192 TATAG ATA GA	
	GTAAATTCC GGTT	
	CATTTAAGG CCAA	
	ATA___ AAA AI	
GAM399 EFG1	TATACGATAAATTCCA-AGG 6193 _ T TTGA	
	TATA GGTAATTCCA AGG	
	ATAT CTATTTAAGGT TCC	
	G _ IIIG	
GAM399 GEM	TATAGGTAAAACTTGCATATTTTGA 6194 TTC___ GG GII	
	TATAGGTAAA CATA TTGA	
	ATATCCATTT GTAT AACT	
	TTGAAC AA III	
GAM399 ILF1	AGGAAATCATTCCATAGGCTGA 6191 TATAGGTAA	
	ATTCCATAGGTTGAG	
	TAAGGTATCCGACTT	
	TTTAG_____	
GAM399 LAMA2	TATAGGTAAAATATATTTGTT 6195 TTCCATAG GAG	
	TATAGGTAAA GTT	
	ATATCCATTT CAA	
	TATATAAA III	
GAM399 TACC1	TATGGAAAAATTCCAT--GTTG 6196 TATA T_ AG A	
	GG AAATTCCAT GTTG	

		CC TTTAAGGTA CAAC		
		ATA_ TT _ I		
GAM400 IGF1	TGAAGTACAAAGTCTGAAAA	6200	TTTTTATAAAAT	
	TGAAGTACAAA			
	ACTTCATGTTT			
	CAGACTTTTIII			
GAM400 ZNF255	TGAAATA-AAATTTTAAATAAAA	6199	C _ TA	
	TGAAGTA AAATTTTAA TAAAA			
	ACTTTAT TTTAAAAAT ATTTT			
	_ T II			
GAM401 BLAME	CCAGAGCTTTTCTAGACAG	6206	T II	
	CCAGAGCTTTTCTAG CA			
	II			
	GGTCTCGAAAAGATC GT			
	T CI			
GAM401 BLAME	CCAGAGCTTTTCTAGACAG	6206	TAACCA T C	
	GAGCTTTTCTAG CAG			
	III			
	CTCGAAAAGATC GTC			
	_ T T			
GAM401 FBXL3A	AATCAGAGCTTTTTACTATTTAG	6204	C _ GTCAI	
	CAGAGCTTTT CTA			
	III			
	GTCTCGAAA GAT			
	_ AT AAII			
GAM401 FBXL3A	AATCAGAGCTTTTTACTATTTAG	6204	TAAC _ GTCAGCCI	
	CAGAGCTTTT CTA			
	III			
	GTCTCGAAA GAT			
	TA_ AT AAATCTII			
GAM401 NRF1	AACCAGAGCAACATTTTAAATAGTCA	6203	TA _ TC GCCII	
	ACCAGAGC TTT TAGTCA			
	TGGTCTCG AAA ATCAGT			
	_ TTGTA TT AIIIC			
GAM401 PTGFRN	CAGAGCTTTTAAAG-CAGC	6205	CT T I	
	CAGAGCTTTT AG CAG			
	II			
	GTCTCGAAA TC GTC			
	TT _ G			
GAM401 PTGFRN	CAGAGCTTTTAAAG-CAGC	6205	TAACCAGA CT T	
	GCTTTT AG CAG			
	II			
	CGAAA TC GTC			
	_ TT _			
GAM401 RECQL5	CCAGAGCTTTT-T--TCAGC	6208	C_ CAI	
	CCAGAGCTTTT TAGT			

	GGTCTCGAAAA GTCG		
	AA III		
GAM401 RECQL5	CCAGAGCTTTT-T--TCAGC 6208 TAACCA CTAG		
	GAGCTTTT TCAG		
	CTCGAAAA AGTC		
	_____ A_____		
GAM401 SIM1	CCAGAGAT---CTAGTCAGC 6207_ CTTT		
	CAGAG TCTAGTCAG		
	GTCTC AGATCAGTC		
	G T_____		
GAM401 SIM1	CCAGAGAT---CTAGTCAGC 6207 TAACCA CTTT		
	GAG TCTAGTCAG		
	CTC AGATCAGTC		
	_____ T_____		
GAM401 UBQLN1	TAACCAGAATCAGCTTTTCTA 6209 _____ GTCAGCC		
	TAACCAGA GCTTTTCTA		
	ATTGGTCT CGAAAAGAT		
	TAGT IIICCGA		
GAM401 UBQLN1	TAACCAGAATCAGCTTTTCTA 6209 _____ IIIT		
	TAACCAGA GCTTTTCT		
	ATTGGTCT CGAAAAGA		
	TAGT TIII		
GAM402 ABCA2	TGTCCTCCCTGGCCCAGCTCTGGGTGG6259 _____ GC_ C III		
	TGTCCTCCCTG CAGC GG GTGG		
	ACAGGAGGGAC GTCG CC CACC		
	CGG AGA _ III		
GAM402 ACAD8	TGCGCTCGCAC-TGGCGGGA 6256 G C GGC		
	TGCGC CGCAC TGGCGGGA		
	ACGCG GCGTG ACCGCCCT		
	A _ III		
GAM402 ACAD8	TGCGCTCGCAC-TGGCGGGA 6256_ G C I		
	GCGC CGCAC TGGCGGG		
	CGCG GCGTG ACCGCC		
	A A _ I		
GAM402 ACHE	GCGCCCAGCGAGGCGGGAGG 6226 G CCT_ II		
	GCGC CA GGCGGGAG		
	CGCG GT CCGCCCTC		
	G CGCT CI		
GAM402 ADAM10	GCGCGCGCATGCGCGCGGGGACG 6231 C CC _ A I		
	GCGCGCA TG GCGGG GGC		

	CGCGCGT GC CGCCC CTG		
	— AC G C I		
GAM402 ADAM10	GCGCGCGCATGCGCGCGGGGACG 6231 TG	CC _ A I	
	CGCGCGCA TG GCGGG GGCG		
	GCGCGCGT GC CGCCC CTGC		
	— AC G C C		
GAM402 BACE2	TGGGCGCGCACCGGGACCGGCGGCG 6254 C	T _ G A II	
	TG GCGCGCACCG GG C GG GGCG		
	AC CGCGCGTGG CC G CC CCGC		
	C C T G G II		
GAM402 BACE2	TGGGCGCGCACCGGGACCGGCGGCG 6254 GC	T _ G A I	
	GCGCGCACCG GG C GG GGC		
	CGCGCGTGG CC G CC CCG		
	C_ C T G G I		
GAM402 C2	TGTCCTCCCT-AGGGGCGGCG 6261	CAGC TG	
	TGTCCTCCCTG GCGGCG		
	ACAGGAGGGAT CGCCGC		
	CCC_ II		
GAM402 CASP8	GCGTGAACC---CGGGAGGCG 6230 C C_ TGG		
	GCG ACC CGGGAGGC		
	CGC TGG GCCCTCCG		
	_ ACT _		
GAM402 CD7	TCCTCCCGGT-G-GCGGCGTGG 6251 TGTC	TGCAGC	
	CTCCC GCGGCGTG		
	GAGGG CGCCGCAC		
	_ CCAC_		
GAM402 CDKN3	CCTCCCTCTGCAGCGCCGGCG 6214 TGTCCT _ _ TGG		
	CC CTGCAGCGC GGCG		
	GG GACGTCGCG CCGC		
	G_ A G TGA		
GAM402 CEBPA	GCCCGCGCACCT-CCGGGTCGCG 6242 _ G	GG AG I	
	C CGCGCACCT CGGG GC		
	G GCGCGTGGA GCCC CG		
	C G G_ AG I		
GAM402 CEBPA	GCCCGCGCACCT-CCGGGTCGCG 6242 TG G	GG AG	
	C CGCGCACCT CGGG GCG		
	G GCGCGTGGA GCCC CGC		
	_ G G_ AG		
GAM402 CHN1	TGTGCGCGCACCGGGGCCAGGGAG 6255 C	T _ GCGI	
	TG GCGCGCACCG GGC GGGAG		

	AC CGCGCGTGG CCG CCCTC	
	A C GGT III G	
GAM402 CHN1	TGTGCGCGCACCGGGGCCAGGGAG 6255 GCG T _ _ I	
	CGCGCACCGGC GGGA	
	III	
	GCGCGTGG CCG CCCT	
	_ C GGT I	
GAM402 COL5A1	GCGCTCGCCACGGGCGGGAGG 6233 CG_ G CT I	
	CGC CAC GGC GGGAG	
	GCG GTG CCGCCCTC	
	CGA G C_ I	
GAM402 COL5A1	GCGCTCGCCACGGGCGGGAGG 6233 T G G CT CG	
	GC CGC CAC GGC GGGAGG	
	CG GCG GTG CCGCCCTCC	
	G A G C_ CI	
GAM402 DGAT2	TCCTCCCTGCAATGGTGCATGG 6252 TGTC CGCG	
	CTCCCTGCAG GCGTGG	
	GAGGGACGTT CGTACC	
	_ ACCA	
GAM402 FBP1	CGCGGG-ACCTGGCGGGAGG 6222 G C_ I	
	CGCG ACCTGGCGGGAG	
	GCGC TGGACCGCCCTC	
	_ CC I	
GAM402 FEZ1	TGACCTCC-TGCAGCGAGGC 6260 T C C GTG	
	TG CCTCC TGCAGCG GGC	
	AC GGAGG ACGTCGC CCG	
	T _ T	
GAM402 GAD2	GCGTGCGTGCCGTGTGGCGGGAGG 6235 C C ACC_ I	
	GCG GC TGGCGGGAG	
	CGC CG ACCGCCCTC	
	_ A GCAC I	
GAM402 GAD2	GCGTGCGTGCCGTGTGGCGGGAGG 6235 TGC C ACC_ CGI	
	GCG GC TGGCGGGAGG	
	CGC CG ACCGCCCTCC	
	GCA A GCAC T	
GAM402 GALGT	GTCC-CACTGGCAGCGCGGGGAGG 6246 TGTCC T_ _ CGT I	
	TCCC GCAGCGCGG GG	
	AGGG CGTCGCGCC CC	
	_ TGAC CCT C	
GAM402 GATA6	CCTCCCTGCCTCCTGGCGGCGTGG 6215 TGTCC T AGC_ _ I	
	CCCTGC GCGGCGTGG	

	GGGACG CGCCGCACC		
	_____ GAGGAC C		
GAM402 GCK	TCCTCCCTGC-GCTTGCGGC 6248 TGTC	A _	GTG
	CTCCCTGC GC GCGGC		
	GAGGGACG CG CGCCG		
	_____ _ AA GTI		
GAM402 HRB	TGCGCGCGCCGCCCGCGCCGGA 6253	A_ _ G	GGCG
	TGCGCGCGC CCTG GC GGA		
	ACGCGCGCG GGGC CG CCT		
	GC G G G		
GAM402 HRB	TGCGCGCGCCGCCCGCGCCGGA 6253	_ A _ G	GI
	GCGCGC GC CC TG CGG		
	CGCGCG CG GG GC GCC		
	G _ C G		
GAM402 HTR1E	CGCGAACC---CGGGAGGCG 6219 _ C		TGG
	GCG ACC CGGGAGGC		
	CGC TGG GCCCTCCG		
	G T _____		
GAM402 IFNAR2	CACCTGAACCCGGGAGGCG 6212	_____	
	CACCTGG CGGGAGGC		
	GTGGA CT GCCCTCCG		
	TGG C		
GAM402 ILF1	GCGGGAGCACGCGCGGGCGGGAGG 6232 _	ACCT	I
	GCGCGCGC GGCGGGA		
	CGTGCGCG CCGCCCT		
	T C_____ C		
GAM402 ILF1	GCGGGAGCACGCGCGGGCGGGAGG 6232 T_____	ACCT	CGI
	GCGCGCGC GGCGGGAGG		
	CGTGCGCG CCGCCCTCC		
	GCCCT C_____ T		
GAM402 IMPDH1	CCTCCCTGCAGCG-GTGGTGG 6218 TGTCCT		CGGC
	CCCTGCAGCG GTG		
	GGGACGTGCG CAC		
	_____ CAC_		
GAM402 INPP1	GCGCGGCCCG-GGCGGGAGG 6229	CA	I
	GCGCG CCTGGCGGGAG		
	CGCGC GGGCCGCCCTC		
	C_ C		
GAM402 JAM2	GCGAGGAGCTGGGGGCGGGAGGCG 6228 CGC	ACCT	I
	GC GGCGGGAGGC		

	CG CCGCCCTCCG				
	CCT ACCC I				
GAM402 KIFC3	GCACG-GCCCCGTGGCGGGAGGC 6236	C A _	I		
	CGCG GC CC TGGCGGGAGG				
	GTGC CG GG ACCGCCCTCC				
	_ G C I				
GAM402 KIFC3	GCACG-GCCCCGTGGCGGGAGGC 6236	TG C A _	G		
	CGCG GC CC TGGCGGGAGGC				
	GTGC CG GG ACCGCCCTCCG				
	_ _ G C G				
GAM402 LASS1	GCGCGCGCA---GGCGGCAGG 6239	CC AI			
	GCGCGCGCA TGGCGGG				
	CGCGCGCGT GCCGTCC				
	CC II				
GAM402 LASS1	GCGCGCGCA---GGCGGCAGG 6239	TG CCT G			
	CGCGCGCA GGCGG AGG				
	GCGCGCGT CCGCC TCC				
	_ _ G				
GAM402 MADD	GTCGCTCCC--CAGCGCGGCG 6244	TG _ TG	G		
	TC CTCCC CAGCGCGGCGT				
	AG GAGGG GTCGCGCCGCG				
	_ C _ I				
GAM402 MCM4	TGCCCTGCTCCGCAGCGCGGACGT 6258	CC_ _	GGI		
	TGTCCT CTGCAGCGCGG CGT				
	ACGGGA GGCCTCGCGCC GCA				
	CGA T III				
GAM402 NCAM1	CCCCCTGCAGCG-AGTGTGG 6217	TGTCCT C C			
	CCCTGCAGCG GG GTG				
	GGGACGTCGC TC CAC				
	_ _ A				
GAM402 NOLA1	TCCTCCCTGACGCTGAGCCGTGG 6250	TGTC CA _ _	I		
	CTCCCTG GCGC GGC GTGG				
	GAGGGAC TGCG TCG CACC				
	_ _ AC G T				
GAM402 NRXN2	GCGGGCGCATGGGGCGGGAGG 6240	C CCT	I		
	CG GCGCA GGCGGGAG				
	GC CGCGT CCGCCCTC				
	C ACC I				
GAM402 NRXN2	GCGGGCGCATGGGGCGGGAGG 6240	TG C CCT	CG		
	CG GCGCA GGCGGGAGG				

	GC CGCGT CCGCCCTCC		
	__ C ACC CI		
GAM402 PACSIN3	GTCCTCCCTGGGCCCTCGGCG 6245 TG	CA G__	TGG
	TCCTCCCTG GC CGGCG		
	II		
	AGGAGGGAC CG GCCGC		
	__ C_ GGGA CII		
GAM402 PCOLCE2	CGCGCGCACCGCCGCGGGGCG 6223 _	T G _ A I	
	GCGCGCACCG G CG GG GGC		
	I II II III		
	CGCGCGTGG C GC CC CCG		
	G _ G G _ I		
GAM402 PCOLCE2	CGCGCGCACCGCCGCGGGGCG 6223 TGCG	TG_ A_ G	
	CGCGCACCG GCGGG GGC		
	III		
	GCGCGTGG CGCCC CCG		
	__ CGG CG I		
GAM402 PDGFB	CTCCGCGC-GCGCGGCGTG 6224 TGTCCTCCCT A		
	GC GCGCGGCGT		
	II		
	CG CGCGCCGCA		
	CG_____		
GAM402 PODXL	TCCTCCCTGCCGCTGCAGC 6249 TGTC	A _	TG
	CTCCCTGC GC GCGGCG		
	II		
	GAGGGACG CG CGTCGT		
	__ G A CI		
GAM402 PPP1CB	GCGCGCGCACACT--C-GGAGGC 6234 _	C C GAI	
	GCGCGCGCAC TGG GG		
	III II		
	CGCGCGTGTG GCC CC		
	G A T GII		
GAM402 PPP1CB	GCGCGCGCACACT--C-GGAGGC 6234 T	CTGGCG	
	GCGCGCGCAC GGAGGC		
	CGCGCGTGTG CCTCCG		
	G AG__		
GAM402 PPP2R5E	CGCTCACATTCCTGGCGGGCGGCG 6221 G	CA A I	
	CGCG CCTGGCGGG GGC		
	III III		
	GTGT GGACCGCCC CCG		
	A AA G I		
GAM402 PPP2R5E	CGCTCACATTCCTGGCGGGCGGCG 6221 TGCG	CA A I	
	CGCG CCTGGCGGG GGCG		
	III III		
	GTGT GGACCGCCC CCGC		
	GA__ AA G G		
GAM402 PSMB2	CACTTGGGCCCGGGAGGCG 6213 C _	III	
	CAC TGG CGGGAGGC		
	III III		

	GTG ACC GCCCTCCG		
	A CGG CII		
GAM402 RB1	GCGCGCGCACGTCTGGGGCACGC 6241	CTGG	AGGI
	CGCGCGCAC CGGG		
	GCGCGCGTG GCCC		
	CA__ CGTG		
GAM402 RB1	GCGCGCGCACGTCTGGGGCACGC 6241 TG	CTGG	AG
	CGCGCGCAC CGGG GCG		
	GCGCGCGTG GCCC TGC		
	__ CA__ CG		
GAM402 S100A11	CTCTGTGC-GCGCGGCGTG 6225	TGTCCTCCC	A
	TGC GCGCGGCGT		
	ACG CGCGCCGCA		
	C_____ _		
GAM402 SCAP1	GCGCGGGC-CCTGGTCTGGGAGGCG 6238	C A _	I
	CGCG GC CCTGG CGGGAGGC		
	GCGC CG GGACC GCCCTCCG		
	C _ A I		
GAM402 SCAP1	GCGCGGGC-CCTGGTCTGGGAGGCG 6238 TG	C A _	I
	CGCG GC CCTGG CGGGAGGCG		
	GCGC CG GGACC GCCCTCCGC		
	__ C _ A C		
GAM402 SERPINB9	GCGTGAACC---CGGGAGGCG 6230	C C__ TGG	
	GCG ACC CGGGAGGC		
	CGC TGG GCCCTCCG		
	_ ACT _		
GAM402 SHOX	GCGCGCGCA---GGAGGGGGGCG 6243 _	CCT C A	
	CGCGCGCA GG GGG GGC		
	GCGCGCGT CC CCC CCG		
	C _ _ T C		
GAM402 SHOX	GCGCGCGCA---GGAGGGGGGCG 6243 TG	CCT C A	
	CGCGCGCA GG GGG GGC		
	GCGCGCGT CC CCC CCG		
	_ _ _ T C		
GAM402 SLC25A1	CGGGCACCC--CGGGAGGCG 6220 _ C	GG	I
	G GCACCT CGGGAGGC		
	C CGTGGG GCCCTCCG		
	G C _ I		
GAM402 SLC25A11	GCGCGCGCAACAGAGCGAG-GGCG 6237	_ CT	A I
	CGCGCGCA C GGCGGG GGC		

	GCGCGCGT G TCGCTC CCG	
	T TC _ I	
GAM402 SLC25A11	GCGCGCGCAACAGAGCGAG-GGCG 6237 TG _ CT A I	
	CGCGCGCA C GGCGGG GGCG	
	I	
	GCGCGCGT G TCGCTC CCGC	
	_ T TC _ G	
GAM402 SOX11	GCTCGC-CCAGAGCGGGAGGC 6227 CG A T_ I	
	CGC CC GGCGGGAGG	
	GCG GG TCGCCCTCC	
	GA _ TC I	
GAM402 SOX11	GCTCGC-CCAGAGCGGGAGGC 6227 TGCGCG A T_	
	CGC CC GGCGGGAGGC	
	GCG GG TCGCCCTCCG	
	_ _ TC	
GAM402 TAPBP	GCGTGAACC---CGGGAGGCG 6230 C C_ TGG	
	GCG ACC CGGGAGGC	
	CGC TGG GCCCTCCG	
	_ ACT _	
GAM402 TJP1	TCCTGAGCTCTGCAGCGCTGGGTGG 6247 TGTCCTCC _ C II	
	CTGCAGCGC GG GTGG	
	GACGTCGCG CC CACC	
	GA CTCGA_ A _ CG	
GAM402 TNFRSF7	CCTCC-TGCAGCGCAGGCG 6216 TGTCCTC _ T	
	CCTGCAGCGC GGCG	
	GGACGTCGCG CCGC	
	_ T G	
GAM402 TPR	TGCGCGCGCAGCCGTTGGAAG 6257 C GC GCG	
	TGCGCGCGCA CTG GGGAG	
	ACGCGCGCGT GGC CCTTC	
	C AA III	
GAM402 TPR	TGCGCGCGCAGCCGTTGGAAG 6257 C GC I	
	GCGCGCGCA CTG GGA	
	CGCGCGCGT GGC CCTT	
	C AA I	
GAM402 VIPR2	GCGTGAACC---CGGGAGGCG 6230 C C_ TGG	
	GCG ACC CGGGAGGC	
	CGC TGG GCCCTCCG	
	_ ACT _	
GAM403 AKAP13	CATGGCCGAAGCAGAGTCT 6266 T C II	
	CAT GCC AGGCAGAGTC	

	GTA CGG TTCGTCTCAG			
	C C AI			
GAM403 AKAP13	CATGGCCGAAGCAGAGTCT	6266	GTGCCATT C	
	GCC AGGCAGAGTCT			
	CGG TTCGTCTCAGA			
	_____ C			
GAM403 APOB48R	TGCTATGCTGCCCAGGCTG-GTCTC	6280	___ CAT	AGA I
	GTGC TGCCCAGGC GTCTC			
	TACG ACGGGTCCG CAGAG			
	CGA _____ AC_ T			
GAM403 APOB48R	TGCTATGCTGCCCAGGCTG-GTCTC	6280	___ CAT	AGA I
	GC TGCCCAGGC GTCT			
	CG ACGGGTCCG CAGA			
	GATA _____ AC_ I			
GAM403 ASL	TGTG---TTGCCCAGGCTGTGTC	6287	CCA	AGAI
	TGTG TTGCCCAGGC			
	ACAC AACGGGTCCG			
	_____ ACAC			
GAM403 ASL	TGTG---TTGCCCAGGCTGTGTC	6287	GCCAT	AGA
	GTGT TGCCCAGGC GT			
	CACA ACGGGTCCG CA			
	_____ ACA			
GAM403 CBFA2T1	GTGCGCC--TGCC-AGGCAGAG	6276	AT C T	
	GTGTGCC TGCC AGGCAGAG			
	CACGCGG ACGG TCCGTCTC			
	_____ I			
GAM403 CBFA2T1	GTGCGCC--TGCC-AGGCAGAG	6276	_ AT C	
	TGTGCC TGCC AGGCAGA			
	ACGCGG ACGG TCCGTCT			
	C _____			
GAM403 CDH5	GCCTTTGCCTCCAGGCAGA	6268	A _____	
	GCC TTGCC CAGGCAG			
	CGG AACGG GTCCGTC			
	A AG TII			
GAM403 CDH5	GCCTTTGCCTCCAGGCAGA	6268	GTG ATTGC	GT
	TGCC CCAGGCAGA			
	ACGG GGTCCGTCT			
	A_ A_____ AT			
GAM403 EIF2C1	TGTCATTGCCCAAAGCTGATTCTC	6281	GC _____ A G I	
	CATTGCCCAG GC GA TCT			

	GTAACGGGTT CG CT AGA		
	A_ T A A I		
GAM403 EIF2C1	TGTCATTGCCCAAAGCTGATTCTC 6281 GTGC	_ A G I	
	CATTGCCCAG GC GA TCTC		
	GTAACGGGTT CG CT AGAG		
	CA_ T A A A		
GAM403 EPB42	TGTGCCAGGAGGCCCAGGCAG 6284 TT_ III		
	TGTGCCA GCCCAGGCA		
	ACACGGT CGGGTCCGT		
	CCTC CII		
GAM403 EPB42	TGTGCCAGGAGGCCCAGGCAG 6284 GT TT_ AGTC		
	GTGCCA GCCCAGGCAG		
	CACGGT CGGGTCCGTC		
	_ CCTC CIII		
GAM403 FZD4	GTGCCATTGCGCCCCAGCCTGGGT 6269 _ ATT CA CAGI		
	GTGCC GCC GG		
	CGCGG CGG CC		
	AA GGT AC AIII		
GAM403 FZD4	GTGCCATTGCGCCCCAGCCTGGGT 6269 GTGT _ A_ AGAGTCI		
	GCCATTGC CC GGC		
	CGGTAACG GG TCG		
	_ C GG GACCCAT		
GAM403 IL2RA	TGCTATGCTGCCCAGGCTG-GTCTC 6280 _ CAT AGA I		
	GTGC TGCCCAGGC GTCTC		
	TACG ACGGGTCCG CAGAG		
	CGA _ AC_ T		
GAM403 IL2RA	TGCTATGCTGCCCAGGCTG-GTCTC 6280 _ CAT AGA I		
	GC TGCCCAGGC GTCT		
	CG ACGGGTCCG CAGA		
	GATA _ AC_ I		
GAM403 IL6R	CATTGCCCAGGCTGA-TCTC 6267 _ A G I		
	ATTGCCCAGGC GA TCT		
	TAACGGGTCCG CT AGA		
	G A _ I		
GAM403 IL6R	CATTGCCCAGGCTGA-TCTC 6267 GTGCCATT A G		
	GCCCAGGC GA TCT		
	CGGGTCCG CT AGA		
	_ A _		
GAM403 MHC2TA	GTGTGAC-TT---CAGGCAGAG 6277 CCATT C_		
	GTGTG GC CAGGCAGAG		

	CACAC	TG	GTCCGTCTC			
	_____	AA				
GAM403 MHC2TA	TGCCATTG-CAAGACACAG	6282	CC	GAI		
	TGCCATTGC	AGGCA				
	ACGGTAACG	TCTGT				
	T_	GTC				
GAM403 MHC2TA	TGCCATTG-CAAGACACAG	6282 GT	CC	G TC		
	GCCATTGC	AGGCA AG				
	CGGTAACG	TCTGT TC				
	_____	T_ G CI				
GAM403 MHC2TA	TGCCATTG-CAAGACACAG	6282 GTGTGC	CC	G		
	CATTGC	AGGCA AG				
	GTAACG	TCTGT TC				
	_____	T_ G				
GAM403 MSX1	TGCCGCCGCGCAGGCAGAGT	6283 A C	I			
	GCC TTGC	CAGGCAGAG				
	CGG GGCG	GTCCGTCTC				
	C C	I				
GAM403 MSX1	TGCCGCCGCGCAGGCAGAGT	6283 GT A C	CT			
	GCC TTGC	CAGGCAGAGT				
	CGG GGCG	GTCCGTCTCA				
	_____	C C AI				
GAM403 MSX1	TGCCGCCGCGCAGGCAGAGT	6283 GTGT ATT C				
	GCC GC	CAGGCAGAGT				
	CGG CG	GTCCGTCTCA				
	G_____	C				
GAM403 NPR2	GTG-GCCATTGCCACCCAG	6275 T	GG	AGT		
	GTG GCCATTGCCCA	CAG				
	CAC CGGTAACGGGT	GTC				
	_____	GG				
GAM403 NPR2	GTG-GCCATTGCCACCCAG	6275_ T	GG	I		
	TG GCCATTGCCCA	CA				
	AC CGGTAACGGGT	GT				
	C_	GG I				
GAM403 OAS3	GTG-GCCATTGCCAAAGACTGAG	6273 T	C_	A TC		
	GTG GCCATTGCC	AGGC GAG				
	CAC CGGTAACGG	TCTG CTC				
	_____	TT A				
GAM403 OAS3	GTG-GCCATTGCCAAAGACTGAG	6273 T	C_	AGAI		
	TG GCCATTGCC	AGGC				

	AC CGGTAACGG TCTG		
	— TT ACTI		
GAM403 PNUTL2	GTGTGGATTTGCCCAGGCCAGACTC 6274	CCA	— G II
	GTGTG TTGCCCAGGC AGA TC		
	CACAC AACGGGTCCG TCT AG		
	CTA G G II		
GAM403 PNUTL2	GTGTGGATTTGCCCAGGCCAGACTC 6274	CCA	— GTI
	GTG TTGCCCAGGC AGA		
	CAC AACGGGTCCG TCT		
	CTA G GII		
GAM403 PNUTL2	TTGCCCAGGCCAGACTCTC 6288	—	G II
	TTGCCCAGGC AGA TCT		
	AACGGGTCCG TCT AGA		
	G G GI		
GAM403 RECQL5	TGCCATGTTGCCCAGGCTG-GTC 6278	G —	AGAGTI
	CCAT TGCCCAGGC		
	GGTA ACGGGTCCG		
	— CA ACCAII		
GAM403 RECQL5	TGCCATGTTGCCCAGGCTG-GTC 6278	GTGTGCCA	AGA
	TTGCCCAGGC GTC		
	AACGGGTCCG CAG		
	GTAC— AC—		
GAM403 RECQL5	TGCCATGTTGCCCAGGCTG-GTCT 6279	G —	AGA I
	CCAT TGCCCAGGC GTC		
	GGTA ACGGGTCCG CAG		
	— CA AC— I		
GAM403 RECQL5	TGCCATGTTGCCCAGGCTG-GTCT 6279	GT —	AGA I
	GCCAT TGCCCAGGC GTCTC		
	CGGTA ACGGGTCCG CAGAG		
	— CA AC— I		
GAM403 SLC4A8	ATTGCCCAGGC-TAGTCTC 6264	AG	I
	ATTGCCCAGGC AGTCT		
	TAACGGGTCCG TCAGA		
	A— G		
GAM403 TNFRSF1A	GTGC--TTGTCCAGGCAGAG 6271	CA C	TC
	GTGC TTG CCAGGCAGAG		
	CACG AAC GGTCCGTCTC		
	— A II		
GAM403 TNFRSF1A	GTGC--TTGTCCAGGCAGAG 6271	— CA C	I
	TGC TTG CCAGGCAGA		

		ACG AAC GGTCCGTCT			
		C _ A I			
GAM403 TNFRSF1A		TGTGC--TTGTCCAGGCAGAG	6286	_ CA C I	
		GTGC TTG CCAGGCAGA			
		CACG AAC GGTCCGTCT			
		A _ A I			
GAM403 TNFRSF1A		TGTGC--TTGTCCAGGCAGAG	6286	GT CA C T	
		GTGC TTG CCAGGCAGAG			
		CACG AAC GGTCCGTCTC			
		_ _ A C			
GAM403 TNXB		GTGGCAGTGACGGGGCAGAGTC	6272	C T CCCA TC	
		GTG CA TG GGCAGAGTC			
		CAC GT AC CCGTCTCAG			
		C C TGCC II			
GAM403 TNXB		GTGGCAGTGACGGGGCAGAGTC	6272	C T CCCA I	
		TG CA TG GGCAGAGT			
		AC GT AC CCGTCTCA			
		C C TGCC I			
GAM403 WSX1		ATTGCCCAGGCTG-GTCTC	6265	AGA I	
		ATTGCCCAGGC GTCT			
		TAACGGGTCCG CAGA			
		AC_ G			
GAM403 XRCC3		GTGCCACGGCCCAGGCAGA	6270	T GTCT	
		GTGCCAT GCCCAGGCAGA			
		CACGGTG CGGGTCCGTCT			
		C IIIC			
GAM403 XRCC3		GTGCCACGGCCCAGGCAGA	6270	T II	
		GTGCCAT GCCCAGGCAG			
		CACGGTG CGGGTCCGTC			
		C TI			
GAM403 XRCC3		TGTGCCACGGCCCAGGCAGA	6285	T I	
		GTGCCAT GCCCAGGCAG			
		CACGGTG CGGGTCCGTC			
		C I			
GAM403 XRCC3		TGTGCCACGGCCCAGGCAGA	6285	GT T GT	
		GTGCCAT GCCCAGGCAGA			
		CACGGTG CGGGTCCGTCT			
		_ C GI			
GAM404 AMT		CCTGGCAGAGTGGGAGAGATG	6291	TGTCCT CTT _ C	
		GGCAGAG GAG GATG			

	CCGTCTC CTC CTAC		
	_____ ACC T C		
GAM404 DRD2	TGCCCTGGCAGAG--TGAGGGTG 6303	CT	ATGC
	TGTCCTGGCAGAG TGAGG		
	ACGGGACCGTCTC ACTCC		
	_____ CACI		
GAM404 MANBA	GTCCTGGCACAGATTCCAGGA 6296 TG	G C_ G	GC
	TCCTGGCA AG TT AGGAT		
	AGGACCGT TC AG TCCTG		
	_____ G TA G II		
GAM404 MAPK8IP1	TGTCCTGGCACTGGCCTGAGG 6302	GA_	ATGC
	TGTCCTGGCA GCTTGAGG		
	ACAGGACCGT CGGACTCC		
	GAC IIIC		
GAM404 PER2	CTGGCAGAGGCCTGAAGCTGC 6293	TGTCCTGG _	A
	CAGAG CTTGAGG TGC		
	GTCTC GGACTTC ACG		
	_____ C G		
GAM404 PML	GTCAGGGCAGAGCTGTAAGGA 6295	TGTCCT _	GC
	GGCAGAGCT TGAGGAT		
	CCGTCTCGA ATTCCTG		
	AGTC_ C II		
GAM404 PML	TCCTGGCAGAGGCCTAGTGGA 6299	TGTC _	A_ TGC
	CTGGCAGAG CTTG GGA		
	GACCGTCTC GGAT CCT		
	_____ C CA CTI		
GAM404 RXRA	GTCCTGGCAGGCCAGCTTCCAAGCATGC6294	TG _ _	G III
	TCCTGGCAG AGCTT GAG ATGC		
	AGGACCGTC TCGAA TTC TACG		
	_____ CGG GG G GII		
GAM404 RXRA	TCCTGGCAGTGCCTG-GGA 6301	TGTC A A T	
	CTGGCAG GCTTG GGA		
	GACCGTC CGGAC CCT		
	_____ A _ C		
GAM404 SHANK2	CTGGGCACAGAACT-GAGGATGC 6292	TGTCCTG T	
	GCAGAGCT GAGGATGC		
	TGTCTTGA CTCCTACG		
	CG_____ _		
GAM404 TACC1	GTCCAGTAAGAGCTTGAGGA 6298	TG TGGC TG	
	TCC AGAGCTTGAGGA		

	AGG TCTCGAACTCCT		
	___ TCAT TI		
GAM404 TCF1	TCCTGGCAGTGC-TCAGGA 6300 TGTC A G		
	CTGGCAG GCTT AGGAT		
	GACCGTC CGAG TCCTG		
	___ A _		
GAM404 TIMM44	GTCCTGGCAGAGCTGGGGG 6297 TG T A ATG		
	TCCTGGCAGAGCT G GG		
	AGGACCGTCTCGA C CC		
	___ _C CGI		
GAM405 ARHGEF1	TCCCTGGGCTC---TGCAAGGCT 6310 A ACCCAG		
	TCCC GGGC TGCAAGGC		
	AGGG CCCG ACGTTCCG		
	A AG___		
GAM405 ASCL2	CCCAGGGCACGC-GTCCTAGG 6308 TC CCA GCA C		
	CCAGGGCAC GT AGG		
	GGTCCCGTG CA TCC		
	___ CG_ GGA A		
GAM405 CD80	CCAGGGCACTTCCCAGGTGCAA 6307 TCCC ___ _ CT		
	AGGGCA CCCAG TGCAAGG		
	TCCCGT GGGTC ACGTTTT		
	___ GAA C II		
GAM405 MADD	CAGGGCACCAA--GCAAGG 6306 TCCCAG CAGT		
	GGCACC GCAAGG		
	CCGTGG CGTTCC		
	___ TT___		
GAM405 TP53BP1	TCCCAGGG--CCCGGGGCAAGG 6309 A CAGT C		
	TCCCAGGGC CC GCAAGG		
	AGGGTCCCG GG CGTTCC		
	_ CCC_ I		
GAM406 ATP2B2	GTACAGGGAAACCTGCGCCG 6325 TG A A CA		
	TACAGGGAGGC TGC CCG		
	ATGTCCCTTTG ACG GGC		
	___ G C CI		
GAM406 CKMT1	ACAGGGAGGGAGGATGCAACCG 6313 TGTAC C _ CAG		
	AGGGAGG ATGCA CCG		
	TCCCTCC TACGT GGC		
	CCC___ _ T CTA		
GAM406 DVL1	ACAGGGGGCCTGTGCACCGCAG 6314 TGTACA A A___		
	GGG GGC TGCACCGCAG		

	CCC CCG ACGTGGCGTC	
	_____ _ GAC	
GAM406 EGLN1	CAGGGAGGCCGGCACCCCA 6323 TGTACAGG AT G	
	GAGGC GCACC CA	
	CTCCG CGTGG GT	
	_____ GC G	
GAM406 FANCE	TGTAACAGGGAGGCAGTTGCA 6326 _ _ CCGCAG	
	TGTA CAGGGAGGCA TGCA	
	ACAT GTCCCTCCGT ACGT	
	T CA GAC	
GAM406 GPR44	ACAGGGAGGC-TGGTCCGC 6316 TGTACA A CA	
	GGGAGGC TG CCGC	
	CCCTCCG AC GGCG	
	_____ _ CA	
GAM406 GYG	TGTACAGGGTGCCACTGCA 6327 AG ATG C	
	TGTACAGGG GC CAC GCA	
	ACATGTCCC CG GTG CGT	
	A_ _ A	
GAM406 ITGAL	ACAGGGAGGCAT-CACGGC 6317 TGTACA G C	
	GGGAGGCAT CAC GC	
	CCCTCCGTA GTG CG	
	_____ _ C	
GAM406 ITIH4	TGTACAGGGTG---GCACAGC 6328 A CAT C A	
	TGTACAGGG GG GCAC GC	
	ACATGTCCC CC CGTG CG	
	A _ _ T I	
GAM406 MB	ACAGGGAGGC--GCATCGC 6315 TGTACA AT C	
	GGGAGGC GCA CGC	
	CCCTCCG CGT GCG	
	_____ _ A	
GAM406 PABPC4	CACGGCCGCA-GCACCGCAG 6324 TGTACAGGGAG T	
	GCA GCACCGCA	
	CGT CGTGGCGT	
	CGG_____ _	
GAM406 PDGFB	CAGGGAGGCAGGCAGGCCGC 6321 TGTA G A A GCA	
	CAGG AGGC TGC CC	
	GTCC TCCG GCG GG	
	CTCC G _ A G	
GAM406 PRKCABP	CAGGGAGGCAGGCCGCCCA 6322 TGTACAGG T A G	
	GAGGCA GC CC CA	

		CTCCGT CG GG GT		
		_____ C C G		
GAM406 SERPIND1		ACAGGGAGGCA--ACAGCAG	6318 TGTACA	T CC
		GGGAGGCA GCA GC		
		CCCTCCGT TGT CG		
		_____ - - -		
GAM406 SLC29A1		ACAGGGAGGGAGGCA-GGCAG	6319 TGTAC	T _ GCA
		AGGGAGGCA GCA CC		
		TCCCTCCGT CGT GG		
		CCC_ C CA		
GAM406 WNT1		CAGGGAGGCATGGCTCACAGC	6320 TGTACAGG	CAC
		GAGGCATG CGCAG		
		CTCCGTAC GTGTC		
		_____ CGA		
GAM407 APPL		AAGGGGGAAA-AAAGATCA	6336 TGAAAG	C A
		GGGGAAA AAAGA CA		
		CCCCTTT TTTCT GT		
		_____ - A		
GAM407 ATP6V1A1		AAACAGGGGAAACAAATAACA	6331 TGAAAG	G G
		GGGGAAACAAA AACA		
		TCCCTTTGTTT TTGT		
		TG_____ A G		
GAM407 CASP2		GAAAGCAGGAA-CAAAGAAC	6347 TG G A	AG
		AAAG GGGAA CAAAGAAC		
		TTTC TCCTT GTTTCTTG		
		_ G _ AI		
GAM407 CCND1		TGGAAGGGGGAAAGAGCAAAG	6351 A	__ AACAGC
		TG AAGGGGGAAA CAAAG		
		AC TTCCCCCTTT GTTTC		
		C CTC CGA		
GAM407 CD1A		GAAAGGGGGGATCTAAATAACTGC	6346 TG	AAACAAAG_ A I
		AAAGGGGG AAC GC		
		TTTCCCCC TTG CG		
		_ CTAGATTTA A T		
GAM407 CDK2AP1		TGAAAAGG--AACAAAGAACA	6356 GAA	G
		TGAAAGGGG ACAAAGAACA		
		ACTTTTCCT TGTTTCTTGT		
		_____ I		
GAM407 COL11A1		GAGAGGGGGGAAAAAGTCAAAG	6345 TGAA	__ AACAGC
		AGGGGGAAA CAAAG		

		TCCCCCTTT GTTTC		
		TC__ TTCA CIIICG		
GAM407 DPYSL3		AGGGGACGTGACAAAGAACAG 6339 TGAAAGGGGGAA	C	
		ACAAAGAACAG		
		TGTTTCTTGTC		
		CTGCAC_____ T		
GAM407 GBE1		TGAAAAAAGAAACAAAGAA 6355	CAG	
		TGAAAGGGGGAAACAAAGAA		
		ACTTTTTTCTTTGTTTCTT		
		III		
GAM407 GBF1		AGTGGGAAACAAAGTGCAG 6340 TGAAAGGG	AA	
		GGAAACAAAG CAG		
		III		
		CCTTTGTTTC GTC		
		_____ AC		
GAM407 HS2ST1		AAGGGGGAAAAAAAATCAG 6335 TGAAA	C A C	
		GGGGGAAA AAAGA CAG		
		III		
		CCCCTTTT TTTT GTC		
		_____ T A T		
GAM407 KLHL3		GAATAGGGGGAAAGCACAAGAA 6341 TGAA	_ _ CAGC	
		AGGGGGAAA CA AAGAA		
		II		
		TCCCCCTTT GT TTCTT		
		TTA_ C G TIII		
GAM407 NSD1		AAGGGGGAAAGAAAGAAAAG 6338 TGAAAG	C C	
		GGGGAAA AAAGAA AG		
		II		
		CCCCTTT TTTCTT TC		
		_____ C T		
GAM407 NXF2		TGAAAAGAGGAAACAAAGA 6354	ACAG	
		TGAAAGGGGGAAACAAAGA		
		ACTTTTCTCCTTTGTTTCT		
		IIIC		
GAM407 NXF5		TGAAAAGAGGAAACAAAGA 6354	ACAG	
		TGAAAGGGGGAAACAAAGA		
		ACTTTTCTCCTTTGTTTCT		
		IIIC		
GAM407 PBX3		TGAA---GGGAAACAAAGA 6353 TGA A	AC	
		A GGGGGAAACAAAGA		
		I		
		A TTCCCTTTGTTTCT		
		___ C II		
GAM407 PCLO		TGGATGGTGGAACAAAGGAGAAACAGC6352 TGAAA G	___ III	
		GG GGAAACAAAG AACAGC		
		II		

	CC CCTTTGTTTC TTGTCG	
	ACCTA A CTCT III	
GAM407 PDCL	AAAAGGGACTACAAAGAACAGC 6332 TGAA AA	
	AGGGGG ACAAAGAACAGC	
	TTCCCT TGTTTCTTGTCTG	
	____ GA	
GAM407 POLG	GGGGGACAGAACAAAGAACAGC 6349 TGAAAGGG A _ I	
	GGAA CAAAGAAC AGC	
	TCTT GTTTCTTG TCG	
	TG_____ _ G G	
GAM407 PTPRJ	AAGGGGGAAAAAAG 6337 TGAAAG C C	
	GGGGAAA AAAGAA AG	
	CCCCTTT TTTTTT TC	
	_____ T T	
GAM407 RAP1	TGAGAAGGGCTCCAAAAAAGAACAGC6350 A ____ C III	
	TGA AGGGG GAAA AAAGAACAGC	
	ACT TTCCC TTTT TTTCTTGTCTG	
	C GAGG _ III	
GAM407 RNF4	GAAGGGGTTGGAACAAAAGAGCAG 6343 TGA ____ _ A CII	
	AAGGGG GAAACAAA GA CAG	
	TTCCCC CTTTGTTT CT GTC	
	____ AAC T C AII	
GAM407 RORB	AAGGGGGAAA-AAAGGAAACAG 6334 T__ AAGAACAGC	
	GAAAGGGGGGAAACA	
	CTTTTTTCCTTTGT	
	CCC CTTTIIICG	
GAM407 RRM2B	GAAATGGTGGGAAACAAAGA 6342 TGAAA _ ACAG	
	GG GGGAAACAAAGA	
	CC CCCTTTGTTTCT	
	TTTA_ A CIII	
GAM407 TAT	GAAAGAAAGAAACAAAGAAAAG 6348 TG GG C C	
	AAAG GGAAACAAAGAA AG	
	TTTC TCTTTGTTTCTT TC	
	_ TT T T	
GAM407 TNFRSF17	AAGGGAGCTACAGAAAGAACAGC 6333 TGAAAG AA _ I	
	GGGG ACA AAGAACAGC	
	CCTC TGT TTCTTGTCTG	
	_____ GA CT G	
GAM407 VAMP1	GAAAGGGGGATAGCAGAGACACA 6344 TG AA_ A _ GCI	
	AAAGGGGGA CA AGA ACA	

	TTTCCCCCT GT TCT TGT	
	___ ATC C G GII	
GAM408 ALS2	CAAATCATTCCTTCTTTACAG 6363 TCAA_ GC TGCT	
	ATTT TCTTTACAGG	
	TAAG AGAAATGTCT	
	TTTAG GA IIIT	
GAM408 ATP11B	CAAAC-TATCTTTACAGG 6365 TCAAAT C TG	
	TTG TCTTTACAGG	
	GAC AGAAATGTCC	
	TTT___ T TI	
GAM408 ESR1	AAAATTG---TTTACAGGTGCT 6362 TCAAATTTGCTC	
	TTTACAGGTGC	
	AAATGTCCACG	
	TTAAC_____	
GAM408 F2R	TCTACTTTGCTCTTGAGGGCAGGT 6368 AAA TA___ GCTI	
	TC TTTGCTCTT CAGGT	
	AG AAACGAGAA GTCCA	
	ATG CTCCC IIIT	
GAM408 FBXL7	AAATTTGCTTTGTTCAGGT 6361 TCAA CTTTA GC	
	ATTTGCT CAGGT	
	TAAACGA GTCCA	
	___ AACAA AA	
GAM408 KIF5C	AAATTTGCTTTGCATTTTAACAGGTGC6360 TCAAA_ TC _ III	
	TTTGC TTTA CAGGTGCT	
	AAACG AAAT GTCCACGG	
	TAAACG TA T TII	
GAM408 KL	AAATTACTTCTCTTTACAG 6359 TCAA G GTGC	
	ATTT CTCTTTACAG	
	TGAA GAGAAATGTC	
	TAA_ _ AGII	
GAM408 MME	TGCTCTGTTTCTTACAGGTGCT 6371 TCAAATTTGC T	
	TCTT ACAGGTGCT	
	AGAA TGTCCACGA	
	AA_____ _	
GAM408 PCDHB12	TCAAAAATACTACTTTACAGG 6366 TT _ TGCT	
	TCAAA TGCT CTTTACAGG	
	AGTTT ATGA GAAATGTCC	
	TT T IIIT	
GAM408 PMCHL1	TCAACCTT-CTCTTTACAG 6369 ATTTG GTG	
	TCAA CTCTTTACAG	

	AGTT GAGAAATGTC			
	GGAA_ III			
GAM408 PTGS2	TCAAACAAGCT-TTTACAGGTG 6370	TT C	CT	
	TCAAAT GCT TTTACAGGTG			
	III			
	AGTTTG CGA AAATGTCCAC			
	TT _ II			
GAM408 SNX6	CAAGTGTTGTTCTTTACAG 6364	TCAAAT C	GTGC	
	TTG TCTTTACAG			
	III			
	AAC AGAAATGTC			
	TTCAC_ A GIII			
GAM408 TRPC5	TCCATTTTGCTCTTCTCCAGG 6367	AAA	A_ TGCT	
	TC TTTGCTCTTT CAGG			
	II III			
	AG AAACGAGAAG GTCC			
	GTA AG IIIT			
GAM409 BBS2	TGTGAT-C-CAA--AGCAAACCAG 6379	G T TC		
	TGTGAT C CAA AGCAAACCA			
	I III			
	ACACTA G GTT TCGTTTGGT			
	_ _ _			
GAM409 BBS2	TGTGAT-C-CAA--AGCAAACCAG 6379_	G T TC		
	GTGAT C CAA AGCAAACCA			
	I III			
	CACTA G GTT TCGTTTGGT			
	A _ _ _			
GAM409 CD3Z	TGCACCACCGGCAAACCAG 6377	TCA A	II	
	TGC ATC GCAAACCA			
	III III			
	ACG TGG CGTTTGGT			
	TGG C CI			
GAM409 GNS	GTGAAGTGCTCAATCTGAAA 6374	_	AGCAIII	
	GTGA TGCTCAATC			
	III			
	CACT ACGAGTTAG			
	TC ACTTTII			
GAM409 GNS	GTGAAGTGCTCAATCTGAAA 6374	TG _	AGCAAACCA	
	TGA TGCTCAATC			
	III			
	ACT ACGAGTTAG			
	_ TC ACTTTAIII			
GAM409 KRT15	GTGA-GTTC--TCAGCAAACC 6376	TGATGCTCAA		
	TCAGCAAAC			
	AGTCGTTTG			
	CACTCAAG_			
GAM409 KRT15	GTGA-GTTC--TCAGCAAACC 6376	TGTGATGCTCAA		
	TCAGCAAACC			

		AGTCGTTTGG			
		ACTCAAG_____			
GAM409 MICB	GTGAATGCCC--TCAGCAAACC	6375 T T	AA	A	
	G GATGCTC TCAGCAAACC				
	A TTACGGG AGTCGTTTGG				
	_C _ A				
GAM409 MICB	GTGAATGCCC--TCAGCAAACC	6375 T__	AA	I	
	GATGCTC TCAGCAAAC				
	TTACGGG AGTCGTTTGG				
	CAC _ I				
GAM409 RAB36	TGTGAAGCTTATGCCAGCAAACC	6378 T CAA__		AGI	
	TGTGA GCT TCAGCAAACC				
	ACACT CGA GGTCTTTGG				
	T ATACG III				
GAM409 RAB36	TGTGAAGCTTATGCCAGCAAACC	6378 GTG____	CAAT	I	
	ATGCT CAGCAAAC				
	TACGG GTCGTTTG				
	CTTCGAA _ I				
GAM410 ABCA3	CCTCTGGAGTGGGGCAGGGCA	6384 C _ _		III	
	CC CTGGA GGGGCAGGGC				
	GG GACCT CCCC GTCCCG				
	_ A CA TII				
GAM410 ABL1	GGCCCCC--GAGGG-CAGGGCAG	6407 TGGA		I	
	GGCCCCC GGGGCAGGGC				
	CCGGGGG TCCCGTCCCG				
	C _ T				
GAM410 ABL1	GGCCCCC--GAGGG-CAGGGCAG	6407 TG TGGA			
	GCCCCC GGGGCAGGGCA				
	CGGGGG TCCCGTCCCGT				
	_ C _				
GAM410 ACP1	GGTCACCTGGAGGGAGTAGGGC	6401 GCCC _C I			
	CCTGGAGGG G AGGG				
	GGACCTCCC C TCCC				
	AGT_ T A I				
GAM410 ACP1	GGTCACCTGGAGGGAGTAGGGC	6401 TGGCCC _C AG			
	CCTGGAGGG G AGGGC				
	GGACCTCCC C TCCCG				
	CAGT_ T A CI				
GAM410 ACPT	GGCCCCCTGGAGGGCCAGCAGGG	6400 GCC G GI			
	CCCTGGAGGG CAG				

	GGGACCTCCC GTC			
	___ G GT			
GAM410 ACPT	GGCCCCCTGGAGGGCCAGCAGGG	6400 TG	___	CAGI
	GCCCCCTGGAGGG GCAGGG			
	CGGGGGACCTCCC CGTCCC			
	___ GGT AIII			
GAM410 ACPT	TGACCATCTTGAGGGGCAG	6415 CC G		GGCA
	TGGCC CT GAGGGGCAG			
	ACTGG GA CTCCCCGTC			
	TA A IIIG			
GAM410 ACPT	TGACCATCTTGAGGGGCAG	6415 CC G		II
	TGGCC CT GAGGGGCA			
	ACTGG GA CTCCCCGT			
	TA A CI			
GAM410 ADRA1A	GGCCACATGAAGGGGCAGGGCA	6404 CCC		I
	GCC TGGAGGGGCAGGGC			
	CGG ACTTCCCCGTCCCG			
	TGT I			
GAM410 ADRA1A	GGCCACATGAAGGGGCAGGGCA	6404 TG CCC		G
	GCC TGGAGGGGCAGGGCA			
	CGG ACTTCCCCGTCCCGT			
	___ TGT A			
GAM410 ALPP	GGCCCCCTGGGGGGGTACAGGG	6402 GC	A ___	I
	CCCCTGG GGGG CAGG			
	GGGGACC CCCC GTCC			
	___ C AT I			
GAM410 ALPP	GGCCCCCTGGGGGGGTACAGGG	6402 TG	A ___	CAG
	GCCCCCTGG GGGG CAGGG			
	CGGGGGACC CCCC GTCCC			
	___ C AT CII			
GAM410 ALPPL2	TGGGCCCTAGGAGGGGCA	6412 T_ CT		GGGCA
	GGCCCC GGAGGGGCA			
	CCGGGG CCTCCCCGT			
	AC AT IIIGA			
GAM410 ALPPL2	TGGGCCCTAGGAGGGGCA	6412 T_ CT		II
	GGCCCC GGAGGGGC			
	CCGGGG CCTCCCCG			
	AC AT TI			
GAM410 ARNT2	TGGCCCC---AAGGGCAGGGCAG	6417 CTGG		
	TGGCCCC AGGGGCAGGGCA			

ACCGGGG TTCCCGTCCCGT

GAM410 ARNT2 TGGCCCC---AAGGGCAGGGCAG 6417_ CTGG
GGCCCC AGGGGCAGGGCA
||||| |||||||||
CCGGGG TTCCCGTCCCGT
A _____

GAM410 AXUD1 GGCCTCCTGGGCAAGGGGCAGG 6396 C ____ III
GGCC CCTGG AGGGGCAG
||| ||||| |||||||
CCGG GGACC TCCCCGTC
A CGT CII

GAM410 AXUD1 GGCCTCCTGGGCAAGGGGCAGG 6396 TG C ____ GCAG
GCC CCTGG AGGGGCAGG
||| ||||| |||||||
CGG GGACC TCCCCGTCC
____ A CGT GIII

GAM410 CACNA1D TGCCCATCTGGACAATGGGGCAGGGCAG6413 GGCCCC ____ I
CTGGA GGGGCAGGGCA
||||| |||||||||
GACCT CCCCCGTCCCGT
TA____ GTTA I

GAM410 CACNA1D TGCCCATCTGGACAATGGGGCAGGGCAG6413 TG C_ ____ III
GCCC CTGGA GGGGCAGGGCAG
||||| ||||| |||||||||
CGGG GACCT CCCCCGTCCCGTC
A_ TA GTTA III

GAM410 CALR TGGCCCACTCCTGG--GGGCAGGGGAG6411 ____ AG C II
TGGCCC CCTGG GGGCAGGG AG
||||| ||||| ||||||| ||
ACCGGG GGACC CCCGTCCC TC
TCA ____ C II

GAM410 CALR TGGCCCACTCCTGG--GGGCAGGGGAG6411 ____ AG CAI
GCCC CCTGG GGGCAGGG
||| ||||| |||||||
CGGG GGACC CCCGTCCC
TCA ____ CII

GAM410 CAPN10 GCCCCCTGGCAGGGCTGGG 6388 A A II
GCCCCCTGG GGGGC GG
||||||| ||||| ||
CGGGGGACC TCCCG CC
G A CI

GAM410 CAPN10 GCCCCCTGGCAGGGCTGGG 6388 TGGC A A C
CCCCTGG GGGGC GGG A
||||||| ||||| ||| |
GGGGACC TCCCG CCC T
____ G A _

GAM410 CAPN7 TGGCCCCGCGCCGGGGCAGGGAAG 6418 C GA CAI
GGCCCC TG GGGGCAGGG
||||| || |||||||

	CCGGGG GC CCCC GTCCC		
	C GG TT I		
GAM410 CAPN7	TGGCCCCGCGCCGGGGCAGGGAAG 6418	C GA	C I
	TGGCCCC TG GGGGCAGGG AG		
	ACCGGGG GC CCCC GTCCC TC		
	C GG T I		
GAM410 CHRM1	TGGGCCAGGCCTGTGTGGGGCAGGGC 6410	___ CCC GA	I
	GGCC TG GGGGCAGGG		
	CCGG AC CCCC GTCCC		
	GT AC_ A_ I		
GAM410 CHRM1	TGGGCCAGGCCTGTGTGGGGCAGGGC 6410	T_ C_ GA_	AGII
	GGCC CCTG GGGGCAGGGC		
	CCGG GGAC CCCC GTCCCG		
	AC TCC ACA G		
GAM410 CYP46	TGGCCCAGGGGACGGGGCAGGGGAG 6414	CCT _	C II
	TGGCCC GGA GGGGCAGGG AG		
	ACCGGG CCT CCCC GTCCC TC		
	TCC G C II		
GAM410 CYP46	TGGCCCAGGGGACGGGGCAGGGGAG 6414	CCT _	CAI
	GCCC GGA GGGGCAGGG		
	CGGG CCT CCCC GTCCC		
	TCC G CII		
GAM410 DYRK1B	GGCCCCAGGGAGGGGGCAGGG 6398	GC T_ _	I
	CCCC GGAGGGG CAGG		
	GGGG CCTCCCC GTCC		
	_ TC C I		
GAM410 DYRK1B	GGCCCCAGGGAGGGGGCAGGG 6398	TG CT _	CA
	GCCCC GGAGGGG CAGGG		
	CGGGG CCTCCCC GTCCC		
	_ TC C II		
GAM410 EPHX1	GGGCCTGTGAGAGAGGCAGGGCAG 6395	CCCT	I
	GCC GGAGGGGCAGGGCA		
	CGG TCTCTCCGTCCCGT		
	ACAC I		
GAM410 EPHX1	GGGCCTGTGAGAGAGGCAGGGCAG 6395	T CCCT	I
	GGCC GGAGGGGCAGGGCAG		
	CCGG TCTCTCCGTCCCGTC		
	_ ACAC C		
GAM410 HTR6	GCCCCCTGGAGGGGGCGGGC 6389	CA I	
	CCCCCTGGAGGGG GGG		

	GGGGGACCTCCCC CCC			
	CG I			
GAM410 HTR6	GCCCCCTGGAGGGGGCGGGC 6389 TGGC	CA	A	
	CCCCTGGAGGGG GGGC			
	GGGGACCTCCCC CCCG			
	CG C			
GAM410 KCNK4	TGCCCCGCTGGAGGGGCGGGC 6416 G _	A	I	
	GCCC CCTGGAGGGGC GGG			
	CGGG GGACCTCCCCG CCC			
	_ C G I			
GAM410 KCNK4	TGCCCCGCTGGAGGGGCGGGC 6416 TG _	A	AG	
	GCCC CCTGGAGGGGC GGGC			
	CGGG GGACCTCCCCG CCCG			
	A_ C G II			
GAM410 LIF	GCCCCCTGGA--AGCAAGACAG 6390 GG I			
	GCCCCCTGGA GGCAGGGC			
	CGGGGGACCT TCGTTCTG			
	T			
GAM410 LIF	GCCCCCTGGA--AGCAAGACAG 6390 TGGC GG			
	CCCCTGGA GGCAGGGCA			
	GGGGACCT TCGTTCTGT			
GAM410 LPIN1	GCCCCGGGGTGGGGCAGGGGAG 6391 CT A CAI			
	CCCC GG GGGGCAGGG			
	GGGG CC CCCCGTCCC			
	CC A CTI			
GAM410 LPIN1	GCCCCGGGGTGGGGCAGGGGAG 6391 TGGC CT A C			
	CCC GG GGGGCAGGG AG			
	GGG CC CCCCGTCCC TC			
	CC A C			
GAM410 MAP3K14	CCCTCTGGCCAGGGGCAGGGCAG 6382 _ CCTGG I			
	TGGCC AGGGGCAGGGCAG			
	ACCGG TCCCGTCCCGTC			
	AG _ C			
GAM410 MAP3K14	CCCTCTGGCCAGGGGCAGGGCAG 6382 CCC _ I			
	CTGG AGGGGCAGGGCA			
	GACC TCCCGTCCCGT			
	A_ GG I			
GAM410 MAX	GGCCACCTGG---GCAGGGCAG 6406 C A_ GI			
	GGCC CCTGG GGGGCAG			

	CCGG GGACC TCCCGTC	
	T CG II	
GAM410 MAX	GGCCACCTGG---GCAGGGCAG 6406 TG C A_ GCA	
	GCC CCTGG GGGGCAGG	
	CGG GGACC TCCCGTCC	
	_ T CG III	
GAM410 NDST1	GGCCTTCTGGGGGTGCAGGGCAG 6408 CC A _ I	
	GCC CTGG GGG GCAGGGCA	
	CGG GACC CCC CGTCCCGT	
	AA _ A I	
GAM410 NDST1	GGCCTTCTGGGGGTGCAGGGCAG 6408 TG CC A _ I	
	GCC CTGG GGG GCAGGGCAG	
	CGG GACC CCC CGTCCCGTC	
	_ AA _ A G	
GAM410 NRXN2	GGCCCTCCCAGGAGGGGCAGCTGGCAG6392 GCC T _ I	
	CCC GGAGGGGCAG GGCA	
	GGG CCTCCCCGTC CCGT	
	A_ T GA I	
GAM410 NRXN2	GGCCCTCCCAGGAGGGGCAGCTGGCAG6392 TG _ _ _ III	
	GCCC CCT GGAGGGGCAG GGCAG	
	CGGG GGG CCTCCCCGTC CCGTC	
	_ A T GA All	
GAM410 PDE4A	GGCCCCGTGGGTGGGGGCAGGG 6397 GC C A_ I	
	CCC TGG GGGGCAGG	
	GGG ACC CCCC GTCC	
	_ C CAC I	
GAM410 PDE4A	GGCCCCGTGGGTGGGGGCAGGG 6397 TG C A_ CAG	
	GCCCC TGG GGGGCAGGG	
	CGGGG ACC CCCC GTCCC	
	_ C CAC CII	
GAM410 PDE4A	GCCCATGGGAGGGGGGCAGGGCA 6387 _ CCCCCT A I	
	TGG GG GGGGCAGGGCAG	
	ACC CC CCCC GTCCGTT	
	GGT CT_ _ C	
GAM410 PDE4A	GCCCATGGGAGGGGGGCAGGGCA 6387 CCCCCT_ A I	
	GG GGGGCAGGGC	
	CC CCCC GTCCCG	
	GTACCCT _ I	
GAM410 PDGFRB	TGGCCTCCCTGGAGGCAGAGGGC 6409 _ _ C AGI	
	TGGCC CCCTGGAGG GG AGGGC	

	ACCGG GGGACCTCC TC TCCCG		
	A G _ III		
GAM410 PDGFRB	TGGCCTCCCTGGAGGCAGAGGGC 6409 G _ _ C I		
	GCC CCCTGGAGG GG AGGG		
	III IIIIIII II IIII		
	CGG GGGACCTCC TC TCCC		
	_ A G _ I		
GAM410 PLXNA1	CCCCCTGGAGGGCCCTGGC 6383 G AG_ II		
	CCCCCTGGAGGG C GG		
	IIIIIIIIII I II		
	GGGGGACCTCCC G CC		
	_ GGA GI		
GAM410 PLXNA1	CCCCCTGGAGGGCCCTGGC 6383 TGGCCC G AG_ A		
	CCTGGAGGG C GGC		
	IIIIIIII I III		
	GGACCTCCC G CCG		
	_____ _ GGA G		
GAM410 PRKCD	GGCTCCCGTTGCAGGGGCAGG 6394 _ C_ G III		
	GGC CCC TG AGGGGCAG		
	III III II IIIIIII		
	CCG GGG AC TCCCCGTC		
	A CA G CII		
GAM410 PRKCD	GGCTCCCGTTGCAGGGGCAGG 6394 TG _ C_ G GCAG		
	GC CCC TG AGGGGCAGG		
	II III II IIIIIII		
	CG GGG AC TCCCCGTC		
	_ A CA G GIII		
GAM410 PTPRS	CCCGGGAGGGGCAGAGGCA 6385 T _ II		
	CCC GGAGGGGCAG GGC		
	III IIIIIII III		
	GGG CCTCCCCGTC CCG		
	C T TI		
GAM410 RPN1	GGCCCCCTGGAGGATGC-GGGCAG 6399 _ A I		
	GCCCCCTGGAGGG GC GGGCA		
	IIIIIIIIII II IIII		
	CGGGGGACCTCCT CG CCCGT		
	A _ I		
GAM410 RPN1	GGCCCCCTGGAGGATGC-GGGCAG 6399 TG _ A I		
	GCCCCCTGGAGGG GC GGGCAG		
	IIIIIIIIII II IIII		
	CGGGGGACCTCCT CG CCCGTC		
	_ A _ C		
GAM410 SCRT1	GGCACCTGGAGGGG-AGGGGAG 6405 _ C C CAI		
	GC CCCTGGAGGGG AGGG		
	II IIIIIIIII III		
	CG GGGACCTCCCC TCCC		
	C T _ CTI		
GAM410 SCRT1	GGCACCTGGAGGGG-AGGGGAG 6405 TG C C C		
	GC CCCTGGAGGGG AGGG AG		
	II IIIIIIIII III II		

		CG GGGACCTCCCC TCCC TC		
		__ T __ C		
GAM410 SLC22A12	CCTGGAGGGACATGGGGAG	6386	_	CAII
	CCTGGAGGGGGCA GGG			
	GGACCTCCCTGT CCC			
	A CTCl			
GAM410 SLC22A12	CCTGGAGGGACATGGGGAG	6386	T_ CCCCT	AGGGCA
	GGC GGAGGGGC			
	CTG CCTCCCCG			
	CC TACC_ GTIIIG			
GAM410 SLC22A12	GGCTCACCTGGAGGGGCAG	6393	CC_	II
	GGC CCTGGAGGGGCA			
	CCG GGACCTCCCCGT			
	AGT CI			
GAM410 SLC22A12	GGCTCACCTGGAGGGGCAG	6393	TG CC_	GGCA
	GC CCTGGAGGGGCAG			
	CG GGACCTCCCCGTC			
	_ AGT GIII			
GAM410 SNX9	GGTCCCCTGGAGGGACATGG	6403	GGC	GI
	CCCCTGGAGGGGCA			
	GGGGACCTCCCTGT			
	A_ AC			
GAM410 SNX9	GGTCCCCTGGAGGGACATGG	6403	TGGC	_ CA
	CCCCTGGAGGGGCA GGG			
	GGGGACCTCCCTGT CCC			
	CA_ A II			
GAM411 ABCA3	TCCTGGAGAGGCAGGGAAGGC	6434	TATCATCCT TC	
	GG GCAGGGAAGGC			
	TC CGTCCCTTCCG			
	C_ TC			
GAM411 ARHGDIA	CAGCCCTGTC-CAGGGAAGG	6424	TATCAT G G	
	CCTG TC CAGGGAAGG			
	GGAC AG GTCCCTTCC			
	G_ _			
GAM411 ARHGDIA	TCCTGGCTGGGTCAGGGAAGGC	6433	TATCATC TCG	
	CTGG CAGGGAAGGC			
	GACC GTCCCTTCCG			
	C_ CA_			
GAM411 ARHGEF12	ATCATCTTTGGACTGCAGGGAAG	6421	TA C_ TC_	GCI
	TCATC TGG GCAGGGAAG			

	AGTAG ACC CGTCCCTTC	
	___ AA TGA GII	
GAM411 CCND1	CATCACAGG-CGCAGGGAAG 6423 TATCATCCT T	
	GG CGCAGGGAAGG	
	II	
	CC GCGTCCCTTCT	
	GTGT_____	
GAM411 CD7	CATGGTGGG-GCAGGGAAGG 6425 TATCATCC TC	
	TGG GCAGGGAAGG	
	III	
	ACC CGTCCCTTCC	
	CC_____ C_	
GAM411 CIT	TCATCCTCTGCAGGCAGGGAAG 6428 TATC G_ C_ GC	
	ATCCT GT GCAGGGAAG	
	II	
	TAGGA CG CGTCCCTTC	
	_____ GA TC AC	
GAM411 CMAR	TCCTGCGCCTCAGGGAAGG 6432 TATCATCCTG G	
	GTC CAGGGAAGG	
	III	
	CGG GTCCCTTCC	
	G_____ A	
GAM411 DBH	TCATCCTGGGCGTGCAGGG 6427 TATC TC__ AAGG	
	ATCCTGG GCAGGG	
	TAGGACC CGTCCC	
	_____ CGCA GAI	
GAM411 DDEF2	TCCTGGGCTAGAAGGGAAGGC 6435 TATCATC TCGC	
	CTGG AGGGAAGGC	
	GATC TCCCTTCCG	
	CC_____ T_____	
GAM411 IKBKG	TCATCCTGG--GCTAGGCAGGC 6431 TATC TC A A	
	ATCCTGG GC GGG AGG	
	II	
	TAGGACC CG TCC TCC	
	_____ A G	
GAM411 KRT4	ATCATCCTGG-GGCAGAGA 6422 TA TC AG	
	TCATCCTGG GCAGGGA	
	AGTAGGACC CGTCTCT	
	_____ C_ CI	
GAM411 LAMC3	TCAGTCCTGCTGGCAGGGAAG 6426 TATCA GTC C	
	TCCTG GCAGGGAAGG	
	AGGAC CGTCCCTTCT	
	TC_____ GAC T	
GAM411 LZTS1	TCAGCCCGCACTCAGGGAAGG 6430 TATCAT GTCG C	
	CCTG CAGGGAAGG	

	GGGC GTCCCTTCC		
	TC___ GTGA C		
GAM411 SGT	TCCTTCGGGTCGGCCAGGGAAGG 6429 TATCA CT	___	CI
	TC GGTCG CAGGGAAGG		
	AG CCAGC GTCCCTTCC		
	GA___ C_ CG TG		
GAM412 ACRC	ACATGTGAAAAATATGGAAGTCAA 6439 TGAC	TCT___	AI
	ATGTGAAAA GACTCAA		
	TACACTTTT TTGAGTT		
	___ TATACC CA		
GAM412 ACYP1	ACATTCAAAAATCTGACATTAAA 6441 TGACATGT	TCAAAI	
	GAAAATCTGAC		
	TTTTTAGACTG		
	TAAG___ TAATTT		
GAM412 AKAP2	ACA-GAGAAAATCTGGCTC 6442 TGACATGT	A A	
	GAAAATCTG CTC		
	CTTTTAGAC GAG		
	TCT___ C A		
GAM412 CNGB3	TGACATGTGTAGAGTCTGCCT 6446	AAAA_ A CAAA	
	TGACATGTG TCTG CT		
	ACTGTACAC AGAC GG		
	ATCTC _ A		
GAM412 FIGF	CATGTGTCTTAAATCTGACACA 6445 TGACA GA_	T AA	
	TGT AAATCTGAC CA		
	ACA TTTAGACTG GT		
	C___ GAA T CT		
GAM412 M6PR	ACTTGTGAAAATGTGTTTAAAA 6444 TGACA	C ACTCAAA	
	TGTGAAAAT TG		
	ACACTTTTA AC		
	A___ C AAATTTT		
GAM412 PSG4	ACATGTGAAATTCTAATGACT 6440 TGAC	A ___ CAAA	
	ATGTGAAA TCT GACT		
	TACACTTT AGA CTGA		
	___ A TTA CG		
GAM412 PSG7	ACATGTGAAATTCTAATGACT 6440 TGAC	A ___ CAAA	
	ATGTGAAA TCT GACT		
	TACACTTT AGA CTGA		
	___ A TTA CG		
GAM412 RAD54B	TGACCGGCGAAAATCTGACAGAAA 6450 AT	TCAAAI	
	TGAC GTGAAAATCTGAC		

	ACTG CGCTTTT	AGACTG		
	GC	TCTTTI		
GAM412 SLC4A7	TGTGCAAAAATCTGATTA	AAAA 6451 TGACATGT	CTCAAA	
	GAAAATCTGA			
	TTTTTAGACT			
	_____	AATTTT		
GAM412 SYT4	TGACAC---AAAACCTGACTCAA	AAA 6449 GTG		
	TGACAT AAAATCTGACTCAA			
	ACTGTG TTTTGGACTGAGTTT			

GAM412 TNFAIP1	TGACAAG--AAAATCTGAC	6447 TGT TCA		
	TGACA GAAAATCTGAC			
	ACTGT CTTTTAGACTG			
	T_ III			
GAM412 TNFRSF8	TGAAATGTGAAAA---ACCCAAA	6448 C ATCT		
	TGA ATGTGAAA GACTCAA			
	ACT TACACTTT TTGGGTT			
	T _____			
GAM412 TOB1	ACATGTAAGACACTGACTCAA	6443 TGAC AAAT		
	ATGTGA CTGACTCAA			
	TACATT GACTGAGTTT			
	_____ CTGT			
GAM412 ZNF236	ACATGAAGGAAAATCTGAC	6438 TGACATGT TCAA		
	GAAAATCTGAC			
	TTTTTAGACTG			
	TACTTC_ TAT			
GAM413 A1BG	GACATTAAAAGGCATAGGCATATTA	6468 TG _ A G II		
	ACATTAAAA CA GGG ATATTA			
	TGTAATTTT GT TCC TATAAT			
	_ CC A G CI			
GAM413 BMP4	TGACAG-AAAACAA-GGCATAT	6471 TT GGATATT		
	TGACA AAAACAAGG			
	ACTGT TTTTGTTC			
	C_ GTATAII			
GAM413 BMP4	TGACAG-AAAACAA-GGCATAT	6471 TT GGATI		
	TGACA AAAACAAGG			
	ACTGT TTTTGTTC			
	C_ GTATA			
GAM413 CML66	ACATTAAACTTAAGAGGTTA	6454 _ ATIII		
	ACATTAAAAC AAGGGG			

		TGTAATTTTG TTCTCC			
		AA AATII			
GAM413 CML66		ACATTAAAACTTAAGAGGTTA	6454 TGAC	___ A TA	
		ATTAAAC AAGGGG TAT			
		TAATTTTG TTCTCC ATG			
		___ AA A TI			
GAM413 COL4A5		ACATTAAACAGGGGGCATAT	6459 C	A ATAI	
		ATTAAACA GGGG			
		TAATTTTGT CCCC			
		_ C GTAT			
GAM413 COL4A5		ACATTAAACAGGGGGCATAT	6459 TGAC	A _ TA	
		ATTAAACA GGGG ATAT			
		TAATTTTGT CCCC TATA			
		___ C G CC			
GAM413 CRY2		GACATTTATAAAACAAGTGAATATT	6467 ACAT	G I	
		TAAACAAG GGATAT			
		ATTTGTTC CTTATA			
		AAAT A I			
GAM413 CRY2		GACATTTATAAAACAAGTGAATATT	6467 TG	___ G All	
		ACAT TAAACAAG GGATATT			
		TGTA ATTTGTTC CTTATAA			
		_ AAT A GII			
GAM413 DSC3		ACATTAAAGAAGACGACTTTA	6462 C G ATTI		
		CATTAAAA AAGG GAT			
		GTAATTTT TTCT CTG			
		C G AAAl			
GAM413 DSC3		ACATTAAAGAAGACGACTTTA	6462 TGAC	C G ATTA	
		ATTAAAA AAGG GAT			
		TAATTTT TTCT CTG			
		___ C G AAAT			
GAM413 FBXL3A		ACATTAAAAAAATTCGGAGATAT	6457 TGACATTAAACAA	TAI	
		GGGGATAT			
		CCTCTATA			
		TAATTTTTTTTAAG CTI			
GAM413 FGF2		GACATTTAAACATGTTAGGGGATATT	6469 ACATTA	___ I	
		AAACA AGGGGATAT			
		TTTGT TCCCCTATA			
		AA___ ACAA I			
GAM413 FGF2		GACATTTAAACATGTTAGGGGATATT	6469 TG	A ___ All	
		ACATT AAACA AGGGGATATT			

	TGTAA TTTGT TCCCCTATAA	
	— A ACAA AII	
GAM413 IKBKB	ACATTAAAATGCGGGAATCTTA 6463 CAA ATTI	
	CATTAAAA GGGGAT	
	GTAATTTT CCCTTA	
	ACG GAAI	
GAM413 IKBKB	ACATTAAAATGCGGGAATCTTA 6463 TGAC CAA ATTA	
	ATTAAAA GGGGAT	
	TAATTTT CCCTTA	
	— ACG GAAT	
GAM413 LILRB2	ATTAAAAAATGTAGGGATATTA 6464 TGACATTAAAACAA	
	GGGGATATTA	
	TCCCCTATAAT	
	TTTTTACA—	
GAM413 LILRB2	ATTAAAAAATGTAGGGATATTA 6464 TTAAAACAA I	
	GGGGATATT	
	TCCCCTATAA	
	TTTTTTACA I	
GAM413 MBL2	ACATTAAA--AAGGACATATT 6461 CA G I	
	ACATTAAAA AGGG ATA	
	TGTAATTTT TCCT TAT	
	— G A	
GAM413 MBL2	ACATTAAA--AAGGACATATT 6461 TGAC CA G	
	ATTAAAA AGGG ATATT	
	TAATTTT TCCT TATAA	
	— — G	
GAM413 MECP2	ACTTTAAAACAAGCGCAGGTATAT 6458 TGACA — — TAI	
	TTAAAACAAG GGG ATAT	
	AATTTTGTTT TCC TATA	
	A— GCG A TAI	
GAM413 PCLO	ACATTAAA--AAGTGGATA 6460 CA G I	
	ACATTAAAA AG GGAT	
	TGTAATTTT TC CCTA	
	— A T	
GAM413 RABIF	ATTAAAACAATGAAATACTA 6466 G GG I	
	TTAAAACAA G ATATT	
	AATTTTGTT C TATGA	
	A TT I	
GAM413 RABIF	ATTAAAACAATGAAATACTA 6466 TGACATTA G GG	
	AAACAA G ATATT	

	TTTGTT C TATGA		
	_____ A TT		
GAM413 RNGTT	ACATTAAAACTCAGGTGAATAT 6455 CA A_ _ I		
	TTAAAC AGG GGATA		
	AATTTTG TCC CTTAT		
	_____ AG A I		
GAM413 RNGTT	ACATTAAAACTCAGGTGAATAT 6455 TGAC A_ _ TA		
	ATTAAC AGG GGATAT		
	TAATTTTG TCC CTTATA		
	_____ AG A TT		
GAM413 SFPQ	TTAAAACAAGGGGGCAATTA 6472 ATATT		
	TTAAAACAAGGGG		
	AATTTTGTTTCCC		
	CCGTTAAT		
GAM413 SLC20A1	ACATTAAACATAATGGA-ATT 6456 TGAC AG__ ATTA		
	ATTAACAA GGGAT		
	TAATTTTGTT CCTTA		
	_____ ATTA ACTI		
GAM413 SLC20A1	ACATTAAACATAATGGA-ATT 6456 AG__ ATI		
	CATTAAACAA GGGAT		
	GTAATTTTGTT CCTTA		
	ATTA		
GAM413 SPAG8	TTAAAACAATGGCAT-TTA 6473 G G ATT I		
	TTAAAACAA GG AT		
	AATTTTGTT CC TA		
	A G AATI		
GAM413 TNFSF4	TAAACATAAGGGGATACTA 6470 TA _ II		
	AAACA AGGGGATATT		
	TTTGT TCCCCTATGA		
	A_ AT TI		
GAM413 VEGF	ATTAAAA--AGGG-ATATTA 6465 TTAAAC		
	AAGGGGATATT		
	TTTCCCTATAA		
	TAATT__		
GAM414 ALDH3B2	TGGCAG-GCAGGATGCAGT 6488 T AGA		
	TGGCAG GCAGGATGCAGT		
	ACCGTC CGTCCTACGTCA		

GAM414 BIG1	CAGTGCAGGAAGAACTATAT 6477 TGGCAG TGCAGTAGAT		
	TGCAGGA		

ACGTCCT
 _____ TCTTGATATA
 GAM414 COLQ GGCACGGTGACAGCGGATGCAGT 6480 _____ GCA AGATGI
 TGGCAGT GGATGCAGT
 ||||| |||||
 ACTGTCG CCTACGTCA
 CGTGCC _____ GIIIGT
 GAM414 DGCR2 CAGCCCAGGATGCA-TCGATG 6478 TGGCAGTG GTA
 CAGGATGCA GAT
 ||||| ||
 GTCCTACGT CTA
 GG_____ AG_
 GAM414 FUT6 GGCAGTGCA--AAGCAGAAG 6483 TG AT T A
 GCAGTGCAGG GCAG AG
 ||||| ||| ||
 CGTCACGTTT CGTC TC
 _____ T A
 GAM414 GRM7 TGGCAGTGC-TGATGTCAGT 6486 AG _ AGAT
 TGGCAGTGC GATG CAGT
 ||||| ||| |||
 ACCGTCACG CTAC GTCA
 A_ A IIIG
 GAM414 MLPH GCAGTGCAGGACTGAATGTCGCTG 6479 TGGC GCA__ AGA I
 AGTGCAGGAT GT TG
 ||||| || ||
 TCACGTCCTG CA AC
 _____ ACTTA GCG A
 GAM414 MNT GGGACTGGCTCAGGATGCAG 6481 _____ AGTG TAGAT
 TGGC CAGGATGCAG
 ||| |||||
 ACCG GTCCTACGTC
 CGTG A_____ CIIIG
 GAM414 NOTCH2 TGCCAGGCCATGGATGCAGTA 6485 G T A__ GATG
 TG CAG GC GGATGCAGTA
 || ||| || |||||
 AC GTC CG CCTACGTCAT
 G _ GTA IIIG
 GAM414 PITPNB GGTATTGCA--ATGCAGTAG 6484 TGGCAG GG A
 TGCA ATGCAGTAG
 ||| |||||
 ACGT TACGTCATC
 CATA__ _ A
 GAM414 STAU CAGTGCAGGTTAATTTCAGT 6476 TGGCAG ATG__ AGAT
 TGCAGG CAGT
 |||| |||
 ACGTCC GTCA
 _____ AATTAA CGAI
 GAM414 TCFL4 GGGACTGCAGGATGTCAGAAGA 6482 T AG _ T TG
 GGC TGCAGGATG CAG AGA
 || ||||| ||| |||

	CTG ACGTCCTAC GTC TCT	
	C _ A T CI	
GAM414 XT3	TGGAA-TGAAGGATGCAGT 6487 C C AGA	
	TGG AGTG AGGATGCAGT	
	ACC TTAC TCCTACGTCA	
	_ T	
GAM415 APAF1	GATCTATTCCCTTACCCTCT 6496 GAG CT GTTGC	
	AT CCTTACCCTCT	
	TA GGAATGGGAGA	
	AGA AG GG	
GAM415 CAPN10	AGATCTGCTGCCCTACCCTCTG 6491 GA _ TTGCA	
	GATCT CCTTACCCTCTG	
	CTAGA GGGATGGGAGAC	
	_ CGAC C A	
GAM415 LPP	ATCTTTTT-CTCTCTGTTGCA 6495 GAGATCTCCTTACC	
	CTCTGTTGC	
	GAGACAACG	
	AAAAAGA_	
GAM415 MAN1A2	GATCTCCTTCGACGCTTCTATTCCA 6497 GAGA _ C _ G	
	TCTCCTT AC CT CTGTT CA	
	AGAGGAA TG GA GATAA GT	
	_ GC C A G CT	
GAM415 MANBA	TCTCCTTGTC-TCTGTTGC 6499 GAGATCTCCTTACC	
	CTCTGTTG	
	GAGACAAC	
	GAACA_	
GAM415 MB	AGATCTCCT---CCTC-ATTGCA 6493 GA TAC T	
	GATCTCCT CCTC GTTGC	
	CTAGAGGA GGAG TAACG	
	_ _ _	
GAM415 NKTR	GACCACCTTACCCTGTTTT 6498 GAGAT T CT GC	
	C CCTTACCCT GTT	
	G GGAATGGGA CAA	
	G_ T _ AA	
GAM415 NR1I2	AGATCTCCTTATACTTCCTCCTTTGTTG6492 GA C_ G CA	
	GATCTCCTTA CCTCT TTG	
	CTAGAGGAAT GGAGG AAC	
	_ ATGAA A AACTI	
GAM415 RARG	ATCTGTCCCTTTACCCTCTGTT 6494 GAGA C_ GCAI	
	TCTC TTACCCTCTGTT	

	AGGG AGTGGGAGACAA		
	AC__ AA GGAI		
GAM416 ACP1	TGTCCGGAGGAGGAGGAGCTGCG 6508	ATTC_ G ATI	
	TGTCCGGAG GGAGC GCG		
	ACAGGCCTC CCTCG CGC		
	CTCCT A III		
GAM416 ACP1	TGTCCGGAGGAGGAGGAGCTGCG 6508 G	ATTC_ G I	
	TCCGGAG GGAGC GC		
	AGGCCTC CCTCG CG		
	_ CTCCT A I		
GAM416 ALPPL2	GTCTGGAAGCAGTCGGAGAGCGGCGA 6507 TCC	AT_ _ I	
	GGAG TCGGA GCGGCG		
	CTTC AGCCT CGCCGC		
	_ GTC CT I		
GAM416 ALPPL2	GTCTGGAAGCAGTCGGAGAGCGGCGA 6507 TGTCC	AT_ _ TII	
	GGAG TCGGA GCGGCGA		
	CTTC AGCCT CGCCGCT		
	AGAC_ GTC CT CII		
GAM416 APPBP2	CCGGAGGATTCGGAGGGGCG 6502	_ C II	
	CCGGAG ATTCGGAG GGC		
	GGCCTC TAAGCCTC CCG		
	C C CI		
GAM416 APPBP2	CCGGAGGATTCGGAGGGGCG 6502 TGTCC GA	C A	
	G GATTCGGAG GGCG		
	I		
	C CTAAGCCTC CCGC		
	_ TC C C		
GAM416 CD44	TGTCCGGAGCGAACGGAG-GGCG 6510	ATT_ C AT	
	TGTCCGGAG CGGAG GGCG		
	ACAGGCCTC GCCTC CCGC		
	GCTT _ II		
GAM416 CD44	TGTCCGGAGCGAACGGAG-GGCG 6510	ATT_ C I	
	GTCCGGAG CGGAG GGC		
	CAGGCCTC GCCTC CCG		
	GCTT _ I		
GAM416 CDX2	GGGGACTCGAGGAGCGGCG 6506_ A _	III	
	GG GATTC GGAGCGGC		
	CC CTGAG CCTCGCCG		
	C _ CT CII		
GAM416 CDX2	GGGGACTCGAGGAGCGGCG 6506 TGTCCGGAGATTC	A	
	GGAGCGGCG		

			CCTCGCCGC		
			GAGCT_____ C		
GAM416 ENTPD3		TGTGCGGAGCCGATTCGGAGAAGGCGA6509	C ____ C_ TIII		
		TGT CGGA GATTCGGAG GGCGA			
		ACA GCCT CTAAGCCTC CCGCT			
		C CGG TT IIIT			
GAM416 ENTPD3		TGTGCGGAGCCGATTCGGAGAAGGCGA6509 GTCC ____ C_ I			
		GGA GATTCGGAG GGCG			
		CCT CTAAGCCTC CCGC			
		____ CGG TT I			
GAM416 GAL		CCGG-G-TTCGGAGCGTCG 6504 AGA GCI			
		CCGG TTCGGAGCG			
		GGCC AAGCCTCGC			
		C_ AGC			
GAM416 GAL		CCGG-G-TTCGGAGCGTCG 6504 TGTCCGGAGA G			
		TTCGGAGCG CG			
		AAGCCTCGC GC			
		CC_____ A			
GAM416 NAP1L3		CGGAGGTG-GCAGCGGCGAT 6505 _ ATTC _ I			
		GGAG GG AGCGGCGA			
		CCTC CC TCGCCGCT			
		G CA_ G I			
GAM416 PPP4R1		CCGGGGCTACATGGAGCGGCG 6503 AG_ TC III			
		CCGG AT GGAGCGGC			
		GGCC TG CCTCGCCG			
		CCGA TA CII			
GAM416 PPP4R1		CCGGGGCTACATGGAGCGGCG 6503 TGTCC AG TC AT			
		GG AT GGAGCGGCG			
		CC TG CCTCGCCG			
		C_ GA TA GC			
GAM416 SNRP70		TGTCCGGAGGCTCGCGGCGGC 6513 AT GA GAT			
		TGTCCGGAG TCG GCGGC			
		ACAGGCCTC AGC CGCCG			
		CG GC III			
GAM416 SNRP70		TGTCCGGAGGCTCGCGGCGGC 6513 AT GA I			
		GTCCGGAG TCG GCGG			
		CAGGCCTC AGC CGCC			
		CG GC I			
GAM416 TEM8		TGTCCGGAG---GGAGCAGGCG 6511 ATTC _ A			
		TGTCCGGAG GGAGC GGCG			

	ACAGGCCTC CCTCG CCGC	
	_____ T I	
GAM416 TEM8	TGTCCGGAG---GGAGCAGGCG 6511_ ATTC _	
	GTCCGGAG GGAGC GGC	
	CAGGCCTC CCTCG CCG	
	A _____ T	
GAM416 TJP1	TGTCTGGTT-TTCGGAGCGG 6512 C AGA CGA	
	TGTC GG TTCGGAGCGG	
	ACAG CC AAGCCTCGCC	
	A AA_	
GAM416 TJP1	TGTCTGGTT-TTCGGAGCGG 6512_ C AGA I	
	GTC GG TTCGGAGCG	
	CAG CC AAGCCTCGC	
	A A AA_ I	
GAM417 CEP1	GAAAGACCTAGGCTGAAGAAG 6525 TGA TA _ CC	
	GA GCC AGGCTGAAGAAG	
	TT TGG TCCGACTTCTTC	
	_____ TC A AI	
GAM417 DYRK2	GATAGTTTCCCAGGCTGAGAGAA 6526 TGAGATAG _ G I	
	CCAGGCTGA AGAA CC	
	GGTCCGACT TCTT GG	
	TCAAAG_ C _ A	
GAM417 EGLN3	AGAGAGCCAAGTGAGCTGAAGAA 6518 TGAGAT _____ CCI	
	AGCCA GGCTGAAGAAG	
	TCGGT TCGACTTCTTT	
	TC_____ TCAC CII	
GAM417 GJA5	GAGTTCAGCCAGGCT-AAGGAG 6522 TGAGA A AGCC	
	TAGCCAGGCTGA GA	
	GTCGGTCCGATT CT	
	TCAA_ C CCII	
GAM417 IL13	TGAGGTCGGCTAGGCTGAAGA 6528 ATA_ C AGCC	
	TGAG GC AGGCTGAAGA	
	ACTC CG TCCGACTTCT	
	CAGC A IIIC	
GAM417 LDHB	AGATAG--AG-CTGAAGAAG 6521 TGAG CCA	
	ATAG GGCTGAAGAAG	
	TATC TCGACTTCTTC	
	_____ _____	
GAM417 MFAP2	GAGGTGGCCACAGGCTGAAGGAG 6523 TGAGATA _ A CCI	
	GCCA GGCTGAAG AG	

	CGGT CCGACTTC TC	
	TCCAC__ GT C CII	
GAM417 NPEPPS	AGAAAGGCCTGGCTGAAGA 6517 TGAGATA A AGC	
	GCC GGCTGAAGA	
	CGG CCGACTTCT	
	TTTC__ A AGI	
GAM417 PRKY	TGAGA-AGCACAGGCTGAA 6527 T _ GAAG	
	TGAGA AGC CAGGCTGAA	
	ACTCT TCG GTCCGACTT	
	_ T IIIC	
GAM417 RFP	GAGGAAGCCAGGCTGAGCCAAGAAGC 6524 TG AT ____ CII	
	AG AGCCAGGCTGA AGAAGC	
	TC TCGGTCCGACT TCTTCG	
	_ CT CGGT AII	
GAM417 SUV39H1	AGATATGCAGCCCTGAAGAAG 6519 TGAGA AGG CC	
	TAGCC CTGAAGAAG	
	GTCGG GACTTCTTC	
	TATAC ____ TC	
GAM417 TNFRSF10C	AGATAGAGCCAGGCTGGAGA 6516 TGAGAT A AGC	
	AGCCAGGCTG AGA	
	TCGGTCCGAC TCT	
	TATC__ C GTI	
GAM417 UMOD	AGA-AGGCAGGCTGAACAA 6520 TGAGAT C G	
	AG CAGGCTGAA AAG	
	TC GTCCGACTT TTT	
	T__ C G	
GAM418 ABCB11	TAAAATATTAACATTCTTCT 6538 TA_ G ATTT	
	TAAAATATT AT CTTCT	
	ATTTTATAA TA GAAGA	
	TTG A IIIA	
GAM418 ADH4	TATAATATTTAAAGC-TCT-TTTA 6546 A T CTAI	
	AATATTTAA GCTT	
	TTATAAATT CGAG	
	A T AAAI	
GAM418 ADH4	TATAATATTTAAAGC-TCT-TTTA 6546 TAA T CTATTTA	
	AATATTTAA GCTT	
	TTATAAATT CGAG	
	ATA T AAAATII	
GAM418 ARHGEF7	TATAATAAATAATACATTCTATTTA 6540 AA TT _ I	
	AATA TAATGC TTCTATTT	

	TTAT ATTATG AAGATAAA	
	A_ TT T I	
GAM418 ARHGEF7	TATAATAATAATACATTCTATTTA 6540 TAA TT _ II	
	ATAA TAATGC TTCTATTTA	
	TTAT ATTATG AAGATAAAT	
	ATA TT T II	
GAM418 C18orf1	TAATATATAATAATGCTTCCTTCTTTA6536 T_ ATTTI	
	ATAT TAATGCTTCT	
	TATA ATTACGAAGG	
	TT AAGII	
GAM418 C18orf1	TAATATATAATAATGCTTCCTTCTTTA6536 TAA T_ A AIII	
	ATAT TAATGCTTCT TTT	
	TATA ATTACGAAGG AGA	
	ATTA TT A AATI	
GAM418 CCR9	AAGTAATTAATGCTTCATAT 6534 AAA T TAI	
	TA TTAATGCTTC	
	AT AATTACGAAG	
	TTC T TATA	
GAM418 CCR9	AAGTAATTAATGCTTCATAT 6534 TAAAA T TATTT	
	TA TTAATGCTTC	
	AT AATTACGAAG	
	C_ T TATAT	
GAM418 COL19A1	TAAAATATTTA--GCTT-TAT 6542 AT CI	
	TAAAATATTTA GCTT	
	ATTTTATAAAT CGAA	
	_ AT	
GAM418 COL19A1	TAAAATATTTA--GCTT-TAT 6542 AT CTATT	
	TAAAATATTTA GCTT	
	ATTTTATAAAT CGAA	
	_ ATAI	
GAM418 CSF2	TAAAATATTCCCATTTCTTCT 6537 AATG_ ATTT	
	TAAAATATTT CTCT	
	ATTTTATAAG GAAGA	
	GGTAA IIIA	
GAM418 EHF	AAAACATTTAATGCCCTCTGATTT 6532 _ ATTI	
	ATATTTAATGCT TCT	
	TGTAAATTACGG AGA	
	G CTII	
GAM418 EHF	AAAACATTTAATGCCCTCTGATTT 6532 TA _ _ AI	
	AAATATTTAATGCT TCT ATTT	

	TTTGTAATTACGG AGA TAAA			
	— G C AI			
GAM418 ERBB4	TAAAATATTTCTTGCTTAAATT 6543	AA	CTATTTA	
	TAAAATATTT TGCTT			
	ATTTTATAAA ACGAA			
	GA TTAAII			
GAM418 ERBB4	TAAAATATTTCTTGCTTAAATT 6543	AA	CTATI	
	AAAATATTT TGCTT			
	TTTTATAAA ACGAA			
	GA TTTAI			
GAM418 ETF1	TAAAGTATTTT-TGCTTCTATGTA 6545	A AA	TTAI	
	TAAA TATTT TGCTTCTAT			
	ATTT ATAAA ACGAAGATA			
	C A_ CATI			
GAM418 ETF1	TAAAGTATTTT-TGCTTCTATGTA 6545	AAA_ AA	TI	
	TATTT TGCTTCTAT			
	ATAAA ACGAAGATA			
	TTTC A_ CI			
GAM418 GLRA3	TAAAGTCTTTTAATGCTCTTATTTA 6535	AAAATA	TC I	
	TTTAATGCT TATTT			
	AAATTACGA ATAAA			
	TTCAGA GA I			
GAM418 GLRA3	TAAAGTCTTTTAATGCTCTTATTTA 6535	TAAAATA_	TC II	
	TTTAATGCT TATTTA			
	AAATTACGA ATAAAT			
	ATTCAGA GA II			
GAM418 IFNGR1	TAAAAAATATACACGTTTCTATTTA 6539	_ TTA C	I	
	AAAATAT ATG TTCTATTT			
	TTTTATA TGC AAGATAAA			
	T TG_ A I			
GAM418 IFNGR1	TAAAAAATATACACGTTTCTATTTA 6539	T_ TTA C	II	
	AAAATAT ATG TTCTATTTA			
	TTTTATA TGC AAGATAAAT			
	ATT TG_ A II			
GAM418 ITGA1	TAAAATATTTTCATTTCTCCATTT 6544	A GC	AI	
	TAAAATATTT AT TTCTATTT			
	ATTTTATAAA TA GAGGTAAA			
	G AA II			
GAM418 MYO1D	AAAATAAGATTTAATGCTT-TATT 6531	AAAT	CTAI	
	ATTTAATGCTT			

	TAAATTACGAA		
	ATTC ATAI		
GAM418 MYO1D	AAAATAAGATTTAATGCTT-TATT	6531 TAAAAT_	C TAI
	ATTTAATGCTT TATT		
	TAAATTACGAA ATAA		
	TTTATTC _ CII		
GAM418 PDK4	AAAATAGTTGA-GCTTCTATT	6533 AAATATTTAAT	I
	GCTTCTAT		
	CGAAGATA		
	TTTTATCAACT I		
GAM418 PDK4	AAAATAGTTGA-GCTTCTATT	6533 TAAAATATTTAAT	T
	GCTTCTATT		
	CGAAGATAA		
	TTTATCAACT____ T		
GAM418 SMARCC1	TAAAATATTTAGCACTATCTACTT	6541 AT _ AI	
	TAAAATATTTA GCT TCTATTT		
	ATTTTATAAAT TGA AGATGAA		
	CG T II		
GAM418 SMARCC1	TAAAATATTTAGCACTATCTACTT	6541 A AT _ I	
	AAATATTTA GCT TCTATT		
	TTTATAAAT TGA AGATGA		
	_ CG T I		
GAM419 MAML1	CCATTGTTT-TCCG-CGCTA	6549 TAACCA CT _ CG	
	TTGTTT CG GC CT		
	AACAAA GC CG GG		
	_____ AG G AT		
GAM420 CD53	CCCCAGAACTCCCTTCAACTAGTCTC	6558 CA____ AA CII	
	CCCCAG CCTTCAACTA CTC		
	GGGGTC GGAAGTTGAT GAG		
	TTGAG CA III		
GAM420 CREBL2	CAGCACCTTCTCCTGGACTCC	6556 CCCCAG AA AA	
	CACCTTC CT ACTCC		
	GTGGAAG GA TGAGG		
	_____ AG CC		
GAM420 FKBP1A	CAGCACCTTCAATTGAAACT	6554 CCCCAG CT_ C	
	CACCTTCAA AAAC		
	GTGGAAGTT TTTGA		
	_____ AAC C		
GAM420 GLRA3	CAGCACCTTAGAC--AGCTCC	6555 CCCCAG CA TAAA	
	CACCTT AC CTC		

		GTGGAA TG GGG	
		_____ TC TCGA	
GAM420 PAG	AGCAC-TTCAACTAGGCTCC	6552 CCCCAGCAC	AA
	CTTCAACTA CTC		
	GAAGTTGAT GAG		
	_____ CC		
GAM420 PRDM4	CCAGCACCTGC--CGAAACT	6557 CCCC	TCAA _
	AGCACCT CT AAAC		
	TCGTGGA GG TTTGA		
	_____ C__ C		
GAM420 RAD54L	CCCCAGCACCTCTC-TCTCAAC	6559	_____ TAAACTCC
	CCCCAGCACCT TCAAC		
	GGGGTCGTGGA AGTTG		
	GAGAG IIICCTCA		
GAM420 SORCS1	CAGCACCTTGCCCTACTAATCTCC	6553 CCCCAG	CA__ A I
	CACCTT ACTAA CTCC		
	GTGGAA TGATT GAGG		
	_____ CGGAG A A		
GAM420 TSLP	CCCCAGT---TTCACACTAAACTC	6560 CACC	_ C
	CCCCAG TTCA ACTAAACTC		
	GGGGTC AAGT TGATTTGAG		
	A__ G I		
GAM421 APC4	CCGGCAGACTAACACGGCCCC	6571 TCC	_ C TTTC
	CAG CTGAC ACGGCCCC		
	GTC GATTG TGCCGGGG		
	CC_ T _ TCII		
GAM421 BCL11B	CCCAGCTGAATCACCAGCTCCTTT	6578 TC	C_ _ C CI
	CCAGCTGA CAC GGC CCTTT		
	GGTCGACT GTG TCG GGAAA		
	_____ TA G A AI		
GAM421 BCL2	TCCCACC---CCACGGCCCC	6588 G TGA	TT
	TCCCA C CCACGGCCCC		
	AGGGT G GGTGCCGGGG		
	G__ II		
GAM421 BCR	CCAGACTCTGGCCACGGCCC	6569 TCCCAG	A CTTT
	CTG CCACGGCCC		
	GAC GGTGCCGGG		
	TCTGA_ C CGII		
GAM421 CARD4	TCCCGCCTGCGCA-GGCCCTTT	6590 AG AC C	C
	TCCC CTG CA GGCCCTTT		

	AGGG GAC GT CCGGGGAAA	
	CG GC _ I	
GAM421 DDX11	TCCCAGCTGACCACAGCCCCTTTC 6592	I
	TCCCAGCTGACCACGGCCCCCTTTC	
	AGGGTCGACTGGTGTCTCGGGGAAAG	
	I	
GAM421 DUSP4	TCCCAGCTGCTCA-GTCCCAACTTTC 6587	ACCA _ _ II
	TCCCAGCTG CGG CCC CTTC	
	AGGGTCGAC GTC GGG GAAAG	
	GA_ A TT II	
GAM421 EPB72	AGCTGACCAGCTTCCTCTTTC 6563 TC	GA A_ CCCTTTC
	CCAGCT CC CGGC	
	GGTCGA GG GTCG	
	CT A_ AGAAA T CTT	
GAM421 HEXA	CCAGC--ACC--GGCCCCTTTC 6576 TCCC	TGACCA
	AGC CGGCCCCTT	
	TCG GCCGGGGAA	
	_ TG_	
GAM421 HMGB3	CCAGCTGACC---CCCCTTT 6575 TCCC	ACGG
	AGCTGACC CCCCTT	
	TCGACTGG GGGGAA	
	_ _	
GAM421 HSD17B2	AGCAGCCC-CAGCCCCTTTC 6565 TCCCAGCTGA A	
	CC CGGCCCCTTT	
	GG GTCGGGGAAA	
	CG_ _	
GAM421 INPP1	CCGGC-GACGCACGGCCCC 6572 TCCCA T _ TT	
	GC GAC CACGGCCCC	
	CG CTG GTGCCGGGG	
	C_ _ C CG	
GAM421 KCNA5	CCCAGCTGAC--CGGCTCC 6580 TC	AC _ TT
	CCAGCTGACC GGC CCC	
	GGTCGACTGG CCG GGG	
	_ _ A II	
GAM421 LDOC1	CCAGGCTGA--ACGGCCCCTT 6570 TCCCA CC	
	GCTGA ACGGCCCTTT	
	C GACT TGCCGGGGAAG	
	TC_ _	
GAM421 LIMK1	TCCCAGCTGAGGGCCACCTCCC 6583	CCAC _ TT
	TCCCAGCTGA GGCC CCT C	
	I	

	AGGGTCGACT CCGG GGA G	
	C___ T GG	
GAM421 LRRC2	CCACCACACC-CGGCCCCTTT 6574 TC GCTG A	
	CCA ACC CGGCCCCTTT	
	GGT TGG GCCGGGGAAA	
	T_ G___ _	
GAM421 MAPK12	CCCAGGCTGCGCACGGCCCCT 6577 TC _ AC TC	
	CCAG CTG CACGGCCCCTT	
	GGTC GAC GTGCCGGGGAG	
	_ C GC II	
GAM421 MBTPS2	CAGCTGACCGCGCGCGCCTT 6567 TCCCAG A _ C T	
	CTGACC CG GC CCTT	
	GA CTGG GC CG GGAA	
	_____ C G C T	
GAM421 NEU1	CAGCTGACC-CG GACCCTTT 6568 TCCCAG A C	
	CTGACC CGG CCCTTT	
	GA CTGG GCC GGGAAA	
	_____ _ T	
GAM421 PAX5	CTGACCATCGCGGCCCTT 6581 TCCCAGCTGACCA T	
	CGGCCCTT	
	GCCGGGGAA	
	TAGC_____ T	
GAM421 POV1	CAGCTGGCACCTCAGGCCCTTTC 6566 TCCCAG _ A _ I	
	CTG ACC C GGCCCTTTC	
	GAC TGG G CCGGGGAAAG	
	_____ CG A T G	
GAM421 RBP3	AGCTCAGCA-GGCCCTTT 6564 TCC TGACCAC	
	CAGC GGCCCTT	
	GTCG CCGGGGAA	
	_____ T_____	
GAM421 RFXANK	TCCCTGCGTCTCACACAGCCCCTTTC 6582 A TGAC_ II	
	TCCC GC CACGGCCCCTTTC	
	AGGG CG GTGTCGGGGAAAG	
	A CAGAGT II	
GAM421 SH3GL1	TCCCAGCTGGCCTCTGTCCC 6589 A ACGG_ CTTT	
	TCCCAGCTG CC CCC	
	AGGGTCGAC GG GGG	
	C AGACA IIIC	
GAM421 SLC13A3	TCCCAGCTGGCCAAGCGCTCCT 6585 A CG_ C TTC	
	TCCCAGCTG CCA GC CCT	

	AGGGTCGAC GGT CG GGA		
	C TCG A III		
GAM421 SLC4A1	TCCCAGCTG--CACGGCTCAGTTC 6591	AC	CCCTTTC
	TCCCAGCTG CACGGC		
	AGGGTCGAC GTGCCG		
	— AGTCAAG		
GAM421 SMAC	CCAGCTCCCC-CGGCCCCTT 6573	TCCC	GA A
	AGCT CC CGGCCCCTTT		
	TCGA GG GCCGGGGAAG		
	— GG —		
GAM421 TCF8	TCCCAGCTGCCCA--GCCC 6586	A A	CTT
	TCCCAGCTG CC CGGCCC		
	AGGGTCGAC GG GTCGGG		
	— — III		
GAM421 TPS1	CCCAGCTGACCACGCCCGCCT 6579	TC	G _ TTC
	CCAGCTGACCACG CC CCT		
	GGTCGACTGGTGC GG GGA		
	— G C CII		
GAM421 XRCC3	TCCCAGCTGTGCCACGGCCC 6584	A_	CTTT
	TCCCAGCTG CCACGGCCC		
	AGGGTCGAC GGTGCCGGG		
	AC IIIC		
GAM422 ABCA3	GTGCTGGTCC-ACTC---GCTAC 6604	ACAC	GI
	GTGCTGGTCCG CTG		
	CACGACCAGGT GAT		
	GAGC GI		
GAM422 ABCA3	GTGCTGGTCC-ACTC---GCTAC 6604	ACACCTGG	
	GTGCTGGTCCG GCTA		
	CACGACCAGGT CGAT		
	GAG_		
GAM422 ATP8A2	GTGCTGGTCTGTTAACACCT 6602	C_	GGGCTA
	GTGCTGGTC GACACCT		
	CACGACCAG TTGTGGA		
	ACAA IIICAT		
GAM422 ATP8A2	GTGCTGGTCTGTTAACACCT 6602	C_	III
	GTGCTGGTC GACACC		
	CACGACCAG TTGTGG		
	ACAA AII		
GAM422 CACNB3	TGCTCTGAGTCCTGGGCTA 6610	G C CA	II
	TG TC GA CCTGGGCT		

	AC AG CT GGACCCGA	
	G A CA TI	
GAM422 CACNB3	TGCTCTGAGTCCTGGGCTA 6610 GTGCTGGTCC CA	
	GA CCTGGGCTA	
	CT GGACCCGAT	
	GA_____CA	
GAM422 DGCR2	GCAGGTCAGAGGGCACCTGGGCT 6597 CTG C ____ I	
	GTC GA CACCTGGGC	
	CAG CT GTGGACCCG	
	____ T CCC I	
GAM422 DGCR2	GCAGGTCAGAGGGCACCTGGGCT 6597 GTGCT C ____ ACI	
	GGTC GA CACCTGGGCT	
	CCAG CT GTGGACCCGA	
	T____ T CCC GAI	
GAM422 FLRT2	GCTGGTCTGGAACCTCCTGGGCTA 6595 ____ TCC A I	
	CTGG GAC CCTGGGCT	
	GACC TTG GGACCCGA	
	CCA ____ A I	
GAM422 FLRT2	GCTGGTCTGGAACCTCCTGGGCTA 6595 GTGC C__ A CI	
	TGGTC GAC CCTGGGCTA	
	ACCAG TTG GGACCCGAT	
	____ ACC A TT	
GAM422 GAB2	TGCTGGTCCTTGACTCCCTGGG 6606 ____ A_	
	TGCTGGTCC GAC CCTGG	
	ACGACCAGG CTG GGACC	
	AA AG CII	
GAM422 GAB2	TGCTGGTCCTTGACTCCCTGGG 6606 GT ____ A_ CTAC	
	GCTGGTCC GAC CCTGGG	
	CGACCAGG CTG GGACCC	
	____ AA AG AIII	
GAM422 HIRA	TGCTGGCCCCAGGGCACCTGGGC 6607 GCT GA____ I	
	GGTCC CACCTGGG	
	CCGGG GTGGACCC	
	____ GTCCC I	
GAM422 HIRA	TGCTGGCCCCAGGGCACCTGGGC 6607 GT GA____ TACI	
	GCTGGTCC CACCTGGGC	
	CGACCGGG GTGGACCCG	
	____ GTCCC TIII	
GAM422 IGHMBP2	TGGTCTGCCAGCGCCCTGGGCTAC 6609 G CGACA I	
	GTC CCTGGGCTA	

	CGG GGACCCGAT			
	A TCGCG I			
GAM422 IGHMBP2	TGGTCTGCCAGCGCCCTGGGCTAC	6609	G TG CCGACA	I
	TGC GT CCTGGGCTAC			
	ACG CG GGACCCGATG			
	G GT CG_____ G			
GAM422 ISG20	GCTGCTCCATCTCCTGGGCTAC	6599	G ACA	I
	CTG TCCG CCTGGGCTA			
	GAC AGGT GGACCCGAT			
	G AGA I			
GAM422 ISG20	GCTGCTCCATCTCCTGGGCTAC	6599	GTGC G ACA	
	TG TCCG CCTGGGCTAC			
	AC AGGT GGACCCGATG			
	_____ G AGA			
GAM422 ITCH	GCTGGTCTTTAACTCCTGGGCTA	6596	CT C__ A	I
	GGTC GAC CCTGGGCT			
	CCAG TTG GGACCCGA			
	__ AAA A I			
GAM422 ITCH	GCTGGTCTTTAACTCCTGGGCTA	6596	GTGC C__ A	CI
	TGGTC GAC CCTGGGCTA			
	ACCAG TTG GGACCCGAT			
	_____ AAA A TT			
GAM422 OSR1	GTGCTGTTCC---ACCTGGGC	6603	G GAC	T
	GTGCTG TCC ACCTGGGC			
	CACGAC AGG TGGACCCG			
	A _____ I			
GAM422 OSR1	GTGCTGTTCC---ACCTGGGC	6603	_ G GAC	
	TGCTG TCC ACCTGGG			
	ACGAC AGG TGGACCC			
	C A _____			
GAM422 PXF	GTGCTGGTCAGTGAACACCT	6601	C_____ GGGCTA	
	GTGCTGGTC GACACCT			
	CACGACCAG TTGTGGA			
	TCAC IIICAT			
GAM422 PXF	GTGCTGGTCAGTGAACACCT	6601	C_____	
	GTGCTGGTC GACACC			
	CACGACCAG TTGTGG			
	TCAC AII			
GAM422 RLN1	TGCTGTGGCCTACACACCTGGGC	6605	G_ C CG_	ACI
	TG TGGTC ACACCTGGGCT			

	AC ACCGG TGTGGACCCGG		
	CG _ ATG III		
GAM422 RLN1	TGCTGTGGCCTACACACCTGGGC 6605 GC CG_ I		
	TGGTC ACACCTGGG		
	ACCGG TGTGGACCC		
	C_ ATG I		
GAM422 SURF5	GCGGGACCCAC-CCTGGGCTA 6598 CT_ T G A I		
	GG CC AC CCTGGGCT		
	CC GG TG GGACCCGA		
	CGC T G _ I		
GAM422 SURF5	GCGGGACCCAC-CCTGGGCTA 6598 GTGCT T G A		
	GG CC AC CCTGGGCTA		
	CC GG TG GGACCCGAT		
	C_ T G _		
GAM422 SYNGR1	TGCTGGTCC--CATGTGGGCCAC 6608 _ GA CC I		
	GCTGGTCC CA TGGGCTA		
	CGACCAGG GT ACCCGGT		
	A _ AC I		
GAM422 SYNGR1	TGCTGGTCC--CATGTGGGCCAC 6608 GT GA CC		
	GCTGGTCC CA TGGGCTAC		
	CGACCAGG GT ACCCGGTG		
	_ _ AC		
GAM422 TCF2	GTGCTGGTCAGGTCA-CTGGGCT 6600 CGA_ C AC		
	GTGCTGGTC CAC TGGGCT		
	CACGACCAG GTG ACCCGA		
	TCCA _ II		
GAM422 TCF2	GTGCTGGTCAGGTCA-CTGGGCT 6600 CGA_ C I		
	TGCTGGTC CAC TGGGC		
	ACGACCAG GTG ACCCG		
	TCCA _ I		
GAM423 ADD2	CTTAGCTATCTCCGGTCCGC 6616 TAACTTGGATA ATG		
	CCGGTCCGC		
	GGCCAGCCG		
	TCGATAGA_ GTG		
GAM423 CARL	GCTCTTCGCC-CAGGGGGGCGG 6618 GTGC AGAAGTT		
	TCTTCGCC GGCGG		
	AGAAGCGG CCGCC		
	_ GTCCCC_		
GAM423 CMAR	GCTCTTCGCCTCCAAG-TGGAGG 6617 GTGC AG_ T C		
	TCTTCGCC AAGT GG GG		

	AGAAGCGG TTCA CC CC		
	_____ AGG _ T		
GAM423 ESR2	TGCTCTTCGCCCTGCAAGTT 6622 GT	AG__	GGCG
	GCTCTTCGCC AAGTT		
	CGAGAAGCGG TTCAA		
	_____ GACG AIII		
GAM423 LGALS3BP	GTGCTCTTCG--AGCTGTTGG 6621	CC AA	CG
	GTGCTCTTCG AG GTTGG		
	CACGAGAAGC TC CAACC		
	_____ GA II		
GAM423 MUC4	CTCTGAGCGTGAAGTTGGC 6615 GTGCTCTTC CA		
	GC GAAGTTGGCG		
	CG CTTCAACCGT		
	ACT_____ CA		
GAM423 PRX	AATTTGGATACC-TTCAGCTTGG 6613 TAAC	GG	A
	TTGGATACC TCGGC TGG		
	AACCTATGG AGTCG ACC		
	TA_____ A_ A		
GAM423 PRX	ACCTGG-TAC---TCGGCATGG 6614 TAACT A CGG		
	TGG TAC TCGGCAT		
	ACC ATG AGCCGTA		
	G_____ _ _		
GAM423 RNMT	GTGCTCTTCCTGGCCCGACGGTGG 6619	_____ AGAAGT	I
	GTGCTCTTC GCC TGGCGG		
	CACGAGAAG CGG GCTGCC		
	GAC _____ A		
GAM423 ZNF76	GTGCACTCAGACATGAAGTTGGC 6620	__ TG	TTC CA GGI
	G CTC GC GAAGTTGGC		
	I		
	C GAG TG CTTCAACCG		
	CA GT TC_ TA		
GAM424 ABCB9	TGCAGGCCTGG-GCTCGGAGGGC 6665 TT	_____ T	AGAGC
	GCAGGCCTGG TGG GGG		
	CGTCCGGACC GCC CCC		
	_____ CGA T GTIII		
GAM424 ADAM11	TGCAGACCCCGTGGTGGGAG 6662 TT	G	AG
	GCAGGCCT GTGGTGGGAG		
	CGTCTGGG CACCACCCTC		
	_____ G GI		
GAM424 ADAM11	TTGC---CCTGGTGGTAGAAG 6671	AGG	A
	TTGC CCTGGTGGTGGGAG		

	AACG GGACCACCATCTTC		
	____ I		
GAM424 ALDH3B1	GCAGGCGCGATGGTGGGAGA 6656 TTGC C		
	AGGC TGGTGGTGGGAGAG		
	TCCG GCTACCACCCTCTT		
	____ C		
GAM424 B29	CCCTCCTTCTTCCCTCATG-CCA 6643	G C A T	
	CCCTCCTTCTTC TTC TG CCA		
	GGGAGGAAGAAG GAG AC GGT		
	G T _ I		
GAM424 B29	CCCTCCTTCTTCCCTCATG-CCA 6643 _	G C A I	
	CCTCCTTCTTC TTC TG CC		
	GGAGGAAGAAG GAG AC GG		
	G G T _ I		
GAM424 BLTR2	CCCTCCTTCTTTG-TCCAGCCC 6642	C T TGA AT	
	CCCTCCTTCTT GT CC CC		
	GGGAGGAAGAA CA GG GG		
	A _ TCG II		
GAM424 BLTR2	CCCTCCTTCTTTG-TCCAGCCC 6642 _	C CTGACI	
	CCTCCTTCTT GTTC		
	GGAGGAAGAA CAGG		
	G A TCGII		
GAM424 CA11	CCCTCCTTCTGGGACCCTGTCC 6641	TCGT A AT	
	CCCTCCTTCT TCCTG CC		
	GGGAGGAAGA GGGAC GG		
	CCCT A II		
GAM424 CA11	CCCTCCTTCTGGGACCCTGTCC 6641	TCGT ACI	
	CCTCCTTCT TCCTG		
	GGAGGAAGA GGGAC		
	CCCT AGI		
GAM424 CAPNS1	TGCAGGGCCTGGTGGGAATGGGGAGA 6661 TT _ T_____ GCII		
	GCAGG CCTGGTGG GGGAGA		
	CGTCC GGACCACC CCCTCT		
	_ C CTTAC GIII		
GAM424 CASR	CCCTCCTTCCACTCTCCTG 6635	TCG ACCA	
	CCCTCCTTCT TTCCTG		
	GGGAGGAAGG GAGGAC		
	TGA IIIT		
GAM424 CASR	CCCTCCTTCCACTCTCCTG 6635	TCG II	
	CCCTCCTTCT TTCCT		

	GGGAGGAAGG GAGGA		
	TGA CI		
GAM424 DMD	CTCCTTCTTCATCTGTCATGAC 6650	CCTGAI	
	CTCCTTCTTCGTT		
	GAGGAAGAAGTAG		
	ACAGTACT		
GAM424 DMD	CTCCTTCTTCATCTGTCATGAC 6650 CCCT	___ C CAT	
	CCTTCTTCGT TC TGAC		
	GGAAGAAGTA AG ACTG		
	___ GAC T ACI		
GAM424 DVL3	TTTCAGGCCTGGAGGTGAGATGAGC 6669 TTG	T _ II	
	CAGGCCTGG GGTGGGA GAGC		
	GTCCGGACC CCACTCT CTCG		
	AAA T A II		
GAM424 ELF3	TTGCAGGCCTCGAGTGGTCCGTGAG 6668	___ GG___ AGCII	
	TTGCAGGCCT GGTGGT GAG		
	AACGTCCGGA TCACCA CTC		
	GC GGCA IIICG		
GAM424 EPHB2	AGGCCTGGTGGCAGGTGGGAG 6626 TTGCA CT TG AGC		
	GGC GGTGG GGAG		
	CCG CCACC CCTC		
	GACCA T_ CT CII		
GAM424 F2RL3	GGCCTGGTGGGGCCACAGC 6660 TTGCA _ GG GAGAG		
	GGCC TGGT TGG		
	CCGG GTCG ACC		
	CCACC T TA IIICG		
GAM424 FGFR1	GCAGTGCCTGGTGGCAGGGAG 6651 TTGCAG	_ AGC	
	GCCTGGTGGT GGGAG		
	CGGACCACCG CCCTC		
	TCA___ T CCI		
GAM424 FOXD2	GCAGTGGTTGGTGGTGGGGGA 6652 TTGCA CC	A GC	
	GG TGGTGGTGGG GA		
	CC ACCACCACCC CT		
	TCA_ A_ C AA		
GAM424 GAB2	CCTTCCTTCTTCCTCCACTGGACC 6634	G _ ACI	
	TCCTTCTTC TTC CTG		
	AGGAAGAAG AGG GAC		
	G T CII		
GAM424 GAB2	CCTTCCTTCTTCCTCCACTGGACC 6634 C	G _ _ ATI	
	CC TCCTTCTTC TTC CTG ACC		

	GG AGGAAGAAG AGG GAC TGG	
	A G T C III	
GAM424 HIPK2	CCCTCCTTCTCTCCCTCCT 6633 _ G GACCA	
	CCCTCCTTCT TC TTCCT	
	II	
	GGGAGGAAGA AG GAGGA	
	G G IIITA	
GAM424 HIPK2	CCCTCCTTCTCTCCCTCCT 6633 _ G II	
	CCCTCCTTCT TC TTCC	
	II	
	GGGAGGAAGA AG GAGG	
	G G AI	
GAM424 HOXB1	CAGGCCTGG-GTTGGGAGAGC 6628 TTGCAG TGG	
	GCCTGG TGGGAGAG	
	CGGACC ACCCTCTC	
	_____ CA_	
GAM424 HPSE	CCTTCGCTTCCTTGCTTCCTGACCAT 6629 C _ C _ II	
	CC TC CTTCTT GTT CCTGACCAT	
	II II III	
	GG AG GAAGGA CGA GGA CTGGTA	
	A C A A II	
GAM424 HPSE	CCTTCGCTTCCTTGCTTCCTGACCAT 6629 CC _ C _ I	
	TC CTTCTT GTT CCTGACCA	
	II III	
	AG GAAGGA CGA GGA CTGGT	
	_ C A A I	
GAM424 IGFBP5	TGCAGCCGAGAGGGGTGGGAGA 6664 TT G T T_ C	
	GCAG CC GG GGTGGGAGAG	
	II	
	CGTC GG TC CCACCCTCTT	
	_____ C TC I	
GAM424 KAI1	GCAGGCCTGGAGGAGGGAG 6655 TTGC T T AG	
	AGGCCTGG GG GGGAG	
	II	
	TCCGGACC CC CCCTC	
	_____ T T GG	
GAM424 KCNK3	CCCTCCTTCTTTCTGTCCTG 6631 _GT ACCA	
	CCCTCCTTCTT C TCCTG	
	I	
	GGGAGGAAGAA G AGGAC	
	A AC IIIT	
GAM424 KCNK3	CCCTCCTTCTTTCTGTCCTG 6631 _GT II	
	CCCTCCTTCTT C TCCT	
	I	
	GGGAGGAAGAA G AGGA	
	A AC CI	
GAM424 KCNMB3	CCCTCCTTCTCCTCCTCTCTGGCCA 6632 G_ _ A TII	
	CCCTCCTTCTTC TTC CTG CCA	
	III	

	GGGAGGAAGAGG GAG GAC GGT		
	AG A C III		
GAM424 KCNMB3	CCCTCCTTCTCCTCCTCTCTGGCCA 6632 CC	G_ _ A I	
	TCCTTCTTC TTC CTG CC		
	III III II		
	AGGAAGAGG GAG GAC GG		
	AG A C I		
GAM424 LOXL1	AGGCCTGGTGGACAGAGAG 6627 TTGCAGGC	TG	
	CTGGTGG GGAGAG		
	GACCACC TCTCTC		
	TG		
GAM424 LZTR1	TGCGGG---GGTGGTGGG-GAGC 6666 TT A CCT	A	
	GC GG GGTGGTGGG GAG		
	CG CC CCACCACCC CTC		
	C _ _ _		
GAM424 MAP3K8	TGCAGGCCT---GTGGGAG 6663 TT	GGTG	
	GCAGGCCT GTGGGAG		
	CGTCCGGA CACCCTC		
	CCCTCCTTCTTC---CCTG 6637	G CCT	
GAM424 MN1	CCCTCCTTCTTC TT		
	GGGAGGAAGAAG GA		
	G CII		
GAM424 MN1	CCCTCCTTCTTC---CCTG 6637	GTT AC	
	CCCTCCTTCTTC CCTG		
	GGGAGGAAGAAG GGAC		
	II		
GAM424 NDUFS2	CCTCCTTCTTGGCTTCTCACC 6648	C C G I	
	CTCCTTCTT GTT CT AC		
	GAGGAAGAA CGA GA TG		
	C A G I		
GAM424 NDUFS2	CCTCCTTCTTGGCTTCTCACC 6648 CC	C C G AT	
	CTCCTTCTT GTT CT ACC		
	GAGGAAGAA CGA GA TGG		
	C A G AI		
GAM424 NHLH1	TTGAAAGC-TGGTGGTGGGAG 6670	C C AG	
	TTG AGGC TGGTGGTGGGAG		
	AAC TTCG ACCACCACCCTC		
	T _ II		
GAM424 NLGN2	GCAGGCGCGTGGTGGTGGTGAAGAGC 6654 TTGC	C_ _ _ II	
	AGGC TGGTGGTGG GA GAGC		

	TCCG ACCACCACC CT CTCG	
	_____ CGC A T AG	
GAM424 NR4A2	GGTCGGGTAGGGGTGGGAGAGC 6659 TTGCA CCT T	
	GG GG GGTGGGAGAGC	
	CC CC CCACCCTCTCG	
	_____ AT_ _	
GAM424 PFKFB3	CCCAACATCTACGTTCTGA 6638 TCCT T CCA	
	CCC TCT CGTTCCTGA	
	GGG AGA GCAAGGACT	
	TTGT T	
GAM424 PFKFB3	CCCAACATCTACGTTCTGA 6638 TCCT T I	
	CC TCT CGTTCCTG	
	GG AGA GCAAGGAC	
	TTGT T I	
GAM424 PYGM	AGGCCCTCGGCGGTGGGAGA 6625 TTGCAGG _	
	CCT GGTGGTGGGAGAG	
	GGA CCGCCACCCTCTT	
	_____ G	
GAM424 RAB7L1	CCCTCCTTCTGCATTCCAGA 6639 T T CCA	
	CCCTCCTTCT CGTTCC GA	
	GGGAGGAAGA GTAAGG CT	
	C T	
GAM424 RAB7L1	CCCTCCTTCTGCATTCCAGA 6639 T TGI	
	CCTCCTTCT CGTTCC	
	GGAGGAAGA GTAAGG	
	C TCI	
GAM424 SEPN1	CCTTCCTTCTTCCT--CTG-CCA 6644 _ G TC A	
	CCT CTTCTTC T CTG CC	
	GGA GGAAGAAG A GAC GG	
	A G _ _	
GAM424 SEPN1	CCTTCCTTCTTCCT--CTG-CCA 6644 C G TC A	
	CC TCCTTCTTC T CTG CCA	
	GG AGGAAGAAG A GAC GGT	
	A G _ _	
GAM424 SIGLEC11	GCAGGAAGCCTGGTGGAGGG 6653 TTGC T AGAG	
	AGGCCTGGTGG GGG	
	TTCGGACCACC CCC	
	TCC_ T CG	
GAM424 SLC10A2	CCTCCTGCCACCTCCCTGACCAT 6649 T TCG I	
	CTCCT CT TTCCTGACCA	

	GAGGA GG AGGGACTGGT			
	C TGG I			
GAM424 SLC10A2	CCTCCTGCCACCTCCCTGACCAT 6649 CC T TCG I			
	CTCCT CT TTCCTGACCAT			
	GAGGA GG AGGGACTGGTA			
	__ C TGG C			
GAM424 SLC19A1	GCTGCCCTTAGGGTGGGAGAG 6658 TTGCAG __ T C			
	GCCT GG GGTGGGAGAG			
	CGGG TC CCACCCTCTC			
	A ____ AA _ T			
GAM424 SLC6A8	CCCTCCTTC--CCTTCCTCAC 6640 CG G CA			
	CCCTCCTTCTT TTCCT AC			
	GGGAGGAAGGG AAGGA TG			
	__ G			
GAM424 SLC6A8	CCCTCCTTC--CCTTCCTCAC 6640 CG GI			
	CCCTCCTTCTT TTCCT			
	GGGAGGAAGGG AAGGA			
	__ GT			
GAM424 SMG1	TTGCAGGCCATGGTGTTGGG 6667 _ G AGAG			
	TTGCAGGCC TGGTG TGGG			
	AACGTCCGG ACCAC ACCC			
	T A C			
GAM424 SOX13	GCAGGGCTGG--GTGGGAGAG 6657 TTGC C TG			
	AGG CTGG GTGGGAGAG			
	TCC GACC CACCCTCTC			
	__ C __			
GAM424 SYN3	TTGAGGCGCTGGT-TTGGG-GAGC 6672 C GG A			
	TTG AGGCCTGGT TGGG GAGC			
	AAC TCCGGACCA ACCC CTCG			
	C A_ _			
GAM424 TAF7L	CCTCTTGCTCCCTCTCCTGACCA 6646 CC__ TTCGT I			
	CTCCTTC TCCTGACCAT			
	GAGGGAG AGGACTGGTG			
	GAGAAC ____ I			
GAM424 TRC8	CCCTCCTTCCTC--TCCTG 6636 GT ACC			
	CCCTCCTTCTTC TCCTG			
	GGGAGGAAGGAG AGGAC			
	__			
GAM424 TRC8	CCCTCCTTCCTC--TCCTG 6636 GT I			
	CCCTCCTTCTTC TCCT			

	GGGAGGAAGGAG AGGA			
	— C			
GAM424 TRHDE	CCTCCTTCTTCTTCTTCCT 6645	G__ III		
	CCTCCTTCTTC TTCC			
	GGAGGAAGAAG AAGG			
	AAG AII			
GAM424 TRHDE	CCTCCTTCTTCTTCTTCCT 6645 CC	G__ GACCA		
	CTCCTTCTTC TTCCT			
	GAGGAAGAAG AAGGA			
	— AAG GIIT			
GAM424 TRIM39	CCTC-TCCTTCCTTCCTGACC 6647 _ C	G I		
	CTC TTCTTC TTCCTGAC			
	GAG AGGAAG AAGGACTG			
	G _ G I			
GAM424 TRIM39	CCTC-TCCTTCCTTCCTGACC 6647 CC	TCG A		
	CTCCTTCT TTCCTGACC			
	GAGGAAGG AAGGACTGG			
	GA _ G			
GAM424 VASP	CCCTCCTTCCTTCCCCCTTCCTG 6630	_ G ACCATI		
	CCCTCCTTCT TC TTCCTG			
	GGGAGGAAGG GG AAGGAC			
	AAGG G IITAC			
GAM424 VASP	CCCTCCTTCCTTCCCCCTTCCTG 6630	_ G IIIC		
	CCCTCCTTCT TC TTCCT			
	GGGAGGAAGG GG AAGGA			
	AAGG G CII			
GAM425 CENTD2	GGAATCCTAGAGCCAAGGAT 6676 TGGC	A C_ TT		
	ATCCTAGAG CC GGAT			
	TAGGATCTC GG CCTA			
	CT_ _ TT CI			
GAM425 CSH2	TGGGATCCTAGAG--CCGG 6677 C	AC ATT		
	TGG ATCCTAGAG CCGG			
	ACC TAGGATCTC GGCC			
	C _ III			
GAM425 RAB6A	CAGCCTAGAGACCTCCCGGA 6675 TGGCAT	_ T		
	CCTAGAGA CCCGATT			
	GGATCTCT GGGCCTGG			
	— GGA C			
GAM425 RNASE6	TGGCATCCTAGGCACTCGAATT 6678	AG C TA		
	TGGCATCCTAG AC CGGATT			

	ACCGTAGGATC TG GCTTAA	
	CG A II	
GAM426 ARF4L	GGACTGCCAGCCTCTTCTCC 6692 A A I	
	GACTGCCA CCTCT CTC	
	CTGACGGT GGAGA GAG	
	C A I	
GAM426 ARF4L	GGACTGCCAGCCTCTTCTCC 6692 GAAGGA A A	
	CTGCCA CCTCT CTCC	
	GACGGT GGAGA GAGG	
	C A	
GAM426 CACNB2	CTTCCCACCTTCTACTCCC 6689 CTG A _ II	
	CC ACCT CTACTCC	
	GG TGGA GATGAGG	
	GAA G A GI	
GAM426 CORO2B	AAGGACTGCAGAACTTTA 6681 CAACCTCTII	
	AAGGACTGC	
	TTCCTGACG	
	TCTTTGAAAT	
GAM426 CRYZ	AGGACTGCCACACCT-T-CTCC 6685 _ _ _ ACTCI	
	GGACTGCCA ACCT CT	
	CCTGACGGT TGGA GA	
	T G A GIIIC	
GAM426 CRYZ	AGGACTGCCACACCT-T-CTCC 6685 GAAG _ CTA	
	GACTGCCA ACCT CTCC	
	CTGACGGT TGGA GAGG	
	G A _	
GAM426 F8A	GAAG-ACAGCCATGTCCTCTACTC 6691 AA T A _ I	
	GGAC GCCA CCTCTACT	
	TCTG CGGT GGAGATGA	
	_ T ACA I	
GAM426 F8A	GAAG-ACAGCCATGTCCTCTACTC 6691 GA T A _ CCI	
	AGGAC GCCA CCTCTACTC	
	TTCTG CGGT GGAGATGAG	
	C _ T ACA III	
GAM426 GNAZ	AGGACTGCCA--CTC-ACTCC 6686 _ AC T	
	GGACTGCCA CTC ACTC	
	CCTGACGGT GAG TGAG	
	T _ _	
GAM426 GNAZ	AGGACTGCCA--CTC-ACTCC 6686 GAAG AC T	
	GACTGCCA CTC ACTC	

CTGACGGT GAG TGAG

GAM426 HOXD1	AGGACTGCCGCCGTCTGCGCC	6687	AA _	ACTCI
	GGACTGCC CC TCT			
	CCTGACGG GG AGA			
	C_ C CGCGI			
GAM426 HOXD1	AGGACTGCCGCCGTCTGCGCC	6687	GAAG	AA _ ACT C
	GA CTGCC CC TCT CC			
	CTGACGG GG AGA GG			
	C_ C CGC C			
GAM426 HSPB3	CTGCCAACCTTCCACTGCC	6688	_ _	II
	CTGCCAACCT CTACT CC			
	GACGGTTGGA GGTGA GG			
	A C II			
GAM426 IRAK4	ACTGC-AACCTCTACCTCCC	6684	C _	II
	ACTGC AACCTCTAC TCC			
	TGACG TTGGAGATG AGG			
	_ G GI			
GAM426 RAB7L1	ACTGC-AACCTCTAACTCCC	6683	C _	II
	ACTGC AACCTCTA CTCC			
	TGACG TTGGAGAT GAGG			
	_ T GI			
GAM426 SORCS3	CTTCCAACCTCTTTAACTCC	6690	CTG _	III
	CCAACCTCT ACTC			
	GGTTGGAGA TGAG			
	GAA AAT GII			
GAM426 ZNF265	AAGGCATGC--ACCTCTACT	6682	_ AC CA	I
	AGG TGC ACCTCTAC			
	TCC ACG TGGAGATG			
	T GT _ I			
GAM426 ZNF265	AAGGCATGC--ACCTCTACT	6682	GA AC CA	C
	AGG TGC ACCTCTACT			
	TCC ACG TGGAGATGA			
	_ GT _ T			
GAM427 AQP6	TCAGTTCTTCTCAAGGGTG	6708	C TIII	
	TCAGTTCTTC CAGG			
	AGTCAAGAAG GTTC			
	A CCAC			
GAM427 AQP6	TCAGTTCTTCTCAAGGGTG	6708	TATC C _	AACA
	AGTTCTTC CA GGTG			

		TCAAGAAG GT CCAC		
		_____ A TC CCII		
GAM427 CAPN9		TCA-TTCTTCCCAGATCAA	6709 TATCA	G C
		GTTCTTCCCAGGT AA		
		TAAGAAGGGTCTA TT		
		_____ G C		
GAM427 CAPN9		TCA-TTCTTCCCAGATCAA	6709 TCA	GAI
		GTTCTTCCCAGGT		
		TAAGAAGGGTCTA		
		AG_ GTT		
GAM427 CD80		CTTCCCAGGTGCAAAACAG	6705	AACAIII
		CTTCCCAGGTG		
		GAAGGGTCCAC		
		GTTTTGT		
GAM427 CLU		TCTGTTCTTCCCA--TGAGCAG	6712 CA	GG AI
		GTTCTTCCCA TGA		
		III		
		CAAGAAGGGT ACT		
		GA _ CG		
GAM427 CLU		TCTGTTCTTCCCA--TGAGCAG	6712 TATCA	GG A
		GTTCTTCCCA TGA CA		
		III II		
		CAAGAAGGGT ACT GT		
		A_ _ C		
GAM427 CREBL2		AGTTCTTCCCTATTTAACAG	6696	AGGTG I
		GTTCTTCCC AACAA		
		III		
		CAAGAAGGG TTGT		
		ATAAA I		
GAM427 CREBL2		AGTTCTTCCCTATTTAACAG	6696 TATCAGTT	AGGTG
		CTTCCC AACAA		
		III		
		GAAGGG TTGT		
		_____ ATAAA		
GAM427 DISC1		ATGAGTTCTTAGCCAGGTGAACA	6698 TATC	C_ I
		AGTTCTT CCAGGTGAACAG		
		TCAAGAA GGTCCACTTGTT		
		AC_ TC I		
GAM427 DISC1		ATGAGTTCTTAGCCAGGTGAACA	6698 TC	C_ I
		AGTTCTT CCAGGTGAAC		
		TCAAGAA GGTCCACTTG		
		C_ TC I		
GAM427 FEN1		TCAGCTGATTGCCAGGTGAACA	6707 C	C_ C I
		AGTT TT CCAGGTGAAC		
		II		

	TCGA AA GGTCCACTTG	
	_ CT C I	
GAM427 FEN1	TCAGCTGATTGCCAGGTGAACA 6707 TATC C_ C G	
	AGTT TT CCAGGTGAACA	
	TCGA AA GGTCCACTTGT	
	____ CT C A	
GAM427 GGA1	AGTTCTTCCAAGGCTACACAG 6695 G C GA_ I	
	TTCTTCC AGGT ACA	
	AAGAAGG TCCG TGT	
	_ T ATG I	
GAM427 GGA1	AGTTCTTCCAAGGCTACACAG 6695 TATCAGTT C GA_	
	CTTCC AGGT ACAG	
	GAAGG TCCG TGTC	
	_____ T ATG	
GAM427 GNAZ	TCATTTGCTCCCAGGTGAA 6710 G C II	
	TCA TT TTCCCAGGTGA	
	AGT AA GAGGGTCCACT	
	A C TI	
GAM427 GNAZ	TCATTTGCTCCCAGGTGAA 6710 TATCAGTTC CA	
	TTCCCAGGTGAA	
	GAGGGTCCACTT	
	TAAAC_____ TC	
GAM427 MAPRE1	TCTGTT-TTCC-AGGTGAAC 6711 CA_ C C I	
	GTT TTCC AGGTGAA	
	CAA AAGG TCCACTT	
	AGA _ _ I	
GAM427 MAPRE1	TCTGTT-TTCC-AGGTGAAC 6711 TATCA C C	
	GTT TTCC AGGTGAAC	
	CAA AAGG TCCACTTG	
	A_____ _ _	
GAM427 MC1R	CAGTTCTTCCCCTCCAGGTG 6701 TATCAG _ AACA	
	TTCTTC CCAGGTG	
	AAGGGG GGTCCAC	
	AAG_____ A AGGI	
GAM427 MC1R	CAGTTCTTCCCCTCCAGGTG 6701 _____ IIIC	
	CAGTTCTTCCC AGGT	
	GTCAAGAAGGG TCCA	
	GAGG CIII	
GAM427 MLPH	ATCAGTAAA-CCCAGGTGAGCAG 6700_ TCTT ACAI	
	TCAGT CCCAGGTGA	

	AGTCA GGGTCCACT	
	T TTT_ CGTI	
GAM427 MLPH	ATCAGTAAA-CCCAGGTGAGCAG 6700 TA TCTT A	
	TCAGT CCCAGGTGA CAG	
	AGTCA GGGTCCACT GTC	
	_ TTT_ C	
GAM427 NR1I2	CAGTTGTCTTCAGGTGAACA 6704 C CC I	
	AGTT TT CAGGTGAAC	
	TCAA AG GTCCACTTG	
	C AA I	
GAM427 NR1I2	CAGTTGTCTTCAGGTGAACA 6704 TATCA T CC	
	GT CTTC AGGTGAACA	
	CA GAAG TCCACTTGT	
	AA_ _ _	
GAM427 OGG1	CAGTTCTTCACCTTGTGAA 6702 _ AG II	
	CAGTTCTTC CC GTGA	
	GTCAAGAAG GG CACT	
	T AA TI	
GAM427 OGG1	CAGTTCTTCACCTTGTGAA 6702 TATCAG _ AG CA	
	TTCTTC CC GTGAA	
	AAGAAG GG CACTT	
	_ _ _ T AA AG	
GAM427 OVOL1	TCTTCCCAGGCTCAGAACAG 6715 _	
	TCTTCCCAGGT GAACA	
	AGAAGGGTCCG CTTGT	
	AGT CII	
GAM427 OVOL1	TCTTCCCAGGCTCAGAACAG 6715 TA_ TTCTT CA GAACA	
	TCAG CC GGT	
	AGTC GG CCG	
	TCCG TTGTC AG IIIGA	
GAM427 PCDHGA8	TCTTCCAGTAGGTGAACAG 6713 C_	
	TCTTCC AGGTGAACA	
	AGAAGG TCCACTTGT	
	TCA CII	
GAM427 PIP5K1B	CAGTTCTTCACAGTTCAGCA 6703 C GTGAACI	
	AGTTCTTC CAG	
	TCAAGAAG GTC	
	T AAGTCGI	
GAM427 PIP5K1B	CAGTTCTTCACAGTTCAGCA 6703 TAT_ TTCC GAACA	
	CAGTTC CAGGT	

	GTCAAG GTTCG			
	AAGAAGT TC__ IIIGA			
GAM427 PLCG2	TCTTCCCAGAGTGTGAATAG 6714	___	CAIII	
	TCTTCCCAG GTGAA			
	AGAAGGGTC CACTT			
	TCA ATCII			
GAM427 PPP1R12B	ATCAAATCATTCCAGGTGAA 6699	T TTC	I	
	TCAG TC CCAGGTGA			
	AGTT AG GGTCCACT			
	T TAA I			
GAM427 PPP1R12B	ATCAAATCATTCCAGGTGAA 6699	TA T TTC	CA	
	TCAG TC CCAGGTGAA			
	AGTT AG GGTCCACTT			
	___ T TAA TI			
GAM427 TAF4B	TCAGCTTCTTCCTCAGGTGAACA 6706	CAG _	I	
	TTCTTCC CAGGTGAAC			
	AAGAAGG GTCCACTTG			
	CG_ A I			
GAM427 TAF4B	TCAGCTTCTTCCTCAGGTGAACA 6706	TATCAG _	GI	
	TTCTTCC CAGGTGAACA			
	AAGAAGG GTCCACTTGT			
	TCG___ A GT			
GAM427 TNNI1	ATCATTGTCATCCCAGGTGA 6697	GTTCT_	II	
	ATCA TCCCAGGTG			
	TAGT AGGGTCCAC			
	AAACGT TI			
GAM427 TNNI1	ATCATTGTCATCCCAGGTGA 6697	TA GTTCT_	ACA	
	TCA TCCCAGGTGA			
	AGT AGGGTCCACT			
	___ AAACGT AII			
GAM428 ACOX1	GAGTTGCACACAGGC-GCTT 6726_	TGTCA I		
	AGTTGCACAC GCT			
	TCAACGTGTG CGA			
	C TCCG_ I			
GAM428 ACOX1	GAGTTGCACACAGGC-GCTT 6726	TGAGAG	TGTCA	
	TTGCACAC GCTT			
	AACGTGTG CGAA			
	_____ TCCG_			
GAM428 ATSV	AGAGTCTGCACACTGGCAG 6718	_ T II		
	AGAGT TGCACACTG CA			

	TCTCA ACGTGTGAC GT			
	G C CI			
GAM428 ATSV	AGAGTCTGCACACTGGCAG	6718	TGAG _	T CTT
	AGT TGCACACTG CAG			
	TCA ACGTGTGAC GTC			
	___ G C CAI			
GAM428 CALM3	TGAGTGTTGCCCACTGTCAG	6728	A A	CTT
	TGAG GTTGC CACTGTCAG			
	ACTC CAACG GTGACAGTC			
	A G			
GAM428 CALM3	TGAGTGTTGCCCACTGTCAG	6728	A A	I
	GAG GTTGC CACTGTCA			
	CTC CAACG GTGACAGT			
	A G I			
GAM428 CSN10	GAGTTGG-C-CTGTCAGCT	6725	CACA	I
	GAGTTG CTGTCAGC			
	CTCAAC GACAGTCG			
	CG_ A			
GAM428 CSN10	GAGTTGG-C-CTGTCAGCT	6725	TGAGAGTTGCACA	
	CTGTCAGCT			
	GACAGTCGA			
	AACCG_____			
GAM428 GOSR1	AGAGTC-CATCACTGTCAGTCTTG	6720	G G _ _	I
	AGTT CA CACTGTCAG CTT			
	TCAG GT GTGACAGTC GAA			
	_ _ A A I			
GAM428 GOSR1	AGAGTC-CATCACTGTCAGTCTTG	6720	TGAG G _ _	I
	AGTT CA CACTGTCAG CTTG			
	TCAG GT GTGACAGTC GAAC			
	___ _ A A G			
GAM428 IFI27	AGAGTTGCAACAAT-TCATCTT	6719	C TG_ G	I
	GAGTTGCA AC TCA CT			
	CTCAACGT TG AGT GA			
	_ TTA A I			
GAM428 IFI27	AGAGTTGCAACAAT-TCATCTT	6719	TGAG C TG_ G G	
	AGTTGCA AC TCA CTT			
	TCAACGT TG AGT GAA			
	___ _ TTA A A			
GAM428 KIF3C	GAGCAGATGCCCAACTGTCAG	6722	_ T _	C
	GAG AG TGC ACACTGTCA			

	CTC TC ACG TGTGACAGT	
	G T GGT CIII	
GAM428 KIF3C	GAGCAGATGCCCAACACTGTCAG 6722 TG_ _ GC	CTTGI
	AGA GTT ACACTGTCAG	
	TCT CGG TGTGACAGTC	
	TCG A GT CIIIG	
GAM428 MFAP4	GAGAGTGGCTCCTGGCTGTCAGCT 6723 AGA GCACA	I
	GTT CTGTCAGC	
	CGA GACAGTCG	
	CAC GGACC I	
GAM428 MFAP4	GAGAGTGGCTCCTGGCTGTCAGCT 6723 TG T ACA__	TGI
	AGAGT GC CTGTCAGCT	
	TCTCA CG GACAGTCGA	
	_ C AGGACC CII	
GAM428 PTGIR	AGAGAT-CACAGGGTCAGCTTG 6721_ TTG CT	I
	GAG CACA GTCAGCTT	
	CTC GTGT CAGTCGAA	
	T TA_ CC I	
GAM428 PTGIR	AGAGAT-CACAGGGTCAGCTTG 6721 TGAG TTG CT	
	AG CACA GTCAGCTTG	
	TC GTGT CAGTCGAAC	
	_ TA_ CC	
GAM428 PTPN1	GAGAGTTGCTCCCTG-CAGATT 6724 ACA T CI	
	AGAGTTGC CTG CAG	
	TCTCAACG GAC GTC	
	AGG _ TA	
GAM428 PTPN1	GAGAGTTGCTCCCTG-CAGATT 6724 TG ACA T C G	
	AGAGTTGC CTG CAG TT	
	TCTCAACG GAC GTC AA	
	_ AGG _ T G	
GAM428 TCP11	TGAGTTGTTGCACACGGACAGCT 6727 A_ TGT TGI	
	TGAG GTTGCACAC CAGCT	
	ACTC CAACGTGTG GTCGA	
	AA CCT	
GAM428 TCP11	TGAGTTGTTGCACACGGACAGCT 6727 GAGA TGT I	
	GTTGCACAC CAGC	
	CAACGTGTG GTCG	
	TCAA CCT I	
GAM429 CDK7	AAACCAGAAT-TAAATTTTAA 6738 GGAAT GC	
	CTAGAA TAAATTTTAA	

GGTCTT ATTTAAAAAT
T_____ A_
GAM429 CDK7 AAACCAGAAT-TAAATTTTA 6738 TGGAAT GC
CTAGAA TAAATTTTT
||||| |||||||
GGTCTT ATTTAAAAA
_____ A_
GAM429 CNTNAP2 AATCTAGAAACTTGAATTCAATTTA 6735 GGAA A_ TTAII
TCTAGAAGCT AATTT
||||||||| |||||
AGATCTTTGA TTAAG
_____ AC TTAAA
GAM429 CREBL2 ATTTGGAAGCTAAATATTT 6741 GGAATCTA T
GAAGCTAAAT TTT
||||||||| |||
CTTCGATTTA AAA
AC_____ T
GAM429 CREBL2 ATTTGGAAGCTAAATATTT 6741 TGGAATCTA T
GAAGCTAAAT TTT
||||||||| |||
CTTCGATTTA AAA
C_____ T
GAM429 CRYGB GAAAC-ACAAGCTAAATATTTTA 6743 GGAATC G T AI
TA AAGCTAAAT TTT
|| ||||||| |||
GT TTCGATTTA AAA
TTT___ G T AT
GAM429 CRYGB GAAAC-ACAAGCTAAATATTTTA 6743 TGGAATC G T A
TA AAGCTAAAT TTT
|| ||||||| |||
GT TTCGATTTA AAA
TT_____ G T A
GAM429 DAZL AATCTAGAAACAATGCTAACTTTT 6733 GGAA TA_____ II
TCTAGAAGC AATTTTTA
||||||| |||||||
AGATCTTTG TTGAAAAT
_____ TTACGA TI
GAM429 DMD TACGATGTCAG---TACTTCCAAT 6750 AA_ T CAA
GAT TTAG TACTTCCAA
||| ||| |||||||
CTA AGTC ATGAAGGTT
ATG C ____
GAM429 DMD TACGATGTCAG---TACTTCCAAT 6750 TAA T CAA
GAT TTAG TACTTCCAAT
||| ||| |||||||
CTA AGTC ATGAAGGTTA
ATG C ____
GAM429 DSCR1 TGAATTGTATAAGCTAAATT 6751 TG CTAG_ TTT
GAAT AAGCTAAATT
||| |||||||

	CTTA TTCGATTTAA	
	A_ ACATA III	
GAM429 GPR48	GGAATCAAGTA---AAATTTTTA 6749 TAG CT	
	GGAATC AAG AAATTTTTA	
	III	
	CCTTAG TTC TTAAAAAT	
	___ AT	
GAM429 LECT2	AAGTTTGAATGAATACTTCC 6732 TAAGATTTTAGC AA	
	AATACTTCC	
	TTATGAAGG	
	TCAAACCTTAC___ AI	
GAM429 LNK	GGAAATTCTAGAAGCAAAAATTT 6746 ___ T_ TTAI	
	GGAA TCTAGAAGC AAATTT	
	CCTT AGATCTTCG TTAAA	
	TA TT IIIA	
GAM429 LNK	GGAAATTCTAGAAGCAAAAATTT 6746 T _ T_ TTAI	
	GGAAT CTAGAAGC AAATTT	
	CTTA GATCTTCG TTAAA	
	_ A TT CIII	
GAM429 LUZP1	AAGCTTTCGTCATACTTCC 6731 TA A AG_ AAT	
	AG TTTT CAATACTTCC	
	TC AAAG GTTATGAAGG	
	___ G GCA CII	
GAM429 LUZP1	AAGCTTTCGTCATACTTCC 6731 AGA AG_ I	
	TTTT CAATACTTC	
	AAAG GTTATGAAG	
	CG_ GCA I	
GAM429 MEN1	ATTCATCCCCACTTCCAAT 6742 GCAA I	
	TTTTA TACTTCCAA	
	AAAGT GTGAAGGTT	
	AGGG I	
GAM429 MEN1	ATTCATCCCCACTTCCAAT 6742 TAAGATTTTAGCAA	
	TACTTCCAA	
	GTGAAGGTT	
	GTAGGG_____	
GAM429 P23	AATGT-GAAG-TAAATTTT 6737 GGAATCTA C	
	GAAG TAAATTTT	
	CTTC ATTTAAAAA	
	ACA_____	
GAM429 P23	AATGT-GAAG-TAAATTTT 6737 TGGAATCTA C	
	GAAG TAAATTTT	

		CTTC ATTTAAAA		
		CA_____		
GAM429 PSCDBP	AATCTAGAAAATAAATATT	6736 GGAA	C	TTTT
	TCTAGAAG TAAAT			
	AGATCTTT ATTTA			
	_____ T TAAT			
GAM429 SEL1L	GGAAGCTGGGGGCTAAATTTGTA	6748	T AGAA	TTAI
	GGAA CT GCTAAATTT			
	CCTT GA CGATTTAAA			
	C CCCC CATI			
GAM429 SLC22A12	GAGTTTAGCAATCATTTCC	6745	T	ACTTCII
	GA TTTAGCAAT			
	CT AAATCGTTA			
	C GTAAAGG			
GAM429 SLC22A12	GAGTTTAGCAATCATTTCC	6745	TAAGAT	AC_ AA
	TTTAGCAAT TTCC			
	AAATCGTTA AAGG			
	_____ GTA AA			
GAM429 SMARCA3	AATCT-GACTGCTAAATTTCTA	6734	GGAA A A_	
	TCT GA GCTAAATTTTTA			
	AGA CT CGATTTAAAGAT			
	_____ _ GA			
GAM429 SMARCA3	AATCT-GACTGCTAAATTTCTA	6734	TGGAATCTA A_	
	GA GCTAAATTTTTA			
	CT CGATTTAAAGAT			
	GA_____ GA			
GAM429 TAF5	GAACATGGAAGCTAAATTT	6744	GGAATCTA	T
	GAAGCTAAATTTT			
	CTTCGATTTAAAG			
	TTGTAC_ I			
GAM429 TAF5	GAACATGGAAGCTAAATTT	6744	TGGAATCTA	
	GAAGCTAAATTTT			
	CTTCGATTTAAAGA			
	TGTAC_____			
GAM429 TCF12	ATCTAGAAGCTTGAAAAGTCTT	6740	GGAATC	AAATTTTAI
	TAGAAGCT			
	ATCTTCGA			
	_____ ACTTTTCAGA			
GAM429 TRIM34	AGTTTGTACCTGATACTTCCA	6739	TAAGATTTTAGCA	AT
	ATACTTCCA			

		TATGAAGGT		
		AAACATGGAC__ CC		
GAM429 ZNF264		GGGATCTATACGCTGAAAATTTTTA 6747 _ A GAA _ II		
		GGA TCTA GCT AAATTTTTA		
		CCT AGAT CGA TTTAAAAAT		
		C _ ATG CT II		
GAM429 ZNF264		GGGATCTATACGCTGAAAATTTTTA 6747 T A GAA _ II		
		GGA TCTA GCT AAATTTTTA		
		CCT AGAT CGA TTTAAAAAT		
		_ _ ATG CT TI		
GAM430 DLG5		GGATTTCAACCTCCTTGTTGGC 6754 TGGG _ CAGG		
		GTTTCAACT TGTTGGC		
		TAAAGTTGG ACAACCG		
		_ AGGA AGII		
GAM430 EPB41		TGAGGTT---CTTGTTGGCC 6758 TCAA A		
		TGGGGTT CTTGTTGGCC		
		ACTCAA GAACAACCGG		
		_ I		
GAM430 GOLGA4		GGTTTCAACTTGCTAGTCA 6756 TGGGG C		
		TTTCAACTTGTTGG CAG		
		AAAGTTGAACGATC GTT		
		A_ A		
GAM430 PSD		TGGGGTTTCA-CTACGTTGGCCAGG 6757 ACT I		
		TGGGGTTTCA TGTTGGCCAGG		
		ACCCCAAAGT GCAACCGGTCC		
		GAT I		
GAM430 SULT2A1		GGGTTTCAAC-TG-TAGCCA 6755 TGGG T T		
		GTTTCAACT GT GGCCA		
		CAAAGTTGA CA TCGGT		
		_ -		
GAM431 ARHC		TGTCCGGGGGGCTTTGCACA 6764 _CG TCAT		
		TGTCCGGGGGG C TGTACA		
		ACAGGCCCCC G ACGTGT		
		C AA IIIG		
GAM431 ARHC		TGTCCGGGGGGCTTTGCACA 6764 _CG II		
		TGTCCGGGGGG C TGTAC		
		ACAGGCCCCC G ACGTG		
		C AA TI		
GAM431 ARHGAP6		CGGGGGCCGCTTGT-CATC 6762 GTA_ II		
		CGGGGGCCGT CAT		

	GCCCCCGGCG	GTA	
	AACA	GI	
GAM431 ARHGAP6	CGGGGGCCGCTTGT-CATC	6762 TGTCCGGG	GTA_ A
	GGCCGT	CATC	
	CCGGCG	GTAG	
	_____	AACA	G
GAM431 HD	TGGCCGGGGGCCCTGTCCACCA	6765 T	G A TG
	TG CCGGGGGGCC	TGT CATCA	
	AC GGCCCCCGG	ACA GTGGT	
	C	G G	
GAM431 HD	TGGCCGGGGGCCCTGTCCACCA	6765 GT	G A I
	CCGGGGGGCC	TGT CATC	
	GGCCCCCGG	ACA GTGG	
	CC	G G I	
GAM431 MAPT	CGGGGGCCGGGT-CATTAT	6763	T A CAI
	CGGGGGCCG	GT CAT	
	GCCCCCGGC	CA GTA	
	C _	ATA	
GAM431 MAPT	CGGGGGCCGGGT-CATTAT	6763 TGTCCGGG	T A CA
	GGCCG	GT CAT	
	CCGGC	CA GTA	
	_____	C _	AT
GAM431 PSME3	CCGGGCCGGGCCGTGTCCGATC	6761	___ ACATIIIG
	CCGGG	GGCCGTGT	
	GGCCC	CCGGCACA	
	GGC	GGCTAGII	
GAM431 PSME3	CCGGGCCGGGCCGTGTCCGATC	6761 TGTCCGG	AC_ ATG
	GGGCCGTGT	ATC	
	CCCGGCACA	TAG	
	CCGG_	GGC GAG	
GAM432 ALDH1A3	CTGCAGCTA--GGATCGGAATTCC	6779	G CC TC
	CTGCAG	TA GG CGGAATTCC	
	GACGTC	AT CC GCCTTAAGG	
	G _	TA	
GAM432 ALDH1A3	CTGCAGCTA--GGATCGGAATTCC	6779 _	G CC TC I
	TGCAG	TA GG CGGAATTCC	
	ACGTC	AT CC GCCTTAAG	
	G	G _ TA I	
GAM432 ATP1B1	GCAGCTGCCGCGGTCCGGA	6780	_ AC
	GCAG	GT CCGTCCGG	

	CGTC CG GCCAGGCC		
	GA GC TII		
GAM432 ATP1B1	GCAGCTGCCGCGGTCCGGA 6780	AGGTAC	ATTC
	CTGC CGGTCCGGA		
	GACG GCCAGGCCT		
	TC GC_____ CCII		
GAM432 CNTN1	TGC-GGCACAG--CCGGAATTC 6787	_ A	C T
	GC GGTAC GG CCGGAATT		
	CG CCGTG TC GGCCTTAA		
	A _ _ _		
GAM432 CNTN1	TGC-GGCACAG--CCGGAATTC 6787	CT A	C T
	GC GGTAC GG CCGGAATT		
	CG CCGTG TC GGCCTTAA		

GAM432 FCN2	TGCAGGTACGCGGGCCTGGGAA 6785	_ T _	AIII
	TGCAGGTAC CGG CC GG		
	ACGTCCATG GCC GG CC		
	C C A CTTI		
GAM432 FCN2	TGCAGGTACGCGGGCCTGGGAA 6785	CT _ T _	TTCC
	GCAGGTAC CGG CC GGAA		
	CGTCCATG GCC GG CCTT		
	_____ C C AC CIII		
GAM432 GYG	CTGCAGGTAACCATCAGAGAA 6773	_ GTC	ATTCC
	CTGCAGGTA CCG CGGA		
	GACGTCCAT GGT GTCT		
	T A _ CTTII		
GAM432 GYG	CTGCAGGTAACCATCAGAGAA 6773	T _ G C	AI
	GCAGGTA CCG TC GG		
	CGTCCAT GGT AG CT		
	_ T _ T CT		
GAM432 HTR6	CTGCAGGTAAGGGGCCTGGA 6772	CC_ C	ATTC
	CTGCAGGTA GGTC GGA		
	GACGTCCAT CCGG CCT		
	TCC A IIIC		
GAM432 HTR6	CTGCAGGTAAGGGGCCTGGA 6772	CC_ C	II
	CTGCAGGTA GGTC GG		
	GACGTCCAT CCGG CC		
	TCC A TI		
GAM432 IRS2	GCAGGTACCTGCACTGGAAT 6781	G CC_	II
	GCAGGTACC GT GGAA		

	CGTCCATGG CG CCTT	
	A TGA AI	
GAM432 IRS2	GCAGGTACCTGCACTGGAAT 6781 CTGC G CC_	
	AGGTACC GT GGAATTC	
	TCCATGG CG CCTTAGG	
	____ A TGA	
GAM432 LAMR1	CTGCAGGTA---GCACGGAA 6776 ACC TC TT	
	CTGCAGGT GG CGGAA	
	GACGTCCA TC GCCTT	
	____ GT II	
GAM432 LAMR1	CTGCAGGTA---GCACGGAA 6776 _ ACC TC	
	TGCAGGT GG CGGA	
	ACGTCCA TC GCCT	
	G ____ GT	
GAM432 MARK3	CTGC-GGAA--GGATCGGAATTCC 6778 A TACC TC	
	CTGC GG GG CGGAATTCC	
	GACG CC CC GCCTTAAGG	
	_ TT_ TA	
GAM432 MARK3	CTGC-GGAA--GGATCGGAATTCC 6778 _ A TACC TC	
	TGC GG GG CGGAATTC	
	ACG CC CC GCCTTAAG	
	G _ TT_ TA	
GAM432 MARK3	CTGCTGGCCGCCGCTGCGGAATTCC 6770 A A_ GTC II	
	CTGC GGT CCG CGGAATTCC	
	GACG CCG GGC GCCTTAAGG	
	A GC GAC II	
GAM432 MARK3	CTGCTGGCCGCCGCTGCGGAATTCC 6770 T A A_ GTC I	
	GC GGT CCG CGGAATTC	
	CG CCG GGC GCCTTAAG	
	_ A GC GAC I	
GAM432 MYBPH	GCAGGTACCAGGGGCGG--TTCC 6782 _ _ TC AATTCI	
	CAGGTACC GG CGG	
	GTCCATGG CC GCC	
	C T CC AAG	
GAM432 MYBPH	GCAGGTACCAGGGGCGG--TTCC 6782 CTGC _ TC AA	
	AGGTACC GG CGG TTCC	
	TCCATGG CC GCC AAGG	
	____ T CC ____	
GAM432 NRIP1	GCAGGTACC--ACAGGAAT 6784 GTCC I	
	GCAGGTACCG GGAA	

	CGTCCATGGT CCTT		
	GT__ A		
GAM432 NRIP1	GCAGGTACC--ACAGGAAT 6784 CTGC GTCC T		
	AGGTACCG GGAAT		
	TCCATGGT CCTTA		
	____ GT__ C		
GAM432 PHKG2	AGGTACCGGGCTGGTCTTC 6768 TCC AATTII		
	AGGTACCGG GG		
	TCCATGGCC CC		
	CGA AGAAGI		
GAM432 PHKG2	AGGTACCGGGCTGGTCTTC 6768 CTGCAGGT TCC AA		
	ACCGG GG TTC		
	TGGCC CC AAG		
	____ CGA AG		
GAM432 POLR2E	CTGCAGGGAAAGGCAGCCGGAATTC 6771 TACC __ CII		
	CTGCAGG GGT CCGGAATTC		
	GACGTCC CCG GGCCTTAAG		
	CTTT TC		
GAM432 POLR2E	CTGCAGGGAAAGGCAGCCGGAATTC 6771 TG TACC __ I		
	CAGG GGT CCGGAATT		
	GTCC CCG GGCCTTAA		
	__ CTTT TC I		
GAM432 RPL18	CTGCTCGGCCAGGTCCGGAA 6777 A_ ACC TTC		
	CTGC GGT GGTCCGGAA		
	GACG CCG CCAGGCCTT		
	AG GT_		
GAM432 RPL18	CTGCTCGGCCAGGTCCGGAA 6777 A_ ACC I		
	TGC GGT GGTCCGGA		
	ACG CCG CCAGGCCT		
	AG GT_ I		
GAM432 RTN2	CTCCAGCGGCGGGTCCGGAA 6775 T__ A ACC I		
	GC GGT GGTCCGGA		
	CG CCG CCAGGCCT		
	AGGT _ C__ I		
GAM432 RTN2	CTCCAGCGGCGGGTCCGGAA 6775 CT__ A ACC TTC		
	GC GGT GGTCCGGA		
	CG CCG CCAGGCCTT		
	GAGGT _ C__		
GAM432 SLC6A3	CTGCATGCGT-CCGGTCCGG 6769 G A_ AATTC		
	CTGCA GT CCGGTCCGG		

	GACGT CG GGCCAGGCC			
	A CA III CC			
GAM432 SLC6A3	CTGCATGCGT-CCGGTCCGG	6769	G A_ II	
	CTGCA GT CCGGTCCG			
	II			
	GACGT CG GGCCAGGC			
	A CA CI			
GAM432 TDRD1	TGCAG-TCCCCCTGCCGGAATTC	6786	GTA G_ T I	
	GCAG CC G CCGGAATT			
	II			
	CGTC GG C GGCCTTAA			
	AGG GA_ I			
GAM432 TDRD1	TGCAG-TCCCCCTGCCGGAATTC	6786 CT	GTA G_ T C	
	GCAG CC G CCGGAATTC			
	II			
	CGTC GG C GGCCTTAAG			
	_ AGG GA_ T			
GAM432 UNG	GCTGGGCCCCGGTCCGGGAATT	6783 CA TA	AATI	
	GG CCGGTCCGG			
	II			
	CC GGCCAGGCC			
	A_ CG CTTA			
GAM432 UNG	GCTGGGCCCCGGTCCGGGAATT	6783 CTGCA TA	_ CC	
	GG CCGGTCCGG AATT			
	II			
	CC GGCCAGGCC TTAA			
	A_ CG C CC			
GAM432 ZYX	CTGC--GTCCCGGTCCGGA	6774 AG A	ATT	
	CTGC GT CCGGTCCGGA			
	II			
	GACG CA GGCCAGGCCT			
	_ G III			
GAM432 ZYX	CTGC--GTCCCGGTCCGGA	6774 AG A	I	
	CTGC GT CCGGTCCGG			
	II			
	GACG CA GGCCAGGCC			
	_ G T			
GAM433 ADRA1A	TGTCAGTAGGTTGAGCCTGAAA	6799 G _ CA	CCA	
	TG CAGT GGT AGCCTGAAA			
	II			
	AC GTCA CCA TCGGACTTT			
	A T AC III			
GAM433 ADRA1A	TGTCAGTAGGTTGAGCCTGAAA	6799 GG _ CA	I	
	CAGT GGT AGCCTGAA			
	GTCA CCA TCGGACTT			
	A_ T AC I			
GAM433 ALEX3	TGGGACTGGGCTCAAGCCTG	6800 CAG _	AAACC	
	TGG TGG TCAAGCCTG			

	ACC ACC AGTTCGGAC			
	CTG CG IIIAC			
GAM433 ALEX3	TGGGACTGGGCTCAAGCCTG 6800 CAG _ III			
	TGG TGG TCAAGCCT			
	III III IIIIIII			
	ACC ACC AGTTCGGA			
	CTG CG CII			
GAM433 AQP6	GGCCTTGG---AGCCTGAAA 6798 AG TCA I			
	GGC TGG AGCCTGA			
	III III IIIIIII			
	CCG ACC TCGGACT			
	GA _ T			
GAM433 AQP6	GGCCTTGG---AGCCTGAAA 6798 TG AG TCA C			
	GC TGG AGCCTGAAA			
	II III IIIIIII			
	CG ACC TCGGACTTT			
	_ GA _ C			
GAM433 ATP2C1	TGACAGTGGTCACATCCTG 6801 AG_ AAACC			
	TGGCAGTGGTCA CCTG			
	IIIIIIII III			
	ACTGTCACCAGT GGAC			
	GTA IIIAC			
GAM433 ATP2C1	TGACAGTGGTCACATCCTG 6801 AG_ II			
	TGGCAGTGGTCA CCT			
	IIIIIIII III			
	ACTGTCACCAGT GGA			
	GTA CI			
GAM433 FZD4	TGACAGTGGTCATGTACTGAA 6802 AGC_ ACCA			
	TGGCAGTGGTCA CTGAA			
	IIIIIIII III			
	ACTGTCACCAGT GACTT			
	ACAT IIIA			
GAM433 FZD4	TGACAGTGGTCATGTACTGAA 6802 G AGC_ I			
	GCAGTGGTCA CTGA			
	IIIIIIII III			
	TGTCACCAGT GACT			
	_ ACAT I			
GAM433 GOT2	CAGTGGGTGAAGCCTGAACCCA 6791 A TC_ A I			
	GTGG AAGCCTGAA CC			
	III IIIIIII II			
	CACC TTCGGACTT GG			
	_ CAC G I			
GAM433 GOT2	CAGTGGGTGAAGCCTGAACCCA 6791 TGGCAGT C A			
	GGT AAGCCTGAA CCA			
	III IIIIIII III			
	CCA TTCGGACTT GGT			
	AC_ C G			
GAM433 NBS1	GCAATGACAAAGCCTGAAAACA 6793 TC CCI			
	CAGTGG AAGCCTGAAA			
	IIIIII IIIIIIIII			

	GTTACT TTCGGACTTT			
	GT TGI			
GAM433 NBS1	GCAATGACAAAGCCTGAAAACA 6793	TGGC TC CCA		
	AGTGG AAGCCTGAAA			
	TTACT TTCGGACTTT			
	___ GT TGT			
GAM433 OGG1	GCAGTGGTCA---CAGAACCCA 6795	___ AAAl		
	GCAGTGGTCA AGCCTG			
	CGTCACCAGT TTGGGT			
	GTC IIIA			
GAM433 OGG1	GCAGTGGTCA---CAGAACCCA 6795	TGGC AGCCT A		
	AGTGGTCA GAA CC			
	TCACCAGT CTT GG			
	___ GT___ G			
GAM433 PNOC	TGGCAGTGG-CAAGTC-AAAACC 6805	T CC A		
	TGGCAGTGG CAAG TGAAACC			
	ACCGTCACC GTTC GTTTTGG			
	_ A_ I			
GAM433 PNOC	TGGCAGTGG-CAAGTC-AAAACC 6805	_ T CC I		
	GGCAGTGG CAAG TGAAAC			
	CCGTCACC GTTC GTTTTG			
	A _ A_ I			
GAM433 RECK	TGGCAGTGGTCTACCAGGAA 6803	AA T_ ACC		
	TGGCAGTGGTC GCC GAA			
	ACCGTCACCAG TGG CTT			
	A_ TC			
GAM433 RECK	TGGCAGTGGTCTACCAGGAA 6803	AA TGAI		
	GGCAGTGGTC GCC			
	CCGTCACCAG TGG			
	A_ TCCT			
GAM433 RGS9	GCGGTGGCTCAAGCCTGTAA 6792	A _ AAII		
	GC GTGG TCAAGCCTG			
	CG CACC AGTTCGGAC			
	C G ATTI			
GAM433 RGS9	GCGGTGGCTCAAGCCTGTAA 6792	TGGCA _ AAACC		
	GTGG TCAAGCCTG			
	CACC AGTTCGGAC			
	C___ G ATTAG			
GAM433 RNH	AGTGGTCAAGGCAGAGAACA 6790	_ CT_ ACCI		
	GTGGTCAAG C GAA			

		CACCAGTTC G CTT			
		C TCT GIII			
GAM433 RNH	AGTGGTCAAGGCAGAGAACA	6790 T_____	T TCA	GAAACC	
	GGCAG GG AGCCT				
	CCGTC CT TCGGG				
	CAGTT T TG_ IIIACC				
GAM433 SERPINB9	GCGGTGGCTCAAGCCTGTAA	6792 A _	AAII		
	GC GTGG TCAAGCCTG				
	CG CACC AGTTCGGAC				
	C G ATTI				
GAM433 SERPINB9	GCGGTGGCTCAAGCCTGTAA	6792 TGGCA _	AAACC		
	GTGG TCAAGCCTG				
	CACC AGTTCGGAC				
	C_____ G ATTAG				
GAM433 SHOX	GGCAGTGGTTCATGCTTGTA	6796 G _	A C AAI		
	CAGTGGT CA GC TG				
	GTCACCA GT CG AC				
	_ A A A ATI				
GAM433 SHOX	GGCAGTGGTTCATGCTTGTA	6796 TG _	A C AAACCA		
	GCAGTGGT CA GC TG				
	CGTCACCA GT CG AC				
	_ A A A ATTAI				
GAM433 SLC14A2	GGC-GTGCTGAAGCCTGAA	6797 A GTC	I		
	GGC GTG AAGCCTGA				
	CCG CAC TTCGGA				
	_ GAC T				
GAM433 SLC14A2	GGC-GTGCTGAAGCCTGAA	6797 TG A GTC	AC		
	GC GTG AAGCCTGAA				
	CG CAC TTCGGA				
	_ _ GAC AI				
GAM433 SLC26A4	GCAGGGGTC---CTGAAACCA	6794 _ T CAAG			
	CAG GGT CCTGAAACC				
	GTC CCA GGA				
	C C _____				
GAM433 ZNF264	TGGCAGAG---AAGCCTGAAA	6804 T TCA	C		
	TGGCAG GG AGCCTGAAA				
	ACCGTC CT TCGGA				
	T _____ I				
GAM433 ZNF264	TGGCAGAG---AAGCCTGAAA	6804 _ T TCA			
	GGCAG GG AGCCTGAA				

CCGTC CT TCGGACTT
A T ____

GAM434 CARD12 AAAGCTTCCCACCTTTCTAT 6809 AAAC C__ I
CTTCCCACC CTGT
||||||| ||||
GAAGGGTGG GATA
TC__ AAA I

GAM434 CARD12 AAAGCTTCCCACCTTTCTAT 6809 TGCAAAC C__ T
CTTCCCACC CTGTA
||||||| ||||
GAAGGGTGG GATAT
C_____ AAA T

GAM434 ENO2 GCAAGACCT-CCCACCCCAGT 6815 AC TGI
CAA CTTCCCACCCC
||| |||||||||
GTT GGAGGGTGGGG
CT TCI

GAM434 ENO2 GCAAGACCT-CCCACCCCAGT 6815 TG AC T AT
CAA CTTCCCACCCC GT
||| ||||||||| ||
GTT GGAGGGTGGGG CA
__ CT T GI

GAM434 FTSJ2 CCTTCCCACAGTCTGTTTT 6813 CC_ ATII
CCTTCCCAC CTGT
||||||| ||||
GGAAGGGTG GACA
TCA AAAl

GAM434 LEP CAAACATTCCCCACCCCTG 6810 C_ II
CAAAC TTCCCACCCCT
||||| |||||||||
GTTTG AGGGGTGGGGA
TA CI

GAM434 LEP CAAACATTCCCCACCCCTG 6810 TGCAAACC TAT
TTCCCACCCCTG
|||||||||
AGGGGTGGGGAC
TTGTA__ CCI

GAM434 NUMA1 CAAA---TCCCACCCCAGT 6812 CAAACCT TG
TCCCACCCC
|||||||
AGGGTGGGG
GTTT__ TC

GAM434 NUMA1 CAAA---TCCCACCCCAGT 6812 TGCAAACCT T
TCCCACCCC GT
||||||| ||
AGGGTGGGG CA
TT_____ T

GAM434 SPG4 CAAACCTTCAAACCTTCTCTATT 6811 A CC C_ G I
AACCTTC ACC CT TAT
||||||| ||| || |||

	TTGGAAG TGG GA ATA	
	— TT AA G I	
GAM434 SPG4	CAAACCTTCAAACCTTCTCTATT 6811 TGCA CC C_ G I	
	AACCTTC ACC CT TATT	
	TTGGAAG TGG GA ATAA	
	— TT AA G A	
GAM434 TCF20	TGAAAACATGGACCATCCCTGTATT 6816 C CTTC_ C II	
	TG AAAC CCA CCCTGTATT	
	AC TTTG GGT GGGACATAA	
	T TACCT A II	
GAM434 TCF20	TGAAAACATGGACCATCCCTGTATT 6816 GC CTTC_ C I	
	AAAC CCA CCCTGTAT	
	TTTG GGT GGGACATA	
	T_ TACCT A I	
GAM434 TSLP	AAACTCTTCCCACCACGAGTGTA 6808 _ CCTGTIIIT	
	AAAC CTTCCCACC	
	TTTG GAAGGGTGG	
	A TGCTCACAT	
GAM434 TSLP	AAACTCTTCCCACCACGAGTGTA 6808 TGCAAAC CC__ TTI	
	CTTCCCACC TGTA	
	GAAGGGTGG ACAT	
	GA__ TGCTC TCT	
GAM434 ZNF148	GCAACAGCT-CCCACCCCTG 6814 ACC II	
	GCAA TTCCCACCCCT	
	CGTT GAGGGTGGGGA	
	GTC CI	
GAM434 ZNF148	GCAACAGCT-CCCACCCCTG 6814 TG ACC AT	
	CAA TTCCCACCCCTGT	
	GTT GAGGGTGGGGACG	
	_ GTC II	
GAM435 BRCA1	ATGAATATGCCTGGTAGAAGACT 6821 G_ A T TCI	
	TGAATATGC GG TA AAG	
	ACTTATACG CC AT TTC	
	GA _ C TGI	
GAM435 BRCA1	ATGAATATGCCTGGTAGAAGACT 6821 TA G_ A T T I	
	TGAATATGC GG TA AAG CT	
	ACTTATACG CC AT TTC GA	
	_ GA _ C T A	
GAM435 DMC1	TGAATATGCAGTTTGATAT 6824 GATAIII	
	TGAATATGCGG	

	ACTTATACGTC			
	AAACTAT			
GAM435 DMC1	TGAATATGCAGTTTGATAT	6824 TATG	___	AAGTC
	AATATGCGG GATAT			
	TTATACGTC CTATA			
	___ AAA AT			
GAM435 NLGN1	ATGTAAA-GAGGGATATAA	6820 ATGAATATGC		I
	GGGATATA			
	CCCTATAT			
	TACATTTCT_ T			
GAM435 NLGN1	ATGTAAA-GAGGGATATAA	6820 TATGAATATGC		GT
	GGGATATAA			
	CCCTATATT			
	ACATTTCT___ GI			
GAM435 TGM4	TGAATCTGCCCTCATATAAGTC	6825 TATGAATA GGG_		T
	TGC ATATAAGTC			
	ACG TATATTCAG			
	TTAG___ GGAG T			
GAM435 TP53	TATAAAAATG--GGATATAA	6823 TATGC		GT
	TATGAA GGGATATAA			
	ATATTT CCCTATATT			
	TTA___ II			
GAM435 TP53	TATAAAAATG--GGATATAA	6823 ATGAATATGC		I
	GGGATATA			
	CCCTATAT			
	ATATTTTTA_ I			
GAM435 TPM1	ATGCGGGATCCAT-AGTCT	6822 ATA_ II		
	ATGCGGGAT AGTC			
	TACGCCCTA TCAG			
	GGTA AI			
GAM435 ZNF16	ATGAATATGCAGCCTCCATAA-TCT	6819 GA___		GTCT
	GAATATGCGG TATAA			
	CTTATACGTC GTATT			
	GGAG A			
GAM435 ZNF16	ATGAATATGCAGCCTCCATAA-TCT	6819 TA	GA___	G I
	TGAATATGCGG TATAA TCT			
	ACTTATACGTC GTATT AGA			
	___ GGAG _ A			
GAM436 ALDH3A2	TAA-AAT-TGATGCCAATTT	6852 TA A C		CT
	AGAAT TG TGCCAATTT			

	TTTTA AC ACGGTAAAA	
	A_ _ T II	
GAM436 ARSD	AAGCAGATGCTGCCATGCTTCTGT 6830 TA AAT A_ I	
	AG ATGCTGCCA TTTCTGT	
	II IIIIIII IIIII	
	TC TACGACGGT GAAGACA	
	_ GTC AC C	
GAM436 ATP10C	GAATGAGGTGC-AATTTCTGT 6842 TAAGAATATGC C	
	TGC AATTTCTG	
	III IIIIIII	
	ACG TTAAAGAC	
	ACTCC _____	
GAM436 ATRX	TAAGAATAT--TGCACACAATTCTGT 6848 _ T _ T I	
	TAAGAATAT GC GC CAATT CTGT	
	IIIIIIII II II IIII III	
	ATTCTTATA CG TG GTTAA GACA	
	A _ T _ I	
GAM436 BCL11B	AAGAATATGCTG-CAATTTCT 6832 TA C G	
	AGAATATGCTGC AATTTCT	
	IIIIIIII IIIII	
	TCTTATACGACG TTAAAGA	
	_ _ A	
GAM436 CCNT2	TAAGAATATGGTGTCA--TTCTG 6854 C C AT T	
	TAAGAATATG TG CA TTCTG	
	IIIIIIII II II IIII	
	ATTCTTATAC AC GT AAGAC	
	C A _ I	
GAM436 CKTSF1B1	AAGATTACTGCTGCCAACTT 6828 TA ATA_ CTG	
	AGA TGCTGCCAATTT	
	III IIIIIIIII	
	TCT ACGACGGTTGAA	
	_ AATG TII	
GAM436 DAZL	ATAGTGCTTTCAATTTCTG 6840 TAAGAATAT GC	
	GCT CAATTTCTG	
	III IIIIIII	
	CGA GTTAAAGAC	
	_____ AA	
GAM436 DCX	TAA-AATATGCTGTAACATTTC 6850 TA CCA_ TGT	
	AGAATATGCTG ATTTC	
	IIIIIIII IIII	
	TTTTATACGAC TAAAG	
	A_ ATTG III	
GAM436 FGF5	TAAGAATATTTCTGACAAAT 6846 G_ C TTCTG	
	TAAGAATAT CTG CAAT	
	IIIIIIII III IIII	
	ATTCTTATA GAC GTTA	
	AA T IIITG	
GAM436 FHL1	ATATGCTGCTTTATTTCTGT 6841 TAAGAATA GCCA	
	TGCT ATTTCTG	
	III IIIIIII	

ACGA TAAAGAC
 G_____ AA____
 GAM436 GAD1 AAGAATATG-T-CCATTTTC 6831 TA CTG A
 AGAATATG CCA TTTCT
 ||||| || |||||
 TCTTATAC GGT AAAGG
 _____ A_ A
 GAM436 GALK2 AGAAAGTCCTGCCAATTCCT 6837 TAAGAATATG
 CTGCCAATTTCTG
 |||||
 GACGGTTAAGGAT
 TTTTCAG_____
 GAM436 HOXB3 AGGAT-TG-TGTCAATTTCTG 6838 TAAGAATA C C
 TG TG CAATTTCTG
 || || |||||
 AC AC GTTAAAGAC
 CTA_____ _ A
 GAM436 IPP TAGGATATCTGCTGCCAAT 6845 TAAGAATA_ TTCTG
 TGCTGCCAAT
 |||||
 ACGACGGTTA
 ATCCTATAG IIITG
 GAM436 KITLG TAA-AACATTCTGTTCCAATTTCTG 6847 TA G _ TI
 AGAATAT CTG CCAATTTCTG
 ||||| || |||||
 TTTTGTA GAC GGTAAAGAC
 A_ A AA II
 GAM436 LEF1 AATAGGGCTGCCAATTGCT 6836 TAAGAATAT T G
 GCTGCCAATT CT
 ||||| ||
 CGACGGTTAA GA
 CC_____ C T
 GAM436 OGT TAGGAATATGCTGGCTTGAATTT 6849 TAA CCAATTTCTGTI
 GAATATGCTG
 |||||
 CTTATACGAC
 ATC CGAACTTAAAI
 GAM436 PCDHA9 AAGCATTTTCT-CCAATTTCTGT 6835 TA AATATG G
 AG CT CCAATTTCTGT
 || || |||||
 TC GA GGTAAAGACA
 _ GTAAAA _
 GAM436 PDE4D AGAAAATTATGC-AATTTCTGT 6839 T A TGCC
 AAGA TATGC AATTTCTGT
 ||| ||| |||||
 TTTT ATACG TTAAAGACA
 _ A _____
 GAM436 PPP4R1 TAAGGAAAATGCTCTGCCAATT 6844 TAA_ T _ TCTGT
 GAA ATGCT GCCAATT
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	CTT TACGA CGGTTAA		
	ATTC T GA IIITG		
GAM436 PRKY	TAAGAAAATACTGCCAATT 6851	T	TCTG
	TAAGAA ATGCTGCCAATT		
	ATTCTT TATGACGGTTAA		
	T IIIT		
GAM436 PTPRA	AAGCCTATG-TACCAATTTCT 6833	TA AA C	
	AG TATG TGCCAATTTCTG		
	TC ATAC ATGGTTAAAGAT		
	_ GG _		
GAM436 RAD18	AAGAATATGC-GCAATGTTTCT 6829	TA T CAA_ T	
	AGAATATGC GC TTTCTG		
	TCTTATACG CG AAAGAT		
	_ _ TTAC I		
GAM436 SCA1	TAAGAATAT-TTAAAAATTTCT 6853	GCTGCC	GT
	TAAGAATAT AATTTCT		
	ATTCTTATA TTAAAGA		
	AATTT_ II		
GAM436 SFRS1	TAAGGTCAATA-CTGCCAATTTCT 6843	AAT_ TGT	
	TAAG ATGCTGCCAATTTCT		
	ATTC TATGACGGTTAAAG		
	CAGT III		
GAM436 SHMT2	AAGAC-ATGGGCCCAATTTCTGT 6834	TA A CTG	
	AGA TATG CCAATTTCTGT		
	TCT GTAC GGTAAAGACA		
	_ _ CCG		
GAM436 TRAF5	TAAGAATATGAT-C-ATTTCTGT 6855	CTGCCA	
	TAAGAATATG ATTTCTGT		
	ATTCTTATAC TAAAGACA		
	TAG_		
GAM437 ALDH3A2	TAAGATGT---AGAATTCTATAAC 6868	ATA G _ G	
	TAAGATGT AGAA TCT TAAC		
	ATTCTACA TCTT AGA ATTG		
	_ A T I		
GAM437 C11orf8	AGA-GTATGAAAAGAAGTCTT 6864	TAAG TAT AAC	
	ATG AAGAAGTCTT		
	TAC TTCTTCAGAA		
	TCA_ TT_ AAI		
GAM437 ENAM	AAGATGTATCCTAAGAAATCT 6858	TA _ AACG	
	AGATGTA TAAGAAGTCTT		

	TCTACAT ATTCTTTAGAG		
	___ AGG III G		
GAM437 F2R	TAAGATGGGTAGAGAAGTCTT 6867	TA _	AACG
	TAAGATG TA AGAAGTCTT		
	ATTCTAC AT TCTTCAGAA		
	CC C III G		
GAM437 FIGF	AAAATGCAGA-GAAGTCTT 6860	TA TA	AA
	AGATGTA AGAAGTCTT		
	TTTACGT TCTTCAGAA		
	___ C_ CI		
GAM437 MEN1	AATATGAACCTGAAGTCTTAA 6862	TAAG T AA	CG
	ATG AT GAAGTCTTAA		
	TAC TG CTTCAGAATT		
	TA___ T GA CI		
GAM437 PLA2R1	TAAGCTTATGTATAAGACATTTTAA 6865	TAAG___	A C CGI
	ATGTATAAGA GT TTAA		
	TACATATTCT TA AATT		
	ATTCGAA G A III G		
GAM437 RFC4	AGATGGTCTC-GAAGTCTTA 6863	TAAGATGTATAA	AC
	GAAGTCTTA		
	CTTCAGAAT		
	TACCAGAG___ CG		
GAM437 SNRPA	AAG-TGTTGAGGTAAGTCTTAA 6859	TA A ATAAG_	CG
	AG TGT AAGTCTTAA		
	TC ACA TTCAGAATT		
	___ _ ACTCCA TI		
GAM437 SPAP1	TAAGGTTTTATAGCAAGTCTTAA 6866	ATG_ AG	CGI
	TAAG TATA AAGTCTTAA		
	ATTC ATAT TTCAGAATT		
	CAAA CG III		
GAM437 SUV39H2	AAGAT---TAAGAAGTCTT 6861	TA GTA	A
	AGAT TAAGAAGTCTT		
	TCTA ATTCTTCAGAA		
	___ ___ A		
GAM438 BCAT1	AGATGT--GCAGATGT-TCC 6875	AGAGATGTA	G
	TGCAGATGT TCC		
	ACGTCTACA AGG		
	TAC_____ _		
GAM438 BCL11A	AGA-ATGTATGCAGCATG-GTC 6873	A _ T CA	
	AGAG TGTATGCAG ATG GTC		

TCTT ACATACGTC TAC CAG
 _ G _ II
 GAM438 DDEF1 AGAGATGTAAGTGCTAGATG 6871 _ _ TGTCCA
 AGAGATGTA TGC AGATG
 ||||| |||||
 TCTCTACAT ACG TCTAC
 TC A IIITAC
 GAM438 DEFA6 AGAGCAGGA-GCAGATGTGT 6874 ATGTAT CCA
 AGAG GCAGATGTGT
 ||| |||||
 TCTC CGTCTACACA
 GTCCT_ III
 GAM438 ERBB4 ATAGCATGGGTGTTTCAACCATCTGCTT6880 A ATG_ _ III
 ATAGCATGG TGT CATCT CTT
 ||||| || |||||
 TATCGTACC ACA GTAGA GAA
 C AAGTTG C III
 GAM438 EXTL3 ATGTATGCAAGTGTGTGCAT 6883 AGAGATGT A C
 ATGCAG TGTGT CA
 ||||| |||||
 TACGTT ACACA GT
 _ _ C C
 GAM438 GPR48 AGATGTATGGAAAT-T-CCAT 6877 AGAG C GTG
 ATGTATG AGAT TCCA
 ||||| |||||
 TACATAC TTTA AGGT
 _ _ C A_
 GAM438 KCNS3 AGCATGGATTACATGCAT 6878 G_ III
 AGCATGGAT TATGCA
 ||||| |||||
 TCGTACCTA GTACGT
 AAT AII
 GAM438 KCNS3 AGCATGGATTACATGCAT 6878 ATAG G_ CTCT
 CATGGAT TATGCAT
 ||||| |||||
 GTACCTA GTACGTA
 _ _ AAT ACII
 GAM438 LDHB GAGATGTATGGATAAATGT 6884 AG C_ GTCCA
 AGATGTATG AGATGT
 ||||| |||||
 TCTACATAC TTTACA
 _ CTA AIIIT
 GAM438 LNK GATGT---CAGATGTGTCC 6885 AGAGATGTATG
 CAGATGTGTC
 |||||
 GTCTACACAG
 CA_
 GAM438 PROS1 TGGATGTATGTTTCAT-TCTT 6886 _ _ CTII
 TGGATGTATG CAT CT
 ||||| |||||

ACCTACATAC GTA GA
AA A AIII

GAM438 SLC16A7 ATAGCATGGATTCTTTCTATGCAT 6879 G_____ CTCTTI
ATAGCATGGAT TATGCAT
||||||| |||||
TATCGTACCTA ATACGTA
AGAAAG IIITTC

GAM438 SLC16A7 ATAGCATGGATTCTTTCTATGCAT 6879 G_____ IIIA
ATAGCATGGAT TATGCA
||||||| |||||
TATCGTACCTA ATACGT
AGAAAG AIII

GAM438 TGFBR2 ATCGCATGGATGGGGACATCTGTT 6882 A TAT CI
GCATGGATG GCATCT
||||||| |||||
CGTACCTAC TGTAGA
G CCC CI

GAM438 TGFBR2 ATCGCATGGATGGGGACATCTGTT 6882 ATA TAT CTTI
GCATGGATG GCATCT
||||||| |||||
CGTACCTAC TGTAGA
TAG CCC CAAI

GAM438 TRIM9 ATAGTA--GTTGTATGCATCT 6881 CA A CT
ATAG TGG TGTATGCATCT
||| ||| |||||
TATC ATC ACATACGTAGA
_ A II

GAM438 TRIM9 ATAGTA--GTTGTATGCATCT 6881 _ CA A I
TAG TGG TGTATGCATC
||| ||| |||||
ATC ATC ACATACGTAG
T _ A I

GAM438 TRPM2 AGCTGCGTG-AGATGTGTCC 6876 AGAGA TA C A
TG TG AGATGTGTCC
|| || |||||
AC AC TCTACACAGG
G_____ GC _ G

GAM438 ZNF36 AGAGATGTATTTGGAGTTGTTGTTGCCAT6872 GCA TG CCATIIIA
AGAGATGTAT GA TGT
||||||| || |||
TCTCTACATA CT ACA
AAC CA A_____

GAM439 CACNA1C AATTCCT--TGTTTCTTG 6892 TAGAATTA AAA
TCT TGTTTCTT
||| |||||
AGG ACAAAGAA
_____ GA_

GAM439 DDX1 AGAATTC-CTAAGACTAATGTTTCTTGA6893 TA A _____ III
GAATT TCTAA ATGTTTCTTGA
|||| ||||| |||||

		CTTAA GGATT TACAAAGAACT		
		— _ CTGAT GII		
GAM439 DLX4	AAATA-CTCAATGTTTCTTG	6891 ATTAT A	I	
	CT AATGTTTCTT			
	II			
	GA TTACAAAGAA			
	TTTAT G I			
GAM439 DLX4	AAATA-CTCAATGTTTCTTG	6891 TAGAATTAT A		
	CT AATGTTTCTTG			
	II			
	GA TTACAAAGAAC			
	AT_____ G			
GAM439 ECM2	TAGAATTATAGAAAAGTTTC	6901	CT T TTG	
	TAGAATTAT AAA GTTTC			
	III			
	ATCTTAATA TTT CAAAG			
	TC T III			
GAM439 EPHA3	TATAAAAATATAAATGTTTC	6902__ T TC	TTG	
	TAGAA TA TAAATGTTTC			
	II			
	ATTTT AT ATTTACAAAG			
	AT T _ III			
GAM439 ERBB2IP	GAATTTATCTCCCTGATGTTTCTT	6896 AAT AA__	I	
	TATCT ATGTTTCT			
	ATAGA TACAAAGA			
	__ GGGAC I			
GAM439 ERBB2IP	GAATTTATCTCCCTGATGTTTCTT	6896 TAGAA AA__	I	
	TTATCT ATGTTTCTTGA			
	AATAGA TACAAAGAATT			
	TA__ GGGAC I			
GAM439 FLRT2	ATT-TCTAAATGTCTTTCT	6894 ATTA	CII	
	TCTAAATGTTT			
	AGATTTACAGA			
	TAA_ AAG			
GAM439 FOXO1A	TAGAACCATTTAAATGTTT	6900 C	CTTG	
	TAGAATTAT TAAATGTTT			
	ATCTTGGTA ATTTACAAA			
	A IIIA			
GAM439 FOXO1A	TAGAACCATTTAAATGTTT	6900 C	II	
	TAGAATTAT TAAATGTT			
	ATCTTGGTA ATTTACAA			
	A AI			
GAM439 GRM1	GAATAATCTAAATGCTTTGTT	6897 AATT	CTI	
	ATCTAAATGTTT			

		TAGATTTACGAA		
		TAT_ ACA		
GAM439 GRM1		GAATAATCTAAATGCTTTGTT	6897 TAGAATT	CTTGA
		ATCTAAATGTTT		
		TAGATTTACGAA		
		TAT_ ACAAG		
GAM439 IFIT1		GAATTAT---AATGTTTCT	6898 CTA	
		GAATTAT AATGTTTC		
		CTTAATA TTACAAAG		

GAM439 MTCP1		CTAAACTTCTGTTTCTTGA	6895 _____	IIIT
		CTAAA TGTTTCTTG		
		GATTT ACAAAGAAC		
		GAAG TIII		
GAM439 RAD21		AATTATCTACAATGTCTTTT	6889 _	CTII
		AATTATCTA AATGTTT		
		TTAATAGAT TTACAGA		
		G AAI		
GAM439 SCN3A		GAATTATCTCATTTATTCTT	6899 TAGA	AAATGT
		ATTATCT TTCTTG		
		TAATAGA AAGAAT		
		_____ GTAAAT		
GAM439 TFDP2		AATTATCTAAATGTCACTT	6890	T II
		AATTATCTAAATGTT CT		
		TTAATAGATTTACAG GA		
		T AI		
GAM439 TFDP2		AATTATCTAAATGTCACTT	6890 TAGAAT	T
		TATCTAAATGTT CTTG		
		ATAGATTTACAG GAAT		
		_____ T		
GAM440 BAALC		GAAAGCTATGCAAAATTGCAATGTC	6909 TGAAAG TG C	II
		GTG AA TTGCAATGTC		
		TAC TT AACGTTACAG		
		TTTCGA GT T AI		
GAM440 CALCRL		GAAAGA-GTGAAAGCTTTGCAATGT	6910 TGA T C_	CI
		AAGG GTGAA TTGCAATGT		
		TTTC CACTT AACGTTACA		
		_____ T TCGA CI		
GAM440 DCX		TGAAAGGTGTCAGACCTGAAA	6912 GA_ CAATGTC	
		TGAAAGGTGT ACTTG		

	ACTTTCCACA TGGAC		
	GTC TTTIIC		
GAM440 DRD2	TGCAGGGTGTGAACTGTCCATCTC	6915	AAA TGCA G I
	TG GGTGTGAACT AT TC		
	AC CCACACTTGA TA AG		
	GTC CAGG G I		
GAM440 ITK	TGAAAGGTGGTGCACCTTG	6911	_ AA_ CAATGT
	TGAAAGGTG TG CTTG		
	ACTTTCCAC AC GAAC		
	C GTG IICTG		
GAM440 MTF1	TGAAAGGTGAGGA-TTTCAA	6914	T_ ACTTGCAATGT
	TGAAAGGTG GA		
	ACTTTCCAC CT		
	TC AAAGTTIICT		
GAM440 NDRG3	AAGGA-TGGACTTGCAATG	6908	TGAAA T A
	GGTG GA CTTGCAATG		
	CTAC CT GAACGTTAC		
GAM440 OCRL	TGAAAGG-GAGA-CTAATGCAATGTC	6913	TGT ACT_ I
	TGAAAGG GA TGCAATGTC		
	ACTTTCC CT ACGTTACAG		
	CT_ GATT I		
GAM440 RORB	AAAAGTCTTGACCTTGCAATGT	6905	TGAAAGG T A CI
	TG GA CTTGCAATGT		
	AC CT GAACGTTACA		
	TTCAGA_ _ G AT		
GAM440 SRD5A2	AAACATGAGAGTTTGCAATGTC	6906	TGAAAG T AC
	GTG GA TTGCAATGTC		
	TAC CT AACGTTACAG		
	TG_ _ T CA		
GAM440 ZNF215	AAGGTGTGACGTGAC-TGCAA	6907	TGAAA GT AC T
	G GTGA TTGCAA GT		
	C CACT GACGTT CA		
	CACA_ TG _ _		
GAM441 PCDHGA8	AGAATGAT-CAGATTGTAGCATC	6918	TGAG C AT_ G
	AATGATC AGA TAG ATC		
	TTACTAG TCT ATC TAG		
	_ _ AAC G		
GAM441 TXNRD1	TGAGAATGATGAAGACATCAGG	6919	CC _ ATC
	TGAGAATGAT AGA ATTAGG		

	ACTCTTACTA TCT TAGTCC			
	CT G III			
GAM442 ACCN2	TGGACGTGGCCCTCTACAAGGGCC 6932	C	G	A I
	TGG CGTGG CCTC ACAAGGGCC			
	ACC GCACC GGAG TGTTCCTCGG			
	T G A I			
GAM442 APXL	GGCCGTGGG-ATC-GCAAGGG 6926	TG	CC	AA C
	GCCGTGGG TC CAAGGG			
	CGGCACCC AG GTTCCC			
	— T_ C_ T			
GAM442 CACNG8	GGCCGTGGGCCACCAACCGGGGC 6928	TG	TCA	AA C
	GCCGTGGGCC AC GGGC			
	CGGCACCCGG TG CCCG			
	— TGG GC T			
GAM442 HMOX1	TGGCCGTG----TCAACAAGG 6929	GGCC		G
	TGGCCGTG TCAACAAGG			
	ACCGGCAC AGTTGTTCC			
	— I			
GAM442 ING1	CCTTGACCTCAACAAAGGC 6922	TGGCCG		G
	TG GCCTCAACAAGGGC			
	AC TGGAGTTGTTCCG			
	— G			
GAM442 LHX3	TGGGC-TGGGCCTCAGCAAGG 6931	T_ CG	A	GC
	GGC TGGGCCTCA CAAGG			
	CCG ACCCGGAGT GTTCC			
	AC — C II			
GAM442 PACSIN1	GGCCGTGGG----GACAAGG 6925	TG	CCTCA	
	GCCGTGGG ACAAGG			
	CGGCACCC TGTTC			
	— C_			
GAM442 PACSIN1	GGCCGTGGGCAT-GGCAAGGG 6927	TG	CTCAA	C
	GCCGTGGGC CAAGGG			
	CGGCACCCG GTTCCC			
	— TACC_ C			
GAM442 PDE4A	TGGCCGTGGGAATTATTAAGG 6930		CCTCAAC	GCC
	TGGCCGTGGG AAGG			
	ACCGGCACCC TTCC			
	TTAATAA III			
GAM442 PLAUI	CCATGGGCCTC-ACAAATGCC 6923	TGGCCG	A	G
	TGGGCCTCA CAAG GC			

		ACCCGGAGT GTTT CG	
		_____ _ A	
GAM442 STAT1		CCTTGTGCCCCAACAAGGGCC 6924 TGGCCGTGG	
		GCCTCAACAAGGGCC	
		CGGGGTTGTTCCCGG	
		ACA_____	
GAM443 CAPN10		TAAAGTTACATCCTAAAAGTG 6944 _ CTCT	
		TAAGGTTGCA CCTAAAAGTG	
		ATTTCAATGT GGATTTTCAC	
		A IIIT	
GAM443 CAPN10		TAAAGTTACATCCTAAAAGTG 6944 A _ I	
		AGGTTGCA CCTAAAAGT	
		TTCAATGT GGATTTTCA	
		_ A I	
GAM443 FANCF		AGGTTGCACTGAGCAGTGATC 6940 CTAAA CTI	
		GGTTGCAC AGTG	
		CCAACGTG TCAC	
		ACTCG TAI	
GAM443 FANCF		AGGTTGCACTGAGCAGTGATC 6940 TAAG CTAAA C T	
		GTTGCAC AGTG TC	
		CAACGTG TCAC AG	
		_____ ACTCG T T	
GAM443 GJB5		AGGTTGCACCTATGAGAGATGCT 6939 GGT AA _ I	
		TGCACCTA AG TGC	
		ACGTGGAT TC ACG	
		_____ AC TCT I	
GAM443 GJB5		AGGTTGCACCTATGAGAGATGCT 6939 TAAG AA _ CTI	
		GTTGCACCTA AG TGCT	
		CAACGTGGAT TC ACGA	
		_____ AC TCT TCI	
GAM443 IL1R1		AGGAGGCACCT-AAAGAACTCT 6941 _ TT A T I	
		GG GCACCTAAA G GCTC	
		CC CGTGGATTT C TGAG	
		T TC _ T I	
GAM443 IL1R1		AGGAGGCACCT-AAAGAACTCT 6941 TAAGGTT A T	
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		CGTGGATTT C TGAGA	
		CTC_____ _ T	
GAM443 MPL		AAGGTTGCACAGCTAGTAAATGTG 6936 _ AAAGTIIC	
		AAGGTTGCAC CTA	

	TTCCAACGTG GAT		
	TC CATTACAC		
GAM443 MPL	AAGGTTGCACAGCTAGTAAATGTG 6936 TA	__ A_	CTCTI
	AGGTTGCAC CTA AAGTG		
	TCCAACGTG GAT TTTAC		
	__ TC CA ACTII		
GAM443 OPRM1	AGGTTGGATGACCTAAAAGT 6938 C__		
	AGGTTG ACCTAAAAG		
	TCCAAC TGGATTTTC		
	CTAC AII		
GAM443 OPRM1	AGGTTGGATGACCTAAAAGT 6938 TAA T C		CTC
	GG TG ACCTAAAAGTG		
	CC AC TGGATTTTCAT		
	CAA T _ CII		
GAM443 P2RY6	GGTTGCA--TTAAAGTGCTC 6942 CCTA		I
	GGTTGCA AAAGTGC		
	CCAACGT TTTCACG		
	AA__ A		
GAM443 PACE4	AAGGTTGCAGGGTACAAAGT 6935		CCTAAAAGIII
	AAGGTTGCA		
	TTCCAACGT		
	CCCATGTTTCA		
GAM443 PACE4	AAGGTTGCAGGGTACAAAGT 6935 TA	CCTA__	GCTC
	AGGTTGCA AAAGT		
	TCCAACGT TTTCA		
	__ CCCATG AIII		
GAM443 PPP4R1	GTTGCACCTCAGAGCTGATC 6943	AAA T	II
	GTTGCACCT AG GCT		
	CAACGTGGA TC CGA		
	G__ T CT		
GAM443 WASF3	AAGGTGCCATCTAAA-GTGCTCT 6937 _ T AC_ A		I
	AGGT GC CTAAA GTGCTC		
	TCCA CG GATTT CACGAG		
	T _ GTA _ I		
GAM443 WASF3	AAGGTGCCATCTAAA-GTGCTCT 6937 TA T AC_ A		
	AGGT GC CTAAA GTGCTCT		
	TCCA CG GATTT CACGAGA		
	_ _ GTA _		
GAM443 WEE1	TGCAATGCCTACAAAGTGCTC 6945 __ _		IIIG
	TGCA CCTA AAAGTGCT		

	ACGT GGAT TTTACGA		
	TAC G GIII		
GAM444 ADRA2B	TCCCCCTCAGCAGCAGGCCCACT	6952 TT G _ A I	
	CCC CT GGCAGCAGGC CCGCT		
	GGG GA TCGTCGTCCG GGTGA		
	_ G G G C		
GAM444 CHRM1	TTGCGGCTGGATAGCAGGCAC	6955 TTCCC C_ CGCT	
	GCTGG AGCAGGCAC		
	CGACC TCGTCCGTG		
	AACGC TA IIIT		
GAM444 EPM2A	CCTGCAGGCAGCAGGAACTGC	6948 TTCCC T C C T	
	GC GGCAGCAGG AC GC		
	CG CCGTCGTCC TG CG		
	A_ T T A T		
GAM444 FUT7	TCCCGTCTGCCGAGCAGGCACC	6951 TT _ _ GCTI	
	CCCG CTG GCAGCAGGCACC		
	GGGC GAC CGTCGTCCGTGG		
	_ A GG GIII		
GAM444 GYPC	TTCCTCCCTGG--GCAGGCACC	6953 _ _ G CA GC	
	TTC CC CTGG GCAGGCACC		
	AGG GG GACC CGTCCGTGG		
	A A _ _		
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	CCGCTGGCAG CA GC		
	GGCGACCGTC GT CG		
	AAA T A IIITC		
GAM444 MYCL2	TTCCCAGACTGGAGGCAGGCACC	6954 _ CA GCTI	
	TTCCC GCTGG GCAGGCACC		
	AAGGG TGACC CGTCCGTGG		
	TC TC IIIT		
GAM444 PIN1L	CCACTGGCCAGCAGGCAGCG	6949 TTCCCG _ C C	
	CTGGC AGCAGGCA CG		
	GACCG TCGTCCGT GC		
	_ G C C		
GAM444 TCF8	TCCCGGCCAGG--GCAGGCACCGC	6950 TT _ TG CA I	
	CCCG C G GCAGGCACCGCT		
	GGGC G C CGTCCGTGGCGG		
	_ CG GT C_ I		
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	TCTCCTCG CTCAGGGTT		

	AGAGGAGT GAGTCCCAA	
	— III	
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	GG CTCA GGGTCCG C	
	II IIII IIIIII I	
	CC GAGT CCCAAGGC G	
	GA_____ A T C G	
GAM445 BYSL	CTCATCCTCAGGG-TCCACA 6971 TCTCCTCGG T	
	CCTCAGGGT CCGC	
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	A_____ —	
GAM445 CACNB1	TCTCCCCTGGGGCCTCAGGGT 6979 _____ TCCGCA	
	TCTCCTC GGCCTCAGGGT	
	IIIIII IIIIIIII	
	AGAGGGG CCGGAGTCCCA	
	ACC IIIACG	
GAM445 CHRN2	TCCTGGGCCTCAGGGAGCCG 6974 TCTC C TT _	
	CT GGCCTCAGGG CCG C	
	II IIIIIIII IIII	
	GA CCGGAGTCCC GGC G	
	_____ C TC C	
GAM445 COL4A2	TCCTCGGCCT---GGATCCGC 6975 TCTC CA T	
	CTCGGCCT GGGT CCG	
	IIIIII IIII III	
	GAGCCGGA CCTA GGC	
	_____ — —	
GAM445 CPM	CTCCTAA-CCTCAGGGTGATCCGC 6967 TC C _ AI	
	TCCT GGCCTCAGGGT TCCGC	
	III IIIIIIII IIII	
	AGGA TTGGAGTCCCA AGGCG	
	_____ — — CT GI	
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	_____ TCA_____ CI	
GAM445 EPHB3	CTGCACGGTCCTCAGGGTCCC 6964 TCTCCT _ GCA	
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	GCC GGAGTCCCAGGG	
	ACGT_____ A GII	
GAM445 JAG2	CCTCGGCCTCCGGGTCCGGCA 6962 TCTCCT A C	
	CGGCCTC GGGTTC GCA	
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	_____ G C	
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	CGGAGTCCCG AGG	
	GG_____ GA GG	
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	TCCT GG TCAGGGTTC	
	AGGA CC AGTCCCAAG	
	___ _ AT TI	
GAM445 OVOL1	TCGGCCACAGAGGGTTCCG 6977 TCTCCT CCTC	___
	CGG AGGGTTCCG C	
	GTC TCCCAAGGC G	
	GT_____ C	
GAM445 PCSK2	CTCCTTCAGGCCTCA-GGTTCC 6963 TC __ G GCA	
	TCCT C GGCCTCAGG TTCC	
	AGGA G CCGGAGTCC AAGG	
	___ A T _ All	
GAM445 RENBP	CCTCCTCTTCAGGGTTCCGC 6961 TCT GGCC	
	CCTC TCAGGGTTCCGC	
	GGAG AGTCCCAAGGCG	
	___ A___	
GAM445 REPS2	CTCCTCGGCCTCA-GCTGCCGC 6970 TC GGTT A	
	TCCTCGGCCTCAG CCGC	
	AGGAGCCGGAGTC GGCG	
	___ GAC_ G	
GAM445 SLC5A5	TCCCCTCTCACTCTGGGTTCCGC 6981 GGC A AI	
	TCTCCTC CTC GGGTTCCGC	
	AGGGGAG GAG CCAAGGCG	
	AGT A II	
GAM445 TBX6	CTCCT-GGCCTCAGGTGATCTGC 6966 TC C GT_ C A	
	TCCT GGCCTCAGG TC GC	
	AGGA CCGGAGTCC AG CG	
	___ _ ACT A G	
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	CTCGGCC TC GGT CC	
	GAGTCGG AG TCA GG	
	___ G GGG C II	
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	CTCCT GC GGGTTCCGC	

GAGGG CG CCCAAGGCG

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                  GG CCTCAGGGTTCCG
                  || |||||
                  TC GGGGTCCCAAGGT
                  CA_____ A      C
GAM445 ZNF264     CTCCT-GGCCTCAGGTGATCC      6965 TC      C      GT_      C
                  TCCT GGCCTCAGG TCCG
                  ||| ||||| |||
                  AGGA CCGGAGTCC AGGT
                  _ _      ACT      I
GAM446 APC        ATCAAACCTATTTACAAAATTTTTC 6988 TA      TC_____ T      C      TII
                  TCAAACCT      CAA ATT TTC
                  ||||| ||| ||| |||
                  AGTTTGGA      GTT TAA AAG
                  _      TAAAT      T      A      TII
GAM446 B3GNT3     ATCAAACC-TCAAACCTTC      6990 A_____      CAATATTI
                  TCAAACCTTC
                  |||||
                  AGTTTGGAAG
                  TAGTTTGG      IIITATA
GAM446 B3GNT3     ATCAAACC-TCAAACCTTC      6990 TA_____      AATATTCTT
                  TCAAACCTTCC
                  |||||
                  AGTTTGGAAGG
                  AGTTTGG      IIITCTTCT
GAM446 BAZ2A      TCAA---TTCAAATATTCTTC      7006 TATCAAACC      C
                  TTC AATATTCTT
                  ||| |||||
                  AAG TTATAAGAA
                  TT_____ T
GAM446 CAMLG      TATAAATACCTTCCAAT-TTC      6997 TATCAA      ATI
                  ACCTTCCAAT
                  |||||
                  TGGAAGGTTA
                  ATTTA_      AAG
GAM446 CAMLG      TATAAATACCTTCCAAT-TTC      6997 TATCAA_      A      TTC
                  ACCTTCCAAT TTC
                  ||||| |||
                  TGGAAGGTTA AAG
                  ATATTTA      _      |||
GAM446 CNR1       ATCTAACAATACAATATTCTTCT 6993 A      CTTC      I
                  TC AAC      CAATATTCTTC
                  || ||| |||||
                  AG TTG      GTTATAAGAAG
                  A      TTAT      I
GAM446 CNR1       ATCTAACAATACAATATTCTTCT 6993 TA      A      CTTC      I
                  TC AAC      CAATATTCTTCT
                  || ||| |||||
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		__ A TTAT T		
GAM446 CUL3	TATCAAACCTGTGCTCCAA	6998	_____	TATTCTTC
	TATCAAACCT TCCA			
	ATAGTTTGGA AGGT			
	CACG IIITCTTC			
GAM446 CUL3	TATCAAACCTGTGCTCCAA	6998	_____	IIIT
	TATCAAACCT TCCA			
	ATAGTTTGGA AGGT			
	CACG TIII			
GAM446 CUL3	TATCAAACCTT-TAAAATT	7000		CCAATATI
	TATCAAACCTT			
	ATAGTTTGGAA			
	ATTTTAAI			
GAM446 CUL3	TATCAAACCTT-TAAAATT	7000		CCAATATTCTT
	TATCAAACCTT			
	ATAGTTTGGAA			
	ATTTTAAIIIT			
GAM446 CYBB	CAATCAATCCAATATTCTTCT	6995	AAACCT	I
	TCCAATATTCTTC			
	AGGTTATAAGAAG			
	TTAGTT I			
GAM446 CYBB	CAATCAATCCAATATTCTTCT	6995	TA ACCT	
	TCAA TCCAATATTCTTCT			
	AGTT AGGTTATAAGAAGA			

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	AACCTTCCAAT ATTCTTC			
	TTGGAAGGTTG TAAGAAG			
	_____ AGGT I			
GAM446 DMP1	TATGCAACCTTCCAACCTCCAATTCTTCT	6999	TATCA _____	III
	AACCTTCCAAT ATTCTTCT			
	TTGGAAGGTTG TAAGAAGA			
	ATACG AGGT III			
GAM446 DMRT2	ATTAAAATTTT-AATATTCTTC	6992	TATCAAACCTTCC	
	AATATTCTTCT			
	TTATAAGAAGG			
	AATTTTAAAA_____			
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	TCA TTCCAATATT			

		AGT AAGGTTATAG	
		AGTTACG _____ IIIT	
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		CCT CCA TATTCTTC	
		GGG GGT ATAAGAAG	
		TTTCTG T A I	
GAM446 EHF		TATAAAGACCCCAACCATTATTCTTCT 6996 TATCAAA__ T A II	
		CCT CCA TATTCTTCT	
		GGG GGT ATAAGAAGA	
		ATATTTCTG T A II	
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		CAAACCTTCC TTC	
		GTTTGGAAGG AAG	
		A AG__ CAA	
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		AAACCTTCC TCTTC	
		TTTGGAAGG AGAAG	

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		CTTCC TCTTC	
		GAAGG AGAAG	
		_____ CGAAT A	
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		CTTCC TCTTCT	
		GAAGG AGAAGA	
		_____ CGAAT A	
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		AGTTTGGAAGG	
		AAGAAII	
GAM446 IL17		TCAAACCTTCC----TTCTT 7005 TATC AATA	
		AAACCTTCC TTCT	
		TTTGGAAGG AAGA	

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		TTTGGA TTATAAGAAG	
		ATA TT_ I	
GAM446 LAMA4		TAT-AAACCTAA-AATATTCTTCT 7001 TATC TCC	
		AAACCT AATATTCTTCT	

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	ATA_ TT_		
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	TATCA TTCCAATAT CTTCT		
	ATAGT AAGGTTATA GAAGA		
	C__ C		
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	ATCA TTCCAATAT CTTC		
	TAGT AAGGTTATA GAAG		
	A C__ C		
GAM446 MASP1	CAAACCTTCCCAACTTTCT 6994 _ A II		
	CAAACCTTCC AAT TTC		
	GTTTGGAAGG TTG AAG		
	G A AI		
GAM446 MASP1	CAAACCTTCCCAACTTTCT 6994 TATCAA _ A		
	ACCTTCC AAT TTCTTC		
	TGGAAGG TTG AAGAGG		
	_____ G A		
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	ACCTTCCAA CTTC		
	TGGAAGGTT GGAG		
	GTG TCAC I		
GAM446 MKI67	TCACACCTTCCAAAGTGCCTCT 7007 TATCAA TATT		
	ACCTTCCAA CTTCT		
	TGGAAGGTT GGAGA		
	TG__ TCAC		
GAM446 NFIL3	AATCCATC-AATATTCTTC 6986 AAA TTC I		
	CC CAATATTCTT		
	GG GTTATAAGAA		
	TTA TA_ G		
GAM446 NFIL3	AATCCATC-AATATTCTTC 6986 TATCAAACCTTC		
	CAATATTCTT		
	GTTATAAGAA		
	GTA_____		
GAM446 NOX4	ATCATCACATCAAATATTCTTC 6991_ AACCT C T		
	TATCA TC AATATTCTTC		
	GTAGT AG TTATAAGAAG		
	A GT__ T T		
GAM446 PTGFR	ACCTTTTGCCAATATTCTT 6987 _ III		
	ACCTT CCAATATTCT		

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	AAC AII		
GAM446 PTGFR	ACCTTTTGCCAATATTCTT	6987 TATCAAACCTT	C
	CCAATATTCTT		
	GGTTATAAGAA		
	AC_____A		
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	CTTCCAATA		
	GAAGGTTAT		
	TTTA TAAAAGI		
GAM446 SHANK2	AAATCTTCCAATAATTTTC	6985 TATCAAAC	TTC
	CTTCCAATA	TTC	
	III		
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	_____TAA		
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	III III		
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	T G AI		
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	AAACCTTC AAT TTCTT		
	III III		
	TTTGGAAG TTG AAGAG		
	_____T G A		
GAM447 ADAR	TGTG-AGAGCCTGTGTTCCCAGT	7026 _ G	GT I
	GTG AGAGCCTG TTCTCAG		
	III		
	CAC TCTCGGAC AAGGGTC		
	A _ AC I		
GAM447 ADAR	TGTG-AGAGCCTGTGTTCCCAGT	7026 GTGTG	GT
	GAGAGCCTG TTCTCAGT		
	CTCTCGGAC AAGGGTCA		
	CA_____AC		
GAM447 BLTR2	TGTG-AGAGCCTGCCTTGCCAG	7023 _ G	G C I
	GTG AGAGCCTG TTT TCA		
	III III III		
	CAC TCTCGGAC GAA GGT		
	A _ G C I		
GAM447 BLTR2	TGTG-AGAGCCTGCCTTGCCAG	7023 GTGTG	G C T
	GAGAGCCTG TTT TCAG		
	III III		
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	CA_____G C C		
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	AGAGCCTGGTTT CTCAG		

TCTCGGACCAAA GAGTC
 A AI
 GAM447 EGLN2 TGCAGGGCTTGGTTTCTCTGT 7018 G A C AGI
 G AG GC TGGTTTCTC
 I I I I I I I I I I
 C TC CG ACCAAAGAG
 G C A ACI
 GAM447 EGLN2 TGCAGGGCTTGGTTTCTCTGT 7018 GTGTGG A C AGT
 AG GC TGGTTTCTC
 I I I I I I I I I I
 TC CG ACCAAAGAG
 C A ACA
 GAM447 FLII TGTGGAGAGAGTTGGATTTCCAG 7020 GT CC_ _ TI
 GTGGAGAG TGG TTTCTCAG
 I I I I I I I I I I
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 TCA T TI
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 GGAGAG TGG TTTCTCA
 I I I I I I I I I I
 CCTCTC ACC AAAGGGT
 TCA T I
 GAM447 GNL1 GAGAGCCTGTTGACTCTGT 7011 GTTT AGII
 GAGAGCCTG CTC
 I I I I I I I I I I
 CTCTCGGAC GAG
 AACT ACAI
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 GGAGAGC CTGGTTTC
 I I I I I I I I I I
 CCTCTCG GACCAAAG
 TCCT AIII
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 G G GA CTGGTTTCT
 I I I I I I I I I I
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 T_ GT _ _ CAA
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 GTGG GCC GGTTTCTC
 I I I I I I I I I I
 CACC CGG CCAAAGAG
 A G_ _
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 GTGG GCC GGTTTCTCA
 I I I I I I I I I I
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 G_ _
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 GTGG AGCC GGTTTCTCAG
 I I I I I I I I I I

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	GT T I	
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	GTGG AGCC GGTTCCTCAGT	
	CACC TTGG CCAAAGAGTCA	
	__ GT T T	
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	CCTCTCGGAC GAA GAGTCG	
	_____ G C	
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	CCTCTCGGAC GAA GAGT	
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	ACCTCTC CCGA AGA	
	AGT C TII	
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	CACCTCTC CCGA AGA TC	
	__ AGT C T TI	
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	CACCTCTC CCAG GAGT	
	A _ T	
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	CACCTCTC CCAG GAGTC	
	__ _ T	
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	A C _ I	
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	TCTC CG AAAGAGTC	
	__ _ A _	
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	CCTC CG GAT AAAGAGTC	
	A T _ I	
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	GC CTG TTTCTCAGT	
	CG GAT AAAGAGTCA	
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	_ A TT I	
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	ACACCTCT GGAC GAAG GTC	
	_ A TT I	
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	CA TCTCGGACC AAGG	
	A AA C TII	
GAM447 SGCA	TGTTTAGAGCCTGGGTTC-CAG 7025 GT GG T T T	
	GT AGAGCCTGG TTC CAG	
	CA TCTCGGACC AAG GTC	
	_ AA C _ C	
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	CCTTTCGGACCAA AGAG	
	CTA TII	
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	CAC CCTCTCGGA AAAG	
	C A_	
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	CAC CCTCTCGGA AAG	
	C AA I	
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	CAC TCTCGGAC GAA GGT	
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	CTCTCGGAC GAA GGTC	
	CA___ G C C	
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	TCTCGGACCAAA GAGTC	
	A AI	
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	G AG GC TGGTTTCTC	
	C TC CG ACCAAAGAG	
	G C A ACI	
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	AG GC TGGTTTCTC	
	TC CG ACCAAAGAG	
	___ C A ACA	
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	CACCTCTC ACC AAAGGGTC	
	_ TCA T TI	
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	CCTCTC ACC AAAGGGT	
	_ TCA T I	
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	CTCTCGGAC GAG	
	AACT ACAI	
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	CCTCTCG GACCAAAG	
	TCCT AIII	
GAM448 HNRPF	GGAGAGCAGGACTGGTTTCT 7012 GT TG A GC CAG	
	G G GA CTGGTTTCT	

		C C CT GACCAAAGA	
		T_ GT _ _ CAA	
GAM448 IMMP2L		TGTGGCG--CC-GGTTTCTCA 7022 _ AGA T	
		GTGG GCC GGTTTCTC	
		CACC CGG CCAAAGAG	
		A G_ _	
GAM448 IMMP2L		TGTGGCG--CC-GGTTTCTCA 7022 GT AGA T	
		GTGG GCC GGTTTCTCA	
		CACC CGG CCAAAGAGT	
		_ G_ _	
GAM448 MATN2		TGTGGCAAACCAGGTTTCTCAGT 7027 AG T I	
		GTGG AGCC GGTTTCTCAG	
		CACC TTGG CCAAAGAGTC	
		GT T I	
GAM448 MATN2		TGTGGCAAACCAGGTTTCTCAGT 7027 GT AG T I	
		GTGG AGCC GGTTTCTCAGT	
		CACC TTGG CCAAAGAGTCA	
		_ GT T T	
GAM448 NPR2L		GTGGAGAGCCTGCCTTGCTCAG 7014 GTGT G _	
		GGAGAGCCTG TTT CTCAGT	
		CCTCTCGGAC GAA GAGTCG	
		_ G C	
GAM448 NPR2L		GTGGAGAGCCTGCCTTGCTCAG 7014 T G _ I	
		GGAGAGCCTG TTT CTCA	
		CCTCTCGGAC GAA GAGT	
		_ G C I	
GAM448 OAS3		TGTGGAGAGTCAGGCTGTCTAAG 7021 CCT _ CAI	
		TGGAGAG GGTT TCT	
		ACCTCTC CCGA AGA	
		AGT C TII	
GAM448 OAS3		TGTGGAGAGTCAGGCTGTCTAAG 7021 GT CCT _ C TI	
		GTGGAGAG GGTT TCT AG	
		CACCTCTC CCGA AGA TC	
		_ AGT C T TI	
GAM448 PAX4		TGTGGAGAG---GGTCACTCAG 7024 _ CCT T	
		GTGGAGAG GGTT CTCA	
		CACCTCTC CCAG GAGT	
		A _ T	
GAM448 PAX4		TGTGGAGAG---GGTCACTCAG 7024 GT CCT T	
		GTGGAGAG GGTT CTCAG	

	CACCTCTC CCAG GAGTC	
	— — T	
GAM448 PXN	TGGAGAGGCT--TTTCTCAGT 7019 _ C GG I	
	GGAGAG CT TTTCTCAG	
	CCTCTC GA AAAGAGTC	
	A C _ I	
GAM448 PXN	TGGAGAGGCT--TTTCTCAGT 7019 GTGT A CTGG	
	GGAG GC TTTCTCAG	
	TCTC CG AAAGAGTC	
	— _ A _	
GAM448 RDS	TGGAGTGCACTA-TTTCTCAGT 7017 A _ G I	
	GGAG GC CTG TTTCTCAG	
	CCTC CG GAT AAAGAGTC	
	A T _ I	
GAM448 RDS	TGGAGTGCACTA-TTTCTCAGT 7017 GTGTGGAGA _ G	
	GC CTG TTTCTCAGT	
	CG GAT AAAGAGTCA	
	TCA _ _ T _	
GAM448 S100A1	GTGTGGAGA-CCTGTCTTCAACAGT 7016 G G T _ I	
	GTGTGGAGA CCTG TTTC CAGT	
	CACACCTCT GGAC GAAG GTCA	
	_ A TT I	
GAM448 S100A1	GTGTGGAGA-CCTGTCTTCAACAGT 7016 G G T _ I	
	TGTGGAGA CCTG TTTC CAG	
	ACACCTCT GGAC GAAG GTC	
	_ A TT I	
GAM448 SGCA	TGTTTAGAGCCTGGGTTC-CAG 7025 _ GG T CAI	
	GT AGAGCCTGG TTCT	
	CA TCTCGGACC AAGG	
	A AA C TII	
GAM448 SGCA	TGTTTAGAGCCTGGGTTC-CAG 7025 GT GG T T T	
	GT AGAGCCTGG TTC CAG	
	CA TCTCGGACC AAG GTC	
	_ AA C _ C	
GAM448 SHMT1	GGAAAGCCTGGTTGATTCTCA 7013 _	
	GGAGAGCCTGGTT TCTC	
	CCTTTCGGACCAA AGAG	
	CTA TII	
GAM448 TACC1	GTGGGGAGAGCCT-TTTTC 7015 T GG TCA	
	GTG GGAGAGCCT TTTC	

	CAC CCTCTCGGA AAAG	
	C A_ III	
GAM448 TACC1	GTGGGGAGAGCCT-TTTTC 7015 T GG I	
	GTG GGAGAGCCT TTT	
	III III	
	CAC CCTCTCGGA AAG	
	C AA I	
GAM449 AXL	ACCATGGTCCTAGAGAG-GCA 7063 _ _ T CTGG	
	ACCATGGTC TAGA AG GCA	
	III II III	
	TGGTACCAG ATCT TC CGT	
	G C _ IIIT	
GAM449 CNGA1	TCTAGAAGTGGACGTCACTGGT 7073 ACCA TCTAGAA G	
	TGG GT CACTGGT	
	III II	
	ACC CA GTGACCA	
	C_ TG_ _	
GAM449 CRY2	TGGCTCCAGGAGTGCCTG 7074 ACCATGG A G	
	TCTAG AGTGCCTG	
	AGGTC TCACGTGAC	
	_____ C G	
GAM449 CUL3	ATGGTCTAGAACATGTACTG 7065 ACCATG _ C G	
	GTCTAGAA GTG ACTG	
	III	
	CAGATCTT TAC TGAC	
	_____ G A A	
GAM449 CYP3A43	CCATC-TCTT-AAGTGCCT 7070 ACCATG AG_ G	
	GTCT AAGTGCCT	
	III	
	TAGA TTCACGTGA	
	G_ GAA A	
GAM449 MS4A1	ACCAAGG-CTGGA-GTGCCTGGT 7064 T T A A	
	ACCA GG CT GA GTGCCTGGT	
	III II II	
	TGGT CC GA CT CACGTGACCA	
	T _ C _	
GAM449 NAGA	CCATGGTCTAG-GCTCAGTGGT 7071 AC AA G C	
	CATGGTCTAG GT CA TGGT	
	II II	
	GTACCAGATC CG GT ACCA	
	_ _ A C	
GAM449 PCLO	CCAAGGTTCTAGAAAGTTGACTG 7069 AC T _ GC GT	
	CA GGT CTAGAAGT ACTG	
	II III III	
	GT CCA GATCTTCA TGAC	
	_ T A AC AI	
GAM449 PRELP	CCAGGAGTTTGGGTGTGCCTGGT 7068 ACCATGGTCTAGAA I	
	GTGCCTGGT	

	CACGTGACCA	
	GTCCTCAAACCCA_ A	
GAM449 RFX2	CCATGGTCTGGTGGGGCCCTGGT 7072 AC	AGAAGT A I
	CATGGTCT GC CTGGT	
	GTACCAGA CG GACCA	
	_ CCACCC G C	
GAM449 SYK	CATGCT-TAGAAACTGCACTGGT 7066 ACCATG TC _	
	G TAGAAG TGCCTGGT	
	I	
	C ATCTTT ACGTGACCA	
	A_ GA G	
GAM449 TEGT	CCACTGTGTCAAACCTGTGCACTGGT 7067 ACCA _ T AA II	
	TG GTC AG GTGCACTGGT	
	AC CAG TT CACGTGACCA	
	GTG_ A T GA AI	
GAM450 ADCY2	TGACAATGACTCAATGCTTTTAA 7080 TT_ CTTGAATTGI	
	TGAC ACTCAATGC	
	ACTG TGAGTTACG	
	TTAC AAAATTIIIG	
GAM450 BCL6	TGTCTTCAC-CAATGCCTTG 7083 TGAC_ T AATT	
	TTAC CAATGCCTTG	
	AGTG GTTACGGAAC	
	ACAGA _ IIIG	
GAM450 C10orf2	TGAC---CTCACTGCCTTGAAT 7087 TTA A T	
	TGAC CTCA TGCCTTGAAT	
	ACTG GAGT ACGGAACCTTA	
	_ G I	
GAM450 CLCA3	TGGCTTCATGGATGGCTTGAATTG 7089 A ACTCA C I	
	TG CTT ATG CTTGAATTG	
	AC GAA TAC GAACTTAAC	
	C GTACC C I	
GAM450 HAS3	CTTACT-AGTTTCTTGAATTG 7077 TGA CT TACTCAATGC	
	CTTGAATT	
	GAACTTAA	
	TGATCAAA_	
GAM450 NET1	TAGTCAACACTGACTTGAATTG 7079 TGA CT TACT A C	
	CA TG CTTGAATTG	
	GT AC GAACTTAAC	
	TT_ G T	
GAM450 P2RY1	TGACTTTACTCAAT-CTTTG 7081 _ GCCTTGAATT	
	TGACTT ACTCAAT	

	ACTGAA TGAGTTA	
	A GAAACIIIGT	
GAM450 PRKY	TGGCTTTATCAATGCCTATGAA 7086 A AC _ TTG	
	TG CTT TCAATGCCT TGAA	
	II III IIIIIII IIII	
	AC GAA AGTTACGGA ACTT	
	C AT T III	
GAM450 RAB11A	TGACTGACTACAGCAATGCCTT 7084 ____ T T_ GAATTG	
	TGACT AC CAATGCCTT	
	IIII II IIIIIII	
	ACTGA TG GTTACGGAA	
	ACTG _ TC IIIGTT	
GAM450 SCN1A	TGAATGTTCTCAATGCCGAGACATTG 7082 TGACTTA_ TT _ II	
	CTCAATGCC GA ATTG	
	IIIIII II IIII	
	GAGTTACGG CT TAAC	
	ACTTACAA CT G II	
GAM450 SGCG	TGACTTACT---TGCATTAACTG 7088 CAA C	
	TGACTTACT TGC TTGAATTG	
	IIIIII III IIIIIII	
	ACTGAATGA ACG AATTTGAC	
	____ T	
GAM450 SMG1	TTAAACAAT-CCTTGAATT 7090 TGACTTACT G	
	CAAT CCTTGAAT	
	III IIIIIII	
	GTTA GGA ACTTA	
	T_____ _	
GAM450 TAF1	TGACTTACTGAGCTCCCTT 7085 CAATG GAATT	
	TGACTTACT CCTT	
	IIIIII IIII	
	ACTGAATGA GGGA	
	CTCGA AIIIG	
GAM450 ZNF26	GACTTACTCCTAAAGGCTT 7078 TG AAT__ CTTGAATT	
	ACTTACTC GC	
	IIIIII II	
	TGAATGAG CG	
	____ GATTTC AAAIIIGT	
GAM451 CLASP1	GGCCCGTGGCATCGCCGCA 7095 TG CT__ CTGA	
	GCCCGTGGC CCGCA	
	IIIIII IIII	
	CGGGCACCG GGCGT	
	____ TAGC CIII	
GAM451 DUSP4	CCCGGCTCCTCCGCACTGA 7093 TGGCCC GG	
	GT CCTCCGCACTGA	
	II IIIIIIIII	
	CG GGAGGCGTGA CT	
	C____ A_	
GAM451 MEN1	TGGGCGGCGGCCTCCGCGCT 7096 T_ CC A GA	
	GGC GTGGCCTCCGC CT	
	III IIIIIIIII II	

	CCG CGCCGGAGGCG GA	
	AC C_ C II	
GAM451 RAD52	TGGTGCCTGGCCT-CGCTCT 7097 CC C A GA	
	TGG CGTGGCCTC GC CT	
	ACC GCACCGGAG CG GA	
	AC _ A II	
GAM451 RFP	GGCGCCGAG--CTCCGCACTGA 7094 TG _ T C	
	GC CCG GGC TCCGCACTGA	
	CG GGC TCG AGGCGTGACT	
	_ C _ _	
GAM451 TNFRSF4	TGGACC-TGTTCTCCGCACTG 7098 C G GC A	
	TGG CC TG CTCCGCACTG	
	ACC GG AC GAGGCGTGAC	
	T _ AA I	
GAM452 ATP2C1	TAGCAGCAG-C-ATCTGCAAGA 7110 CTTA ACTA _	
	GCAGCAG ATCTG AAG	
	CGTCGTC TAGAC TTC	
	_ G_ G	
GAM452 ATP7A	TTAGCAGCAGTTCAGCAATCT 7113 CT AC_ GAAGA	
	TAGCAGCAG TAATCT	
	ATCGTCGTC GTTAGA	
	_ AAGTC GIIIA	
GAM452 COL9A3	TAGC--CAGTCATTAATCTGAAG 7108 CTTAG _ GAC A	
	CAG CA TAATCTGAAG	
	GTC GT ATTAGACTTC	
	CG_ A A_ C	
GAM452 CREBL2	TTAGCCAGCAAACAGTAATCTGAA 7112 CT _ _ GAI	
	TAGC AGCAGAC TAATCTGAA	
	ATCG TCGTTTG ATTAGACTT	
	_ G TC AII	
GAM452 DAD1	TAGCAGTAAGTGTCAAATCTGAAGA 7107 CTTA C_ ACT_ II	
	GCAG AG AATCTGAAGA	
	CGTC TC TTAGACTTCT	
	_ AT ACAGT TT	
GAM452 FACL2	AGCAGCAGAC--AGCTGCAGA 7103 CTTAGC TAAT A	
	AGCAGAC CTG AG	
	TCGTCTG GAC TC	
	_ TC_ G	
GAM452 HOXA7	CTTAGCAGCAAATTTTCT 7104 CTAA GAAG	
	CTTAGCAGCAGA TCT	

	GAATCGTCGTTT AGA		
	TAAA IIIA		
GAM452 MADH7	TTAGCAGCAAAGTAGTTTGAAG 7114 CT	C ATC A	
	TAGCAGCAGA TA TGAAG		
	II		
	ATCGTCGTTT AT ACTTC		
	___ C CAA A		
GAM452 MPHOSPH9	TAGCAGCAGCAAATCAGA 7111 CTTA	ACT T AG	
	GCAGCAG AATC GA		
	II		
	CGTCGTC TTAG CT		
	___ GTT T AA		
GAM452 NPR2	AGCAGCAGAAGACT-ATCTGA 7101 CTT	C A AG	
	AGCAG AGACTA TCTGA		
	TCGTC TCTGAT AGACT		
	___ T _ GA		
GAM452 RAF1	CTTAGCAGCAG-CTTCTCTGAA 7105	A AA GA	
	CTTAGCAGCAG CT TCTGAA		
	II		
	GAATCGTCGTC GA AGACTT		
	_ AG II		
GAM452 SGCA	AGCAGCAGATATTTATTCTGAA 7102 CTTAGC	C___ A GA	
	AGCAGA TA TCTGAA		
	II		
	TCGTCT AT AGACTT		
	___ ATAA A AC		
GAM452 USH2A	TAGCAGCAG--GAATGCTGGAAG 7109 CTTA	ACT _ _ A	
	GCAGCAG AAT CTG AAG		
	CGTCGTC TTA GAC TTC		
	___ C_ C C C		
GAM452 ZNF10	CTTACCAG-AGA---ATCTGAAGA 7106	G C CTA	
	CTTA CAG AGA ATCTGAAG		
	GAAT GTC TCT TAGACTTC		
	G _ _		
GAM453 FCER1A	ACCAGTTTCACTCAG--TTTA 3104 TA	CA GATTTAT	
	CCAGTTTC TCAG		
	GGTCAAAG AGTC		
	_ TG AAATTII		
GAM453 IFRD1	ACCAGTTTCAAT-AGTATT 3103 TA	C C GATTTA	
	CCAGTTTC AT AG		
	II		
	GGTCAAAG TA TC		
	_ T _ ATAACI		
GAM453 LIFR	TAGCAGTTAAAATCAGGATTCAT 3116 TAC	TCC CI	
	CAGTT ATCAGGATTTAT		

	GTCAA TAGTCCTAAGTA	
	ATC TTT II	
GAM453 PSMA2	TAACAGTTT--ATTAGGATTTAT 3115 TAC CC C C	
	CAGTTT AT AGGATTTAT	
	GTCAAA TA TCCTAAATA	
	ATT _ A I	
GAM453 PSME3	CCAGTTTCCCCATCACGAT 3108 TACCAG TT G TTAT	
	T CCATCA GAT	
	I	
	A GGTAGT CTA	
	TCAA__GG G TCII	
GAM453 RCN1	TACCACTTTCACTTAATCAGGATTT 3113 G C__ ATCII	
	TACCA TTTC ATCAGGATTT	
	ATGGT AAAG TAGTCCTAAA	
	G TGAAT IICT	
GAM453 SCA1	CCAGTTTCCACTGTCCGGCTTGAT 3109 TACC CA__ ATTTATCI	
	AGTTTCCAT GG	
	TCAAAGGTG CC	
	__ ACAGG GAACTAAA	
GAM453 SPON1	AGTCTCCAAAATCAGGATTT 3105 TA TTTCC AT	
	CCAG ATCAGGATTT	
	GGTT TAGTCCTAAA	
	A_ T__ AT	
GAM453 SRGAP2	TACCAGTTTTGATCAGTTGGATT 3114 CC GATTTATCI	
	TACCAGTTT ATCAG	
	ATGGTCAAA TAGTC	
	AC AACCTAAII	
GAM453 TCEB1L	CCAGTTTCCAACATCATGAT 3110 TACC _ G TTAT	
	AGTTTCCA TCA GAT	
	TCAAAGGT AGT CTA	
	__ TG A TTII	
GAM453 WNT8B	CCAGTTTCC-TCAGTTTTT 3111 TACC A GA A	
	AGTTTCC TCAG TTT	
	TCAAAGG AGTC AAA	
	__ _ AA G	
GAM453 ZNF124	TTTACATTTACAGGATTTAT 3117 TACCAGTTTCCAT	
	CAGGATTTAT	
	GTCCTAAATA	
	AAAT__	
GAM454 AF3P21	TGGCAAGGG-CTGCGGCGCCA 7144 GTCCTT GA	
	TGGCAAGGGT CGCCA	

	ACCGTTCCCG	GCGGT	
	ACGCC_ II		
GAM454 AF3P21	TGGCAAGGG-CTGCGGCGCCA	7144_	GTCCTT I
	GGCAAGGGT CGCC		
	CCGTTCCCG GCGG		
	A ACGCC_ I		
GAM454 AMY2B	CATGGGTTCCACATCGCCAGAT	7132 AA	G T_ I
	GGGT TCC TCGCCAGA		
	CCCA AGG AGCGGTCT		
	A_ _ TGT I		
GAM454 AMY2B	CATGGGTTCCACATCGCCAGAT	7132 TGGCAA	G T_
	GGGT TCC TCGCCAGAT		
	CCCA AGG AGCGGTCTA		
	_ _ TGT		
GAM454 CDK6	CAAGGGTGTCTCCGCAGGAT	7133	C C AI
	AAGGGTGT CTTCGC AG		
	TTCCACA GAGGCG TC		
	A _ CT		
GAM454 CDK6	CAAGGGTGTCTCCGCAGGAT	7133 TGGCAA	C CA
	GGGTGT CTTCGC GAT		
	CCCACA GAGGCG CTA		
	_ A TC		
GAM454 COPA	GGCAGGGGGTCTCCTTCGCC	7136 A_ G	II
	GGCA GGGT TCCTTCGC		
	CCGT CCCA AGGAAGCG		
	CC G GI		
GAM454 COPA	GGCAGGGGGTCTCCTTCGCC	7136 TG A_ G	AGA
	GCA GGGT TCCTTCGCC		
	CGT CCCA AGGAAGCGG		
	_ CC G AII		
GAM454 DUSP5	GGCCAGGGTGTCCACGGCCAG	7137 A	TTC I
	GC AGGGTGTCC GCCA		
	CG TCCCACAGG CGGT		
	G TGC I		
GAM454 DUSP5	GGCCAGGGTGTCCACGGCCAG	7137 TG A	TTC AT
	GC AGGGTGTCC GCCAG		
	CG TCCCACAGG CGGTC		
	_ G TGC CI		
GAM454 GAA	TGGCC-GGG-GTCCTTCGC	7142 AA T	CAG
	TGGC GGG GTCCTTCGC		

	ACCG CCC CAGGAAGCG		
	G_ _ III		
GAM454 GAA	TGGCC-GGG-GTCCTTCGC 7142	AA T I	
	TGGC GGG GTCCTTCG		
	III		
	ACCG CCC CAGGAAGC		
	G_ _ G		
GAM454 IL15	TGGCAAGGGGTTTCCAGCAGCCA 7140	TG_ TT_ GATI	
	TGGCAAGGG TCC C GCCA		
	III I		
	ACCGTTCCC AGG G CGGT		
	CAA TC T IIIT		
GAM454 IL15	TGGCAAGGGGTTTCCAGCAGCCA 7140	GG TG_ TT_ I	
	CAAGGG TCC C GCC		
	III I		
	GTTCCC AGG G CGG		
	_ CAA TC T I		
GAM454 KCNK4	GTGTCCTTCTCCCCCAGAT 7139	G___ III	
	GTGTCCTTC CCAGA		
	CACAGGAAG GGTCT		
	AGGG AII		
GAM454 KLHL1	AAGCGTACCCCTCGCCAGAT 7129	TGGCAAGG GT	
	GT CCTTCGCCAGA		
	CA GGGAGCGGTCT		
	_____ TG		
GAM454 KLHL1	AAGCGTACCCCTCGCCAGAT 7129	G GT I	
	AG GT CCTTCGCCAGA		
	TC CA GGGAGCGGTCT		
	G TG I		
GAM454 MADH7	AGGGTGTCT--GCC-GAT 7131	TC AGA	
	AGGGTGTCT GCC		
	III		
	TCCCACAGGA CGG		
	_ CTA		
GAM454 OPHN1	TGGCAAGGGTTTATGTCCT 7141	_____ IIIA	
	TGGCAAGGGT GTCC		
	III		
	ACCGTTCCCA CAGG		
	AATA AIII		
GAM454 OPHN1	TGGCAAGGGTTTATGTCCT 7141	_____ T_____ GCCA	
	TGGCAAGGGT GTCC TC GA		
	III		
	ACCGTTCCCA CAGG AG CT		
	AATA AIIIT ACCG		
GAM454 PRKY	TGGCAAGGGTATACTCCACC 7143	C AGA	
	TGGCAAGGGTGT CTTGCC		

	ACCGTTCCCATAGAGGTGG		
	T III		
GAM454 PRKY	TGGCAAGGGTATACTCCACC 7143	C I	
	GGCAAGGGTGTCTTCGC		
	CCGTTCCCATAGAGGTG		
	T I		
GAM454 SORCS2	GCAAAGGTGTCCTT-G-CAGA 7134	C CAI	
	GCAAGGGTGTCTT GC		
	CGTTCCACAGGAA CG		
	_ TCT		
GAM454 SORCS2	GCAAAGGTGTCCTT-G-CAGA 7134	TGGC C C	
	AAGGGTGTCTT GC AGA		
	TTCCACAGGAA CG TCT		
	_____ - -		
GAM454 TBL2	AGGGTGTCCCCGTTGGCCAG 7130	C___ III	
	AGGGTGTCTT GCCA		
	TCCACAGGGG CGGT		
	CAAC CII		
GAM454 TDE1	GGTGTCTTGGCACTCAGA 7138	__ _ III	
	GGTGTCTT CGC CAG		
	CCACAGGAA GTG GTC		
	CC A TII		
GAM454 VCL	GGCAGGAAGTGTCTTCAGACAG 7135	GC A CCI	
	A GGGTGTCTTCG		
	C TTCACAGGAAGT		
	_ C CTG		
GAM454 VCL	GGCAGGAAGTGTCTTCAGACAG 7135	TG A_ C_ ATI	
	GCA GGGTGTCTTCG CAG		
	CGT TTCACAGGAAGT GTC		
	_ CC CT CII		
GAM455 AKAP2	CATGAGTCAGAGAAAACATGA 7149	___ III	
	CATGGG AGAGAAAACATG		
	GTACTC TCTCTTTGTAC		
	AG TII		
GAM455 AKAP2	CATGAGTCAGAGAAAACATGA 7149	TCTCATGGG I	
	AGAGAAAACATGA		
	TCTCTTTGTACT		
	CTCAG___ T		
GAM455 ALB	TTTTCTTCTCTT-ATTCT 7186	TGTT A G	
	TTCTTCTCTTA TTCT		

		AAGAAAGAGAAT AAGA		
		_____ _ G		
GAM455 APPL	TCTCATGGGAGAAGAGTAAAC	7156	_ _	ATGAI
	TCTCATGGGAGA GA AAAC			
	AGAGTACCCTCT CT TTTG			
	T CA AG			
GAM455 APPL	TCTCATGGGAGAAGAGTAAAC	7156	_	AAAI
	TCTCATGGGAGA GA			
	AGAGTACCCTCT CT			
	T CATTG			
GAM455 APTX	TGATCTCTTTCTCTTCCTGTGTGTT	7169 T	TAA	TII
	TG TTTCTTTCTCT TTCTGT			
	AC AGAGAAAGAGA AGGACA			
	T _____ CAC			
GAM455 B3GALT2	TGTTTTCTTCTC-CTTAATACTATT	7165	CT T	I
	TGTTTTCTTT CTTAAT CTGTT			
	ACAAAAGAAG GAATTA GATAA			
	AG T I			
GAM455 B3GAT1	TTTTCTTTCCCTTTTTTGTGTT	7188 TGTT	AA	C
	TTCTTTCTCTT TT TGTT			
	AAGAAAGGGAA AA ACAA			
	_____ AA C			
GAM455 BAP1	CTCCTAGGAGAGAAAGCAT	7150 A	ACAII	
	CTC TGGGAGAGAAA			
	GAG ATCCTCTCTTT			
	G CGTAI			
GAM455 BAP1	CTCCTAGGAGAGAAAGCAT	7150 TC A	A A	
	TC TGGGAGAGAAA CATG			
	AG ATCCTCTCTTT GTAT			
	_ G C I			
GAM455 BCRP2	TCATGGGAGCCAAGGAAGCA	7152	AG AACIII	
	TCATGGGAG AA			
	AGTACCCTC TT			
	GG CCTTCG			
GAM455 BCRP2	TCATGGGAGCCAAGGAAGCA	7152 TCTC	AG AACATGA	
	ATGGGAG AA			
	TACCCTC TT			
	_____ GG CCTTCGT			
GAM455 CACNA1C	TGTTTTCTTCTGTCTCCATTCT	7163	C_ A	GTTI
	TGTTTTCTTT TCTT ATTCT			

	ACAAAAGAAG AGAG TAAGA		
	AAC G IIIT		
GAM455 CASP8	TCTCCATGGGAGAGGATACA 7155 _ AAA TGA		
	TCTC ATGGGAGAG ACA		
	AGAG TACCCTCTC TGT		
	G CTA III		
GAM455 CASP8	TCTCCATGGGAGAGGATACA 7155 _ AAAACII		
	TCTC ATGGGAGAG		
	AGAG TACCCTCTC		
	G CTATGTI		
GAM455 CD1C	TTTCTTTCTCTCAGAAAAGCTGTT 7174 TGTTTT ATT__ I		
	CTTTCTCTTA CTGTT		
	GAAAGAGAGT GACAA		
	_____ CTTTTC A		
GAM455 CDH7	TTTTCTTTCTTTT--TCCTGT 7187 TGTT C AA		
	TTCTTTCT TT TTCTGT		
	AAGAAAGA AA AGGACA		
	_____ A _		
GAM455 COL13A1	TTTTCTTTCTTTTTTAATAATCTGT 7177 TGTT C__ _ TII		
	TTCTTTCT TTAAT TCTGT		
	AAGAAAGA AATTA AGACA		
	_____ AAA TT TI		
GAM455 COL4A3	TTTTTTTTCTCTTAGCATCTCTGT 7183 TGTTTTTC A__ TI		
	TTTCTCTTA TTCTGT		
	AAAGAGAAT GAGACA		
	AAA_____ CGTA TC		
GAM455 CRH	TGTCTTCCTTTCTCTT--TACTGTT 7162 _ AATT I		
	TGTTTTCT TTTCTCTT CTGTT		
	ACAGAAG AAAGAGAA GACAA		
	G AT__ I		
GAM455 DDEF2	TTTTCTTTCTCTTAGTTGCTTTT 7184 TGTT ATTCTGTI		
	TTCTTTCTCTTA		
	AAGAAAGAGAAT		
	_____ CAACGAAAA		
GAM455 EGLN3	TCTTGGCA-AGAAAACATGA 7154 CA_ GA I		
	TGG GAGAAAACATG		
	ACC TTCTTTTGAC		
	AGA G_ I		
GAM455 EGLN3	TCTTGGCA-AGAAAACATGA 7154 TCTCA GA		
	TGG GAGAAAACATGA		

ACC TTCTTTTGTACT
A___ G_
GAM455 ENTPD5 TTTTCTTTCCTTCTGAATT 7178 TGTT CTAA T
TTCTTTCT TTCTG
||||||| ||||
AAGAAAGG AAGAC
____ T
GAM455 GPR44 TCTGATGG-AGAGAAAACAT 7158 C G GA
TCT ATGG AGAGAAAACAT
||| ||| |||||||||
AGA TACC TCTCTTTTGTA
C _ II
GAM455 GPR44 TCTGATGG-AGAGAAAACAT 7158 CTCATG I
GGAGAGAAAACA
|||||||||
CCTCTCTTTTGT
AGACTA I
GAM455 ITSN1 TCTCATGGGAAATGATAAC 7157 _ A ATGA
TCTCATGGGAGA GA AAC
||||||||| |||
AGAGTACCCTTT CT TTG
A A IIIA
GAM455 ITSN1 TCTCATGGGAAATGATAAC 7157 _ AAII
TCTCATGGGAGA GA
||||||||| ||
AGAGTACCCTTT CT
A ATTGI
GAM455 KLHL1 TGTTTTCTTGTTTCCTACTATTCTGTT7164 TC_ _ III
TGTTTTCTT TCTTA ATTCTGTT
||||||| ||||| |||||||
ACAAAAGAA AGGAT TAAGACAA
CAA GA III
GAM455 KLHL1 TGTTTTCTTT-T-GAAATTCT 7170 CTCTT GT
TGTTTTCTTT AATTCT
||||||| |||||
ACAAAAGAAA TTAAGA
ACT_ II
GAM455 MEF2C TTTTCTTTCTCTT--TCCTGTT 7190 TGTT AA
TTCTTTCTCTT TTCTGT
||||||||| |||||
AAGAAAGAGAA AGGACA

GAM455 MEIS1 TCATTGCAGAAAAAACATGA 7153 GGG I
CAT AGAGAAAACATG
||| |||||||||
GTA TCTTTTTTGTAC
ACG I
GAM455 MEIS1 TCATTGCAGAAAAAACATGA 7153 TCTCATGGG
AGAGAAAACATGA
|||||||||

	TCTTTTTTGTACT		
	TAACG_____		
GAM455 OAS3	CATGTTAGGAGAGAAAACA	7148 CA_____	III
	TGGGAGAGAAAAC		
	ATCCTCTCTTTTG		
	GTACA TII		
GAM455 OAS3	CATGTTAGGAGAGAAAACA	7148 TCTCA	TGA
	TGGGAGAGAAAACA		
	ATCCTCTCTTTTGT		
	CA_____ CCC		
GAM455 PABPC3	TGTTTCCTTGCTCAGTTATCAATTCTGTT7167	T _____	III
	TGTTTCTT CTC TTAATTCTGTT A		
	III I		
	ACAAAGGAA GAG AGTTAAGACAA T		
	C TCAAT III		
GAM455 PAX4	CTCATAGG---GAAAACATGA	7151 _ AGA	
	TCATGGG GAAAACATG		
	AGTATCC CTTTTGTAC		
	G _____		
GAM455 PAX4	CTCATAGG---GAAAACATGA	7151 TC AGA	
	TCATGGG GAAAACATG		
	AGTATCC CTTTTGTAC		

GAM455 PGD	ATTGGAGAAAGAAAACATG	7147 A_ _	III
	TGG GAGAGAAAACAT		
	ACC CTTTCTTTTGTA		
	TA T CII		
GAM455 PGD	ATTGGAGAAAGAAAACATG	7147 TCTCAT	A
	GGGAGAGAAAACATG		
	CTCTTCTTTTGTAC		
	_____ G		
GAM455 PKHD1	TTTTGTTTTTCGTTTTTAATTCTGTT	7181 _ CTTTCTC	II
	TGTTTT TTAATTCTGTT		
	ACAAAA AATTAAGACAA		
	A AGCAA_ CC		
GAM455 PPP1R12B	TTTTCTTCTGCTTAAATGCTG	7179 TGTT _ TT_ TT	
	TTCTTTCT CTAA CTG		
	AAGAAAGA GAATT GAC		
	_____ C TAC TT		
GAM455 PRSS7	TTTTCTTCTTTTTTAAATTCTG	7182 TGTT CTT_____	I
	TTCTTTCT AATTCTGTT		

		AAGAAAGA	TTAAGACGA		
		_____ AAAAAT	I		
GAM455 PUM2		TTCTTTCTCTTGCTCCTGT	7173 TGTTTCT	AA	
		TTCTCTT TTCTG			
		AAGAGAA AGGAC			
		_____ CG			
GAM455 RP1		TTCATGGGA---AAAA-ATGA	7160	AACATG	
		TTCATGGGAGAGAA			
		AGAGTACCCTTTTTT			
		ACTII			
GAM455 RP1		TTCATGGGA---AAAA-ATGA	7160	AACI	
		TTCATGGGAGAGAA			
		AGAGTACCCTTTTTT			
		ACTI			
GAM455 SCA7		TCGTCGTCTTAATTCTGTT	7161 TGTTTCTTTC		
		TCTTAATTCTGT			
		AGAATTAAGACA			
		GC_____			
GAM455 SLC17A5		TTTTCTTTCT-TT-ATTCTTTT	7189 TGTT	CTTA	GT
		TTCTTTCT ATTCT			
		AAGAAAGA TAAGA			
		_____ AA_ AA			
GAM455 TAF7		TTGTCGTTTC-CTTAATTCT	7176 TGTTT _ T	GT	
		TC TTTC CTTAATTCT			
		AG AAAG GAATTAAGA			
		C_ C _ AG			
GAM455 TDO2		TGTATTCTTTCTCATCTTAATGCT	7166 T	TTAATTC	I
		TGT TTCTTTCTC TGTT			
		ACA AAGAAAGAG ACGA			
		T TAGAATT I			
GAM455 TMEM1		TGTGTATTTTCTCTGCTAATTCTGT	7168 _____	CTC	TII
		TGTTTTCTTT TTAATTCTGT			
		ATAAAAGAGA GATTAAGACA			
		ACAC C_ III			
GAM455 TRIM9		TTTCTTTCT-TT-CTTTTGTT	7175 TGT	C AA	GT
		TTTCTTTCT TT TTCT			
		AAAGAAAGA AA AAGA			
		G_ A CA II			
GAM455 TRIM9		TGTTTTCTTTCT-TTCTTTCT	7171	C AA	GT
		TGTTTTCTTTCT TT TTCT			

	ACAAAAGAAAGA AA AAGA		
	_ GA II		
GAM455 TRIM9	TGCTTTCTTTCT-TTCTTTC-GTT 7172	CTTAA GTT	
	TGTTTTCTTTCT TTCT		
	ACGAAAGAAAGA AAGA		
	_____ AAG		
GAM455 TRIM9	TTTTCTTTCT-TTCTTTCT 7185 TG	CTTAA G	
	TTTTCTTTCT TTCT		
	GAAAGAAAGA AAGA		
	AA _____ A		
GAM455 UTX	TTTTCTATCTTCTTAATTC 7180 TGTT T _ TGT		
	TTCT TCT CTTAATTC		
	AAGA AGA GAATTAAG		
	_____ T A TAI		
GAM455 ZNF277	TCTCATAGGAGA-AAAACATGA 7159	A I	
	TCTCATGGGAGAGAGAAA CATGA		
	AGAGTATCCTCTTTTT GTACT		
	_ I		
GAM455 ZNF277	TCTCATAGGAGA-AAAACATGA 7159 _	A I	
	CTCATGGGAGAGAGAAA CATG		
	GAGTATCCTCTTTTT GTAC		
	A _ I		
GAM456 ACK1	CGCCGGAACCTTTCCGGCCC 7195 C _ II		
	CGCT GAACTT CCGGCC		
	GCGG CTTGAA GGCCGG		
	C A GI		
GAM456 ACK1	CGCCGGAACCTTTCCGGCCC 7195 TGGACGCTC _		
	GAACTT CCGGCCCT		
	CTTGAA GGCCGGGG		
	C _____ A		
GAM456 ASB1	GACCCGCGACCACTTCCGGC 7197 GA__ TCGA III		
	CGC ACTTCCGG		
	GCG TGAAGGCC		
	CTGG CTGG GII		
GAM456 ASB1	GACCCGCGACCACTTCCGGC 7197 TGGA TCGA CCT		
	CGC ACTTCCGGC		
	GCG TGAAGGCCG		
	GG__ CTGG CGI		
GAM456 COPA	TGGAACACGAACTTCCGGTCTCTT 7200 C T CC II		
	TGGA GC CGAACTTCCGG CTT		

	ACCT TG GCTTGAAGGCC GAG		
	T T A_ AA		
GAM456 COPA	TGGAAACACGAACTTCCGGTCTCTT 7200 C T CCCTI		
	GA GC CGAACTTCCGG		
	CT TG GCTTGAAGGCC		
	T T AGAGI		
GAM456 DDX1	TGGCGGCGCGCGCTTCCGGCCC 7204 AC T AA TT		
	TGG GC CG CTTCCGGCCC		
	ACC CG GC GAAGGCCGGG		
	GC C GC II		
GAM456 DDX1	TGGCGGCGCGCGCTTCCGGCCC 7204 ____ A T AA I		
	GG CGC CG CTTCCGGCC		
	CC GCG GC GAAGGCCGG		
	CCG _ C ____ I		
GAM456 FUT6	GGA-GCTGAAAC--CCGGCCCTT 7198 C C CT I		
	GGA GCT GAA TCCGGCCC		
	CCT CGA CTT GGGCCGGG		
	_ _ T_ A		
GAM456 FUT6	GGA-GCTGAAAC--CCGGCCCTT 7198 TGGAC C CT		
	GCT GAA TCCGGCCCT		
	CGA CTT GGGCCGGGA		
	CT____ _ T_		
GAM456 GCN5L1	TGGACGCTC-ACCT--CGGC 7201 GA C CC		
	TGGACGCTC ACTTC GGC		
	ACCTGCGAG TGGAG CCG		
	____ _ II		
GAM456 GCN5L1	TGGACGCTC-ACCT--CGGC 7201 _ GA C		
	GGACGCTC ACTTC GG		
	CCTGCGAG TGGAG CC		
	A ____ _		
GAM456 MAPK12	GGGCGCTCCCGCTCCCGGCCCTT 7199 GA GAA I		
	CGCTC CTTCCGGCCCT		
	GCGAG GAGGGCCGGGA		
	CC GGC I		
GAM456 MAPK12	GGGCGCTCCCGCTCCCGGCCCTT 7199 T A GAA I		
	GG CGCTC CTTCCGGCCCTT		
	CC GCGAG GAGGGCCGGGAA		
	_ _ GGC G		
GAM456 MLLT2	ACGCTCGAAGACCGCCGGC 7193 ____ T III		
	ACGCTCGA ACT CCGG		

	TGCGAGCT TGG GGCC		
	TC C GII		
GAM456 MLLT2	ACGCTCGAAGACCGCCGGC 7193 TGGACG	__ T _ T	
	CTCGA ACT CCGGC CC		
	GAGCT TGG GGCCG GG		
	_____ TC C C I		
GAM456 RRM2	CGCGCG--CTCCCGGCCCTT 7196_ T AA	I	
	GC CG CTTCCGGCCCT		
	CG GC GAGGGCCGGGA		
	G C _ I		
GAM456 SOX11	TGGACGCTCCAAC--CCGGGCC 7203	G TT C T	
	TGGACGCTC AAC CCGG CC		
	ACCTGCGAG TTG GGCC GG		
	G _ C I		
GAM456 SOX11	TGGACGCTCCAAC--CCGGGCC 7203	G TT CI	
	TGGACGCTC AAC CCGG		
	ACCTGCGAG TTG GGCC		
	G _ CG		
GAM456 TBL1X	ACCCTGTAACGTCCGGCCCTT 7194 G CG T	I	
	C CT AAC TCCGGCCCT		
	G GA TTG AGGCCGGGA		
	G CA C I		
GAM456 TBL1X	ACCCTGTAACGTCCGGCCCTT 7194 TGGACGCTCG	T	
	AAC TCCGGCCCTT		
	TTG AGGCCGGGAA		
	GACA_____ C		
GAM456 TOP3A	TGG-CG-TGGAACTTCCGCCC 7202 A CTC	G T	
	TGG CG GAACTTCCG CCC		
	ACC GC CTTGAAGGC GGG		
	_ AC_ _ I		
GAM456 TOP3A	TGG-CG-TGGAACTTCCGCCC 7202 A CTC	GI	
	TGG CG GAACTTCCG		
	ACC GC CTTGAAGGC		
	_ AC_ GG		
GAM457 ADAMTS4	CAGGGTGAGGGCTATGAGGGGTC 7213 TC	CA A__ CI	
	AGGGTGAGG GTTA GGGTC		
	TCCCACTCC CGAT CCCAG		
	_ _ ACTC TI		
GAM457 ALEX2	TCCGGGTGAGGCTCTTCAG 7220 A	AGTTAAGGGTC	
	TC GGGTGAGGC		

	AG CCCACTCCG			
	G AGAAGTCIIIC			
GAM457 CACNB1	TCAGGGTGAGG--GTGAAGG 7221	CA T	GT	
	TCAGGGTGAGG GT AAGG			
	II			
	AGTCCCACTCC CA TTCC			
	__ C II			
GAM457 CRHR1	TCAGGGTGAAGGCAG-CAAGG 7219	_ T	GTC	
	TCAGGGTGA GGCAGT AAGG			
	AGTCCCACT CCGTCG TTCC			
	T _ III			
GAM457 FBXL11	AGGGAGAGCACAGTTAAGG 7209	TCAG T _	GTC	
	GG GAG GCAGTTAAGG			
	CC CTC TGTCAATTCC			
	___ T G TGI			
GAM457 GGT1	TCCGGGTCAGG--GTTAAGGGT 7224	A G CA	C	
	TC GGGT AGG GTTAAGGGT			
	AG CCCA TCC CAATTCCCA			
	G G _ I			
GAM457 GGT2	TCCGGGTCAGG--GTTAAGGGT 7224	A G CA	C	
	TC GGGT AGG GTTAAGGGT			
	AG CCCA TCC CAATTCCCA			
	G G _ I			
GAM457 ID1	CAGGCTGGATGCAGTTAAGGG 7211	TC G AG_	CC	
	AGG TG GCAGTTAAGGGT			
	TCC AC CGTCAATTCCCG			
	_ G CTA II			
GAM457 MAP2K2	GGGTGAGGCAG--GAGGGT 7217	TCAGGG	TTA	
	TGAGGCAG AGGGT			
	ACTCCGTC TCCCA			
	___ C_			
GAM457 MAPK4	GGGTGAGGCAAATACAGGG 7216	TCAGGG	TTA_ TC	
	TGAGGCAG AGGG			
	ACTCCGTT TCCC			
	___ TATG CA			
GAM457 MASP1	TCAGGGTGAGGC--TCAGGGGT 7223	AGTTA	TC	
	TCAGGGTGAGGC AGGG			
	AGTCCCACTCCG TCCC			
	AG__ CA			
GAM457 MATN2	CAGGGTGAG--ATTTCGGGTC 7214	TC	CAG AA	
	AGGGTGAGG TT GGGTC			

	TCCCCTCT AA CCCAG		
	___ A___ GG		
GAM457 MPO	TCAGGGTGAGGAAGAAAAAGG 7222	C TT	TCC
	TCAGGGTGAGG AG AAGGG		
	AGTCCCACTCC TC TTTCC		
	T TT III		
GAM457 NIPSNAP1	CAGGGTGAGG--GAACAGGGTC 7215 TC	CAGTTA	
	AGGGTGAGG AGGGTC		
	TCCCCTCC TCCCAG		
	___ CTTG___		
GAM457 NRXN1	GTGACGAAGAAATAAGGGTCC 7218 TCAGGGT	C T	
	GAGG AG TAAGGGTCC		
	CTTC TT ATTCCCAGG		
	___ _ T		
GAM457 PML	AGGGTGAGGGCAGTGCAGG 7208 TCAG	_ TA	TC
	GGTGAGG CAGT AGGG		
	CCACTCC GTCA TCCT		
	___ C CG TI		
GAM457 SLC21A2	AGGGTG--GCACTTAAGGGTC 7210 TCAG	GA G	
	GGT GGCA TTAAGGGTC		
	CCA CCGT AATTCCCAG		
	___ _ G		
GAM457 TMP21	AGGGTAAAGAGAAAGTTAAGGGT 7207 TCA	GT___ C	CCI
	GG GAGG AGTTAAGGGT		
	CC CTCT TCAATTCCCA		
	___ ATTT T CAI		
GAM457 XPNPEP2	CAGGGTGAGGGGAGCTAAG 7212 TC	C_	GGTC
	AGGGTGAGG AGTTAAG		
	TCCCCTCC TCGATTC		
	___ CC GIII		
GAM457 ZNF132	TCAGGGTGGA--AG--AAGGGCCC 7225	CAGTT	
	TCAGGGTGAGG AAGGGTC		
	AGTCCCACTTC TTCCCGG		

GAM458 ABCD4	GGGGT--CCTGCACAGGACC 7253	GG	CI
	GGGGT CCTGCACAGG		
	CCCCA GGACGTGTCC		
	___ TG		
GAM458 ABL1	AGGGGGAG-CCACCACAGGCC 7239	_ T TG	I
	GGGGG GGCC CACAGGCC		

	CCCC TCGG GTGTCCGG		
	T _ TG I		
GAM458 ABL1	AGGGGGAG-CCACCACAGGCC 7239 CAAG T TG		
	GGGG GGCC CACAGGCC		
	CCCC TCGG GTGTCCGGG		
	_____ TG		
GAM458 ADSS	CAAGGGGGTACCATG-ACTGCCCC 7245 G _ C AG I		
	CAAGGGGGTG CC TG AC GCCC		
	GTTCCCCCAT GG AC TG CGGG		
	_ T _ A _ G		
GAM458 ASH1	AGGGGGTGGCC-GC-CAGGC 7235 _ T A I		
	GGGGGTGGCC GC CAGG		
	CCCCACCGG CG GTCC		
	T _ _ I		
GAM458 ASH1	AGGGGGTGGCC-GC-CAGGC 7235 CAAG T A		
	GGGGTGGCC GC CAGGC		
	CCCCACCGG CG GTCCG		
	_____ - -		
GAM458 CACNA2D2	AGGGAGTGG---GCACAGGCC 7237 _ CCT		
	GGGGGTGG GCACAGGC		
	CCCTCACC CGTGTCCG		
	T _____		
GAM458 CACNA2D2	AGGGAGTGG---GCACAGGCC 7237 CAAG CCT		
	GGGGTGG GCACAGGC		
	CCTCACC CGTGTCCG		
	_____ _____		
GAM458 CCR2	TGTTT-CTTGCTTGCATCAG 7261 TGTCTA C CCC		
	CTTGCTTGCA CAG		
	GAACGAACGT GTC		
	ACAAA_ A		
GAM458 CORO2B	AAGGCTGTACCCTGCACAG 7229 GG G II		
	AAGG GTG CCTGCACA		
	TTCC CAT GGACGTGT		
	GA G CI		
GAM458 CORO2B	AAGGCTGTACCCTGCACAG 7229 CA GG G CC		
	AGG GTG CCTGCACAGG		
	TCC CAT GGACGTGTCT		
	_ GA G II		
GAM458 CYFIP2	GGGAGAGCATGCACAGGCC 7254 T_ C II		
	GGG GGC TGCACAGGCC		

	CCC TCG ACGTGTCCGG	
	TC T GI	
GAM458 CYFIP2	GGGAGAGCATGCACAGGCC 7254 CAAGGGGGT C	
	GGC TGCACAGGCC	
	TCG ACGTGTCCGG	
	_____ T	
GAM458 EXTL1	TCCACTCTGCCGCTGCACCAGC 7259 TGTC _ _ CCG	
	TACT TGCT TGCACCAGC	
	GTGA ACGG ACGTGGTCG	
	_____ G CG AGI	
GAM458 GALK1	GGGACTGGCCTG--CAGGCC 7250 _ G CA I	
	GGG TGGCCTGCA GGCC	
	CCT ACCGGACGT CCGG	
	C G _ I	
GAM458 GALK1	GGGACTGGCCTG--CAGGCC 7250 CAAGGGGG CA	
	TGGCCTGCA GGCC	
	ACCGGACGT CCGG	
	TG_____	
GAM458 GSPT1	GGGGGTGGCGGCGCTGC-CGGGCC 7247 CAA G _ ACA I	
	GG GGTGGC CTGC GGCC	
	CC CCGCCG GACG CCGGG	
	_____ A C GC_ G	
GAM458 GSPT1	GGGGGTGGCGGCGCTGC-CGGGCC 7247 GG _ ACA I	
	GGTGGC CTGC GGCC	
	CCGCCG GACG CCGG	
	CA C GC_ I	
GAM458 HDAC7A	AGGGCCTGGTGTGTCTGCACAGGGCC 7231 A GG GC CI	
	GG GTG CTGCACAGG	
	CC CAC GACGTGTCC	
	A A_ A_ CG	
GAM458 HDAC7A	AGGGCCTGGTGTGTCTGCACAGGGCC 7231 CAA_ GG GC _ CII	
	GG GTG CTGCACAGG CC	
	CC CAC GACGTGTCC GG	
	CCGGA A_ A_ C ACI	
GAM458 HOXC9	CAAGGCGCCGGCCTGCACGGGCC 7243 CA G _ A I	
	AGGG GT GGCCTGCAC GGCC	
	TTCC CG CCGGACGTG CCGGG	
	G_ G G C I	
GAM458 HOXC9	CAAGGCGCCGGCCTGCACGGGCC 7243 A G _ A I	
	AGGG GT GGCCTGCAC GGCC	

	TTCC CG CCGGACGTG CCGG		
	_ G G C I		
GAM458 IGHMBP2	CAAGGAGG-GGTTGGCACAGGCC 7242	T CCT	C
	CAAGGGGG GG GCACAGGCC		
	GTTCTCTCC CC CGTGTCCGG		
	_ AAC I		
GAM458 IGHMBP2	CAAGGAGG-GGTTGGCACAGGCC 7242 _	T CCT	I
	AAGGGGGG GG GCACAGGC		
	TTCCTCC CC CGTGTCCG		
	G _ AAC I		
GAM458 IL19	GGATGGCCTG--CAGGCC 7255	CA I	
	GGGTGGCCTGCA GGCC		
	CCTACCGGACGT CCGG		
	_ G		
GAM458 IL6R	AGGGGGTGGCTTCTGCCACAGCGCC 7232 CAAG	___ _ _ CII	
	GGGGTGGC CTGC ACAG GCC		
	CCCCACCG GACG TGTC CGG		
	___ AAG G G CGI		
GAM458 IL6R	AGGGGGTGGCTTCTGCCACAGCGCC 7232 GGG GG	_ _ I	
	GGT CCTGC ACAG GC		
	CCG GGACG TGTC CG		
	A_ AA G G I		
GAM458 IVD	AGGGGGTGGGCTGCAGCAG 7234	C CAII	
	AGGGGGTGG CTGCA		
	TCCCCCACC GACGT		
	C CGTC		
GAM458 IVD	AGGGGGTGGGCTGCAGCAG 7234 CAAG	C CA	
	GGGGTGG CTGCA GGCC		
	CCCCACC GACGT TCGG		
	___ C CG		
GAM458 LAMC1	CTACTTGCTCTACCCAGC 7246 TGTCTA	_ A CC	
	CTTGCT TGC CCAGC		
	GAACGA ATG GGTCG		
	___ G G TA		
GAM458 MAPK4	AGGGGGTGTG-TGCACAGGCC 7238 _	GCC I	
	GGGGGTG TGCACAGGC		
	CCCCCAC ACGTGTCCG		
	T AC_ I		
GAM458 MAPK4	AGGGGGTGTG-TGCACAGGCC 7238 CAAG	GCC	
	GGGGTG TGCACAGGCC		

	CCCCAC ACGTGTCCGG			
	_____ AC_			
GAM458 MLC1	GGGGGTGGCCTGCAGACAGG	7249	___ III	
	GGGGGTGGCCTGC ACAG			
	CCCCACCGGACG TGTC			
	TC CII			
GAM458 MLC1	GGGGGTGGCCTGCAGACAGG	7249 CAAGGG	___ CC	
	GGTGGCCTGC ACAGG			
	CCACCGGACG TGTCC			
	_____ TC CA			
GAM458 NF2	GGAGTTGC-TGCACAGGCC	7252 G C I		
	GGGGT GC TGCACAGGC			
	CCTCA CG ACGTGTCCG			
	A _ G			
GAM458 NF2	GGAGTTGC-TGCACAGGCC	7252 CAAGGGGGTG C		
	GC TGCACAGGC			
	CG ACGTGTCCG			
	AA_____			
GAM458 PLCG1	GGGGGCGGCGGCGGCACAGGCC	7248 _ CT I		
	GG GGTGGC GCACAGGC			
	CC CCGCCG CGTGTCCG			
	G C_ I			
GAM458 PLCG1	GGGGGCGGCGGCGGCACAGGCC	7248 CAA G CT C		
	GG GGTGGC GCACAGGCC			
	CC CCGCCG CGTGTCCGG			
	___ G C_ T			
GAM458 RASGRP2	AGCGGGTGG----CACAGGCC	7236 _ G CTGC		
	G GGGTGGC ACAGGC			
	C CCCACCG TGTCCG			
	T G _____			
GAM458 RASGRP2	AGCGGGTGG----CACAGGCC	7236 CAAGG CTGC		
	GGGTGGC ACAGGC			
	CCCACCG TGTCCG			
	G_____			
GAM458 SAR1	TACTGACCTGCACCAGCACG	7258 TGTCTACTT C		
	GCTTGCACCAGC C			
	TGGACGTGGTCG G			
	C_____ T			
GAM458 SCN4A	AAGGGGGTGGGCTG-GCAGTGCCC	7230 C CA _ I		
	AGGGGGTGG CTG CAG GCC			

	TCCCCCACC GAC GTC CGG	
	C C_ A I	
GAM458 SCN4A	AAGGGGGTGGGCTG-GCAGTGCCC 7230 CA	C CA _ I
	AGGGGGTGG CTG CAG GCCC	
	TCCCCCACC GAC GTC CGGG	
	_ C C_ A A	
GAM458 SFRS7	TAATTACTTTGCACCAGCC 7257 TGTCTACT _ C	
	TGCTT GCACCAGCC	
	ATGAA CGTGGTCGG	
	_ _ _ A A	
GAM458 SH2D1A	TGTCTACTTGCCTTAAACC 7260 GC_ AGCCC	
	TGTCTACTTGCTT ACC	
	ACAGATGAACGGA TGG	
	ATT GC	
GAM458 SOX9	GGGGTGGCCAGTTCACAGCTGCC 7251 GGGT TG_ _ I	
	GGCC CACAG GCC	
	CCGG GTGTC CGG	
	_ TCAA GA I	
GAM458 SSRP1	GGTGGCCTGGGCAGAGCCC 7256 CA _ II	
	GGTGGCCTG CAG GCC	
	CCACCGGAC GTC CGG	
	CC T GI	
GAM458 SSRP1	GGTGGCCTGGGCAGAGCCC 7256 CAAGG _ GCA C	
	GGGT GGCCT CAGGC	
	CCCG TCGGG GTCCG	
	GA_ TC _ A	
GAM458 TBX6	AGGGGGTGG-GTGGGCAGGCCC 7240 _ CC CA I	
	GGGGGTGG TG CAGGCC	
	CCCCCACC AC GTCCGG	
	T C_ CC I	
GAM458 TBX6	AGGGGGTGG-GTGGGCAGGCCC 7240 CAAG CC CA	
	GGGGTGG TG CAGGCC	
	CCCCACC AC GTCCGGG	
	_ C_ CC	
GAM458 TEM6	AGGGGGTGGGGTGCACCCATGCC 7233 CAAG CC AG_ I	
	GGGGTGG TGCAC GCCC	
	CCCCACC ACGTG CGGG	
	_ CC GGTA T	
GAM458 TEM6	AGGGGGTGGGGTGCACCCATGCC 7233 GG CC AG_ I	
	GGGTGG TGCAC GCC	

	CCCACC ACGTG CGG		
	___ CC GGTA I		
GAM458 TNFAIP1	AAGGGGCAGTAGCCTTCTGCACAGGGCC7228 CA	___	___ CIII
	AGGGG GTGGCCT GCACAGG CC		
	TCCCC CATCGGA CGTGTCC GG		
	___ GT AGA C AIII		
GAM458 TNFAIP1	AAGGGGCAGTAGCCTTCTGCACAGGGCC7228 GGG	___	CCI
	GGTGGCCT GCACAGG		
	TCATCGGA CGTGTCC		
	G___ AGA CII		
GAM458 TRPM2	CAAGGGCCCAGC-TGCACAGGCCC 7244	GG C	I
	CAAGGG TGGC TGCACAGGCCC		
	GTTCCC GTCG ACGTGTCCGGG		
	GG _ I		
GAM458 TRPM2	CAAGGGCCCAGC-TGCACAGGCCC 7244_	GG C	I
	AAGGG TGGC TGCACAGGCC		
	TTCCC GTCG ACGTGTCCGG		
	G GG _ I		
GAM458 WNT5A	AGGGGGTGGGGGGC-GAGGCCC 7241_	CCT AC	I
	GGGGGTGG GC AGGCC		
	CCCCACC CG TCCGG		
	T CCC C_ I		
GAM458 WNT5A	AGGGGGTGGGGGGC-GAGGCCC 7241 CAAG	CCT AC	
	GGGGTGG GC AGGCC		
	CCCCACC CG TCCGGG		
	___ CCC C_		
GAM459 ABCG1	ATTTTTTAGGAAGAAACCGGA 7271 ATA	TAA_	III
	TTTTAGGAA CGG		
	AAAATCCTT GCC		
	TAA CTTTG TII		
GAM459 COL15A1	AATAATATTTTAGGGAAAA 7269	AATAII	
	AATGATATTTTAGG		
	TTATTATAAAATCC		
	CTTTI		
GAM459 COL15A1	AATAATATTTTAGGGAAAA 7269 GA	AATAACGG	
	ATGATATTTTAGG		
	TATTATAAAATCC		
	___ CTTTTII		
GAM459 GOCAP1	AATGATATTTTAGGAGATAA 7265	_ ATAI	III
	AATGATATTTT AGGA		

	TTACTATAAAA TCCT		
	A CTATTI		
GAM459 GOCAP1	AATGATATTTTTAGGAGATAA	7265 GA	_ ATAACGGA
	ATGATATTTT AGGA		
	TACTATAAAA TCCT		
	_ A CTATTII		
GAM459 MGAT5	GAATGATATATATATGCTTAATGG	7272	TT_ GGAA C AI
	GAATGATAT TA TAA GG		
	CTTACTATA AT ATT CC		
	TAT ACGA A II		
GAM459 MME	AATG-TATTTTAGGGAAATA	7267 A	AATII
	AATG TATTTTAGG		
	TTAC ATAAAATCC		
	_ CTTTA		
GAM459 MME	AATG-TATTTTAGGGAAATA	7267 GA A	AATAACGG
	ATG TATTTTAGG		
	TAC ATAAAATCC		
	_ _ CTTTATAI		
GAM459 MORC	AATGTT-TTTAAGGAATAAC	7270 GAATGATA	_ G
	TTTTA GGAATAACG		
	AAAAT CCTTATTGT		
	TACA_ T I		
GAM459 POLK	AATTATATTTTTAGGCAAAAAC	7268 AATG	AATAI
	ATATTTTAGG		
	TATAAAATCC		
	A_ GTTTT		
GAM459 POLK	AATTATATTTTTAGGCAAAAAC	7268 GAATG	AAT_ GGA
	ATATTTTAGG AAC		
	TATAAAATCC TTG		
	TAA_ GTTT GII		
GAM459 PTPN2	AAAGATATTTTTAGGAAAAAC	7266 AT	_ TAAI
	GATATTTT AGGAA		
	CTATAAAA TCCTT		
	T_ A TTTI		
GAM459 PTPN2	AAAGATATTTTTAGGAAAAAC	7266 GAAT	_ T GGA
	GATATTTT AGGAA AAC		
	CTATAAAA TCCTT TTG		
	TT_ A T AII		
GAM459 XBP1	AATAAGTATTTTTAGGGAAAAC	7264 GA	_ AAT GGA
	ATGA TATTTTAGG AAC		

	TATT ATAAAATCC TTG	
	___ C CTT All	
GAM460 ARF3	AGCAGGTT-ATGGGCAGCT 7281 TA AGCTTG A	
	AGG ATGGGCAGCT	
	TCC TACCCGTCGA	
	G_ AA___ C	
GAM460 ARHH	AAAGAGCCCTCAGTGGGCAGCT 7276 TA GA___ AGA	
	AGGAGCTT TGGGCAGCT	
	TTCTCGGG ACCCGTCGA	
	___ AGTC CII	
GAM460 FIGF	TAAGCAG-TTGACATCAGGCAGCTAGA7287 G C ___ II	
	TAAG AG TTGAT GGGCAGCTAGA	
	ATTC TC AACTG TCCGTCGATCT	
	G _ TAG II	
GAM460 FRK	AGGAGCT---GGGCAGCT 7282 TAAG TGAT	
	GAGCT GGGCAGCT	
	CTCGA CCCGTCGA	

GAM460 KPNA3	AAGGAGTATCAGTGGGCAGCT 7277 TA C_ GA AGA	
	AGGAG TT TGGGCAGCT	
	TCCTC AG ACCCGTCGA	
	___ AT TC CII	
GAM460 LPL	AAGGGGATGGCAGGGCAGCTAGA 7279 TAA GCTTGAT I	
	GGA GGGCAGCTAGA	
	CCT CCCGTCGATCT	
	TCC ACCGT___ T	
GAM460 NOS2A	TAAAGGGCTTGATGGGGAGC 7288 T_ A C TAG	
	AAGG GCTTGATGGG AGC	
	TTCC CGAACTACCC TCG	
	AT _ C III	
GAM460 PFKFB4	AGGTCCATGCTGGGCAGCT 7284 TAAGGAGCT A AG	
	TG TGGGCAGCT	
	AC ACCCGTCGA	
	CAGGT___ G CC	
GAM460 PRM1	GGAAGTCTG-TGGGCAGCTGAGA 7286 TAAGGA GA _	
	GCTT TGGGCAGCT AGA	
	TGAG ACCCGTCGA TCT	
	___ AC C	
GAM460 SLC12A7	TAGGAAGCCCCATGGGCAGCT 7289 TA _ G AGA	
	AGGA GCTT ATGGGCAGCT	

	TCCT CGGG TACCCGTCGA	
	A_ T G III	
GAM460 SMCX	AAGCAGGCTTGATGGTCAGAAAGA 7275 TAA A G CT I	
	GG GCTTGATGG CAG AGA	
	II IIIIIII III III	
	TC CGAACTACC GTC TCT	
	TCG _ A TT C	
GAM460 SYNGR1	AGGCACCTGCTGGGCAGCT 7283 TAAGGA A AG	
	GCTTG TGGGCAGCT	
	IIII IIIIIII	
	TGGAC ACCCGTCGA	
	CG_ G CC	
GAM460 TACR1	AAGGCTTTTTATGGGCAGC 7278 TA AGCTTG TAG	
	AGG ATGGGCAGC	
	III IIIIIII	
	TCC TACCCGTCG	
	_ GAAAAA TII	
GAM460 WRN	AGGTGCG-GCTGGGCAGCTAGA 7285 TAAGGA TTGA	
	GC TGGGCAGCTAGA	
	II IIIIIIIII	
	CG ACCCGTCGATCT	
	CA_ CCG_	
GAM460 ZNF74	AGGAG---GAGTGGGCAGCT 7280 TA CTTGA A	
	AGGAG TGGGCAGCT	
	IIII IIIIIII	
	TCCTC ACCCGTCGA	
	C_ _ C	
GAM461 ABCD1	GGCA---GGGGCCGGGGACG 5808 TG TCC TC	
	GCA GGGGCCGGGG GC	
	III IIIIIII II	
	CGT CCCC GGCCCC TG	
	_ _ _	
GAM461 AES	GCATACCTGGGACCCGGGGTCGGGG 5804 _ C C TCGCGGII	
	TGG ATCCGGGG CGGGG	
	III IIIIIII IIII	
	ACC TGGGCCCC GCCCC	
	TATGG C A CTIIIGGC	
GAM461 FLNA	GGCGGCCTGGGCCGGGGTTGAGG 5811 T_ ATCCG CGC I	
	GGC GGGCCGGGGT GG	
	III IIIIIII II	
	CCG CCGGGCCCCA CC	
	CG GA_ ACT C	
GAM461 GALNT2	GGGATGCCGGGGCCGAGGCCG 5805 T C _ CGG	
	GG AT CCGGGGCCGGGGTCTG	
	II II IIIIIIIIIII	
	CC TA GGCCCCGGCTCCGGC	
	_ _ C CII	
GAM461 INSM1	TCGGGGGCCGGGGTGGAGG 5812 TGGCAT CC_ T	
	CCGGGG GGGG CGCG	
	IIII III IIII	

	GGCCCC TCCC GCGC	
	CC_____ ACC _	
GAM461 NGB	GGCTGCCGGG--CGGGGTCGC 5810 TG AT GC G	
	GC CCGGG CGGGGTCGC	
	CG GGCCC GCCCAGCG	
	_ AC _ G	
GAM461 PTPRS	GGCATCCGGGGCCAGTGGTGTCCG 5806 TG _ CG I	
	GCATCCGGGGCCCGG GGT CGG	
	CGTAGGCCCGGTC CCA GCC	
	_ A CA C	
GAM461 RPS6KA2	GGC-TCCGAGGCCGGGGTC 5807 TG A GC	
	GC TCCGGGGCCGGGGTC	
	CG AGGCTCCGGCCCCAG	
	_ _ AI	
GAM461 RUNX3	ATCCCGGGCCGGGGTGGGGG 5802 TGGCATCCG CGC	
	GGGCCGGGGT G	
	I	
	CCCGGCCCA C	
	G_____ CCC	
GAM461 SGT	GGCA--CAGGGCCGGGGTGGC 5809 TG TC C G	
	GCA CGGGGCCGGGGT GC	
	CGT GTCCCGGCCCA CG	
	_ _ C G	
GAM461 TRAF1	CATTCGGGGCCGGAGTGGC 5803 TGGCATC C G	
	CGGGGCCGGGGT GC	
	GCCCCGGCCTCA CG	
	A_____ C A	
GAM462 HSF2BP	AGCGAGGAGTGGCCTTGGCGAGGTCCC7303 GCTT _ _ I	
	GGAGTGGCC GC AGGTCC	
	CCTCACCGG CG TCCAGG	
	_ AAC C I	
GAM462 HSF2BP	AGCGAGGAGTGGCCTTGGCGAGGTCCC7303 TA TT _ _	
	GC GGAGTGGCC GC AGGTCCC	
	CG CCTCACCGG CG TCCAGGG	
	_ CT AAC C AII	
GAM462 IL12RB2	GCTGGGCGGTGGCCGCAGG 7305 T A_ II	
	GCT GG GTGGCCGCAG	
	CGA CC CACCGGCGTC	
	C GC CI	
GAM462 IL12RB2	GCTGGGCGGTGGCCGCAGG 7305 TAGCTT A_ TCC	
	GG GTGGCCGCAGG	

		CC CACCGGCGTCC		
		AC___ GC CGI		
GAM462 JUND		GGAGTGGCCGCGGCCTCCC 7307	A	CII
		GGAGTGGCCGC GGTC		
		CCTCACCGGCG CCGG		
		_ AGG		
GAM462 MAP3K11		TAGCTTGGAGGGACCCGAGCTTCC 7308	T	GC G_ CI
		TAGCTTGGAG GGCC AG TCC		
		ATCGAACCTC CTGG TC AGG		
		C GC GA II		
GAM462 MAP3K11		TAGCTTGGAGGGACCCGAGCTTCC 7308	T	GCA CCI
		AGCTTGGAG GGCC GGT		
		TCGAACCTC CTGG TCG		
		C GC_ AAG		
GAM462 MDM2		GCTTGGAGT---CGGGGGTCCC 7306_	GGC	CA
		CTTGGAGT CG GGTCC		
		GAACCTCA GC CCAGG		
		C _ CC		
GAM462 MDM2		GCTTGGAGT---CGGGGGTCCC 7306 TAGC	GGC	CA
		TTGGAGT CG GGTCC		
		AACCTCA GC CCAGG		
		_ _ CC		
GAM462 USP6		CTGGGGGTGGC---AGGTCCC 7304 A_ CGC		
		TTGG GTGGC AGGTCC		
		GACC CACCG TCCAGG		
		CC _		
GAM462 USP6		CTGGGGGTGGC---AGGTCCC 7304 TAGCTT A CGC		
		GG GTGGC AGGTC		
		CC CACCG TCCAG		
		C _ _		
GAM463 CIT		GAAAGCAG-T----TCACAGATG 7322 TGAAAGC GA		
		AGGTAG TCACAGA		
		TTCGTC AGTGTCT		
		T _ _ A_		
GAM463 DDT		AAGCAGCCAGT-TCACAGATG 7317 TGAAAG G GA		
		CAG TAG TCACAGAT		
		GTC GTC AGTGTCTA		
		_ _ G A_		
GAM463 LZTS1		AAGCAGGTAGGGACTCCCAG 7315 TGAAAG A_ A AT		
		CAGGTAGG TC CAG		

	GTCCATCC AG GTC	
	_____ CTG G GG	
GAM463 MSL3L1	GAAAGCAGGCAGCATGACAG 7321 TG	G C AT
	AAAGCAGGTAG AT ACAG	
	TTTCGTCCGTC TA TGTC	
	_____ G C GI	
GAM463 MTR	AAGCAGGTAAGTGTGTCAGCCAGATG 7314 TGAAAG	A_ _ I
	CAGGTAGG TCA CAGATG	
	GTCCATTC AGT GTCTAC	
	_____ AC CG G	
GAM463 POLH	AAGTAGCTGGGATCACAGGTG 7318 TGAA AGGTA	ATG
	AGC GGATCACAG	
	TCG CCTAGTGTC	
	A_ AC_ CAC	
GAM463 PRPS1	AATGCAGGTAGGAGGTCCCAG 7311 TGAAA	_ A ATG
	GCAGGTAGGA TC CAG	
	CGTCCATCCT AG GTC	
	A_ CC G GTI	
GAM463 S100A4	GACAGCAGTCAGGATCACA 7320 TGAA	G GAT
	AGCAG TAGGATCACA	
	TCGTC GTCCTAGTGT	
	TG_ A GII	
GAM463 STAT1	AGCAGGAGGGAATCACAGATG 7319 TGAAAGCA TA _	
	GG GGA TCACAGATG	
	CC CCT AGTGTCTAC	
	_____ TC T	
GAM463 TAX1BP1	AAAGCAGGTAAGATTAACAGA 7312 TGAA	C_ TG
	AGCAGGTAGGAT ACAGA	
	TCGTCCATTCTA TGTCT	
	_____ AT CT	
GAM463 USP14	AAGTAGCTGGGATCACAGGTG 7318 TGAA AGGTA	ATG
	AGC GGATCACAG	
	TCG CCTAGTGTC	
	A_ AC_ CAC	
GAM463 WDR4	AAGCAG--AGGACAAATCACAGATG 7316 TGAA	C TA I
	AG AGG GGATCACAGATG	
	TC TCC TTTAGTGTCTAC	
	G_ _ TG G	
GAM463 XRCC2	AAAGT-GCTAGGATCACAG 7313 TGAAA AGG	A
	GC TAGGATCACAG	

	CG ATCCTAGTGTC		
	TCA__ C		
GAM464 AVP	CATAGAGCAGGGCATGGGGACTC	7326	A__ IIIG
	CATAGAG ATGGGGACT		
	GTATCTC TACCCCTGA		
	GTCCCG GII		
GAM464 AVP	CATAGAGCAGGGCATGGGGACTC	7326	TCCCAGCA AGA I
	TAG ATGGGGACTC		
	GTC TACCCCTGAG		
	C__ CCG T		
GAM464 CTNNA1	CCATCACTAAGAGAATGGGCATCTC	7328	A AT GACTI
	GC AGAGAATGGG		
	TG TCTCTTACCC		
	G AT GTAGI		
GAM464 CTNNA1	CCATCACTAAGAGAATGGGCATCTC	7328	TCCCAG __ GA_ II
	CAT AGAGAATGGG CTC		
	GTG TCTCTTACCC GAG		
	TA__ AT GTA CC		
GAM464 EPHX1	TCCCAGCAT-GGGCA-GGGGAC	7337	AGAGAAT T
	TCCCAGCAT GGGGAC		
	AGGGTCGTA CCCCTG		
	CCCGT__ I		
GAM464 EPHX1	TCCCAGCAT-GGGCA-GGGGAC	7337	_ AGAGAAT I
	CCCAGCAT GGGGA		
	GGGTCGTA CCCCT		
	A CCCGT__ I		
GAM464 FGR	TCCCTGC-TACAGAATGGGG	7335	A A G ACT
	TCCC GC TA AGAATGGGG		
	AGGG CG AT TCTTACCCC		
	A _ G		
GAM464 FGR	TCCCTGC-TACAGAATGGGG	7335	_ A A G I
	CCC GC TA AGAATGGG		
	GGG CG AT TCTTACCC		
	A A _ G I		
GAM464 FXR2	CCAACAGGTGGAGAATGGGG	7327	TA__
	CCAGCA GAGAATGGG		
	GGTTGT CTCTTACCC		
	CCAC CII		
GAM464 FXR2	CCAACAGGTGGAGAATGGGG	7327	TCC CATA ACT
	CAG GAGAATGGGG		

	GTC CTCTTACCCC		
	TT_ CAC_ CAI		
GAM464 HNF3G	CCCATGCCAGAGAGAATGGTGAC 7330	___ CAT	G I
	CCAG AGAGAATGG GA		
	GGTC TCTCTTACC CT		
	TAC ___ A I		
GAM464 HNF3G	CCCATGCCAGAGAGAATGGTGAC 7330	TC _ AT_	G TCI
	CCA GC AGAGAATGG GAC		
	GGT CG TCTCTTACC CTG		
	___ A GTC A CII		
GAM464 IER5	TCCCCGGAGAACGAATGGGGA ACTC 7336	AGCATAGA	_ II
	TCCC GAATGGGGA CTC		
	AGGG CTTACCCCT GAG		
	GCCTCTTG T II		
GAM464 IER5	TCCCCGGAGAACGAATGGGGA ACTC 7336	AGCATAGA	CTI
	CCC GAATGGGGA		
	GGG CTTACCCCT		
	CCTCTTG_ TGA		
GAM464 PRKCABP	CCCAGCTCGGTAGGGGAATGGGGA 7331	CCAGCA A_	I
	TAG GAATGGGG		
	ATC CTTACCCC		
	GAGCC_ CC I		
GAM464 PRKCABP	CCCAGCTCGGTAGGGGAATGGGGA 7331	TC A___ A_	CTCI
	CCAGC TAG GAATGGGGA		
	GGTCG ATC CTTACCCCT		
	___ AGCC CC TIII		
GAM464 PTPN7	CCCTGAACAGAGAATGGAGGCCTC 7332	___ C	ACTI
	G ATAGAGAATGGGG		
	C TGTCTCTTACCTC		
	GA T CIII		
GAM464 PTPN7	CCCTGAACAGAGAATGGAGGCCTC 7332	TC AGC	A_ I
	CC ATAGAGAATGGGG CTC		
	GG TGTCTCTTACCTC GAG		
	___ ACT CG G		
GAM464 RECQL	CCTGCATGGAAAAGAATGGGGA 7329	A ___	III
	CC GCAT AGAGAATGGGG		
	GG CGTA TTTCTTACCCC		
	A CCT TII		
GAM464 RECQL	CCTGCATGGAAAAGAATGGGGA 7329	TCCCA ___	CTC
	GCAT AGAGAATGGGGA		

		CGTA TTTCTTACCCCT			
		A____ CCT CTI			
GAM464 SURF5		TCCCAGCATGGCCAATGGG 7333	AGAG	GA	CT
		TCCCAGCAT AATGGG			
		AGGGTCGTA TTACCC			
		CCGG IIIC			
GAM464 SURF5		TCCCAGCATGGCCAATGGG 7333	AGAG	II	
		TCCCAGCAT AATGG			
		AGGGTCGTA TTACC			
		CCGG CI			
GAM464 TIMM23		CAGCACACAGAATGGGGAATC 7325	G	CTI	
		AGCATA AGAATGGGGA			
		TCGTGT TCTTACCCCT			
		G TAI			
GAM464 TIMM23		CAGCACACAGAATGGGGAATC 7325	TCCCAG	G	CTC
		CATA AGAATGGGGA			
		GTGT TCTTACCCCT			
		____ G TAG			
GAM464 TRIM9		TCCCATTACTGAGAATGGG 7334	GC A	GA	CT
		TCCCA AT GAGAATGGG			
		AGGGT TG CTCTTACCC			
		AA A IIIC			
GAM464 TRIM9		TCCCATTACTGAGAATGGG 7334	GC A	II	
		TCCCA AT GAGAATGG			
		AGGGT TG CTCTTACC			
		AA A CI			
GAM465 BACH1		TGGAGAACCAAGACTGTATCC 7347	C A	C	GAG
		TGGAGAACCAG GC GTA CC			
		ACCTCTTGGTT TG CAT GG			
		C A A III			
GAM465 BACH1		TGGAGAACCAAGACTGTATCC 7347	C A	CCI	
		GGAGAACCAG GC GTA			
		CCTCTTGGTT TG CAT			
		C A AGI			
GAM465 GNA11		GGAGAACCAGTCTCGGTGCC 7343	CGCAGTACII		
		GGAGAACCAG			
		CCTCTTGGTC			
		AGAGCCACGG			
GAM465 GNA11		GGAGAACCAGTCTCGGTGCC 7343	TG	CGCA_ A	CGA
		GAGAACCAG GT CC			

	CTCTTGGTC CA GG	
	AGAGC C AII	
GAM465 HUNK	AGAACCA--GCTGTAACCG 7340	GCAGT CI
	AGAACCAGC ACC	
	III	
	TCTTGGTCG TGG	
	ACAT_ CI	
GAM465 HUNK	AGAACCA--GCTGTAACCG 7340	TGGAGA GCA C
	ACCAGC GTA CCG	
	III III	
	TGGTCG CAT GGC	
	A_ T	
GAM465 KCNK5	AGAACCAGC-CAG-AGCTGAG 7341	G TACCCGI
	AGAACCAGC CAG	
	III	
	TCTTGGTCG GTC	
	_ TCGACTC	
GAM465 KCNK5	AGAACCAGC-CAG-AGCTGAG 7341	TGGAGA G TACCC
	ACCAGC CAG GA	
	III II	
	TGGTCG GTC CT	
	_ TCGA_	
GAM465 RAB5A	TGGAGACTACAATGCAGTACCC 7346	AC_ C GAG
	TGGAGA CAG GCAGTACCC	
	III	
	ACCTCT GTT CGTCATGGG	
	GAT A III	
GAM465 RAB5A	TGGAGACTACAATGCAGTACCC 7346	G AC_ C I
	GAGA CAG GCAGTACC	
	III	
	CTCT GTT CGTCATGG	
	_ GAT A I	
GAM465 SYNGR1	GGAGAAACAGATGGGCGAGTACCCTGAG7344	AAC C_ GAI
	CAG GCAGTACCC	
	III	
	GTC CGTCATGGG	
	TT_ TACC III	
GAM465 SYNGR1	GGAGAAACAGATGGGCGAGTACCCTGAG7344	TG C C_ _ III
	GAGAA CAG GCAGTACCC GAG	
	III III	
	CTCTT GTC CGTCATGGG CTC	
	_ T TACC A CII	
GAM465 TMPRSS3	AGAACGAA---AGTACCCGAG 7342	GAACC C_
	AGCG AGTACCCGA	
	TTGC TCATGGGCT	
	TC_ TT	
GAM465 TPMT	GGAGAACCA-C-CCGAACCCG 7345_	GCGCAGT I
	GAGAACCA ACCC	

	CTCTTGGT TGGG		
	C GGGCT__ I		
GAM465 TPMT	GGAGAACCA-C-CCGAACCCG 7345 TG	GCGCAGT A	
	GAGAACCA ACCCG		
	CTCTTGGT TGGGC		
	__ GGGCT__ C		
GAM466 CCND2	TAAGAAGTGGAGAGGAAGAAA 7360	C CAC CTT	
	TAAGAAGTGGGA AG GAAA		
	ATTCTTCACCT TC CTTT		
	C CTT		
GAM466 CCR9	AAGA--TGGACATTTTCACGAAACTT 7350 TAAGAA	G__ I	
	GTGGACA CACGAAACTT		
	TACCTGT GTGCTTTGAA		
	TC__ AAAA A		
GAM466 ENO2	AAGAAGTGGAAAGTGCGGAAC 7353 TA	C CA A T	
	AGAAGTGGGA AG CG AACT		
	TCTTCACCT TC GC TTGG		
	__ T AC C I		
GAM466 ESR1	AGAAGTGGACTCTACTGAACCTT 7355 TAAG	AGC GA I	
	AAGTGGAC AC AACTT		
	TTCACCTG TG TTGGA		
	__ AGA AC A		
GAM466 F8A	TAAGAAGTGAGGGGCAGGATGAAA 7359	ACA C AACTTI	
	TAAGAAGTGG GCA GA		
	ATTCTTCACT CGT CT		
	CCC C ACTTTI		
GAM466 NFYC	AAGAAGTGG-CAGTAACAAAC 7352 TA	A C_ ACT	
	AGAAGTGG CAG ACGAA		
	TCTTCACC GTC TGTTT		
	__ _ AT GTI		
GAM466 PLXNA2	GAACTGGCTATGACGAAACTT 7358 TAAGAAG	ACAGC	
	TGG ACGAAACTT		
	ACC TGCTTTGAA		
	G__ GATAC		
GAM466 RNF26	AAGAAGTGGGTAAGACGGAA 7351 TA	AC_ C AACT	
	AGAAGTGG AG ACG		
	TCTTCACC TC TGC		
	__ CAT _ CTTCI		
GAM466 SLC24A1	GAAGCTGGACAGCAGGGAAC 7356 TAAGAAG	C_ _	
	TGGACAGCA GAA ACT		

ACCTGTCGT CTT TGG
 CG_____ CC G
 GAM466 SYK AGAAGTGGAAAGACATGAAA 7354 TAAG C _ C CT
 AAGTGGA AG CA GAAA
 ||||| || || ||||
 TTCACCT TC GT CTTT
 _____ T T A CC
 GAM466 TSN GAAGTGGACCGCGCAGGCAAC 7357 TAAGAA A__ CGA T
 GTGGAC GCA AACT
 ||||| || ||||
 CACCTG CGT TTGG
 _____ CGG CCG T
 GAM467 ANKRD3 TCAGTCCCCA-GCACTGAGGT 7373 TGTC G C
 AGTCCCCAG C CTGAGGT
 ||||| || |||||
 TCAGGGGTC G GACTCCA
 _____ _ T
 GAM467 CRY2 TGGCAGTCCCCA-TCCCTGAG 7378 T GG GT
 TG CAGTCCCCA CCCTGAG
 || ||||| |||||
 AC GTCAGGGGT GGGACTC
 C A_ ||
 GAM467 CSK TCCCCAGGCCCCACAGGTG 7374 TGTCA _ CCC A
 GTCCC CAGG TG GGT
 |||| ||| || |||
 CGGGG GTCC AC CCA
 C_____ T _____
 GAM467 CSK TCAGTCCCCACAGGCCCATGA 7368 TGTC _ _ GGTG
 AGTCCCCA GGCCC TGA
 ||||| |||| |||
 TCAGGGGT CCGGG ACT
 _____ GT T GGII
 GAM467 EGFL3 TCAG--CCCAGGCCCAGAGCGTG 7371 TGTCAGTC T _
 CCCAGGCCC GAG GTG
 ||||| || |||
 GGGTCCGGG CTC CAC
 TC_____ T G
 GAM467 GADD45G GTCTGTCCTTCTGGCCCTGAGG 7366__ AG CCA GI
 TGTC TCC GGCCCTGAGGT
 ||| || |||||
 ACAG AGG CCGGGA CTCCG
 AG GA A_____ II
 GAM467 GMFG TCAGTCCCCA-GCCCAGAG 7370 TGTC G T
 AGTCCCCAG CCC GAGG
 ||||| || |||
 TCAGGGGTC GGG CTCT
 _____ _ T
 GAM467 GRIK3 CAGCCCCCAGG-CCTGAGGT 7364 TGTCAGT C
 CCCCAGGCC TGAGGT
 ||||| |||||

	GGGGTCCGG ACTCCA		
	G_____		
GAM467 ITGAV	TCA-TCCCCAGGCCTTGAGG 7372 TGTCA	C	T
	GTCCCCAGGCC TGAGG		
	TAGGGGTCCGG ACTCC		
	_____ A T		
GAM467 MFGE8	CAGTCCCCA-GCCCTATGGTG 7365 TGTCAG	G	A
	TCCCCAG CCCTG GGT		
	AGGGGTC GGGAT CCA		
	_____ A		
GAM467 MYO1C	CAGCCCCCAGGCCCTTGAGG 7363 TGTCAGT	_	T
	CCCCAGGCCCT GAGG		
	GGGGTCCGGGA CTCC		
	G_____ A C		
GAM467 RBM8A	TGTTCTGTCTCCGGGCCCTGAG 7379 CA C A		GTG
	TGT GTC CC GGCCCTGAG		
	ACA CAG GG CCGGGACTC		
	AG A C		
GAM467 SET	TCAATCCACATAGCCCTGAGGT 7369 TGTC	C	_ G
	AGTCC CA GGCCCTGAGGT		
	TTAGG GT TCGGGACTCCA		
	_____ T A G		
GAM467 SLC5A5	TGTCAGTCCCGCGGCTGGCCCTG 7376	CA_____	AGGTGI
	TGTCAGTCCC GGCCCTG		
	ACAGTCAGGG CCGGGAC		
	CGCCGA GTG		
GAM467 STS	TGTCTGGTCCCCAGGCGCTG 7375 A_	C	AGGT
	TGTC GTCCCCAGGC CTG		
	ACAG CAGGGGTCCG GAC		
	AC C G		
GAM467 TCF3	GTCAGTCCCC--TTCCTGAGG 7367 TG	AGGC	T
	TCAGTCCCC CCTGAGG		
	AGTCAGGGG GGA CTCC		
	_____ AA_ C		
GAM467 TNFAIP2	TGACAGTCCCCAGAGCCTG 7377 T	GC	AGGT
	TG CAGTCCCCAG CTG		
	AC GTCAGGGGTC GGAC		
	T TC G		
GAM468 ANK3	ACAGCAGCCTTATTAACCT 7382 TGAC	_	T CTC
	AGCAGCC ATTA CTG		

	TCGTCGG TAAT GGAT	
	____ AA T TII	
GAM468 ARHGEF7	CAGACGCATTTTTCTGCTCC 7385 TGACA GCCATTA	
	GCA TCCTGCTCC	
	III IIIIIII	
	CGT AGGACGAGG	
	TG____ AAAA____	
GAM468 FKBP1B	TGAGCAGCAGCCA-TCTCCAGC 7386 _ A T TCC	
	TGA CAGCAGCCATT TCC GC	
	III IIIIIIIII III II	
	ACT GTCGTCGGTAG AGG CG	
	C _ T III	
GAM468 HSPD1	TGACAGCAGTAAACCATTAT 7387 _____ CCTGCTC	
	TGACAGCAG CCATTAT	
	IIIIIIII IIIIIII	
	ACTGTCGTC GGTAATA	
	ATTT IIICCTC	
GAM468 MAP4K2	TGACAGCAGC--TCCCCCTGGTCC 7393 CATT A C	
	TGACAGCAGC TCCTG TCC	
	IIIIIIII IIIII III	
	ACTGTCGTCG GGGAC AGG	
	AGG____ C	
GAM468 MAPK8IP1	TGTCAGCAGCCAGCTGTCCTG 7389 TGA _ A CTCC	
	CAGCAGCCA TT TCCTG	
	IIIIIIII II IIIII	
	GTCGTCGGT GA AGGAC	
	ACA C C IIIC	
GAM468 MASP2	TGACAGCAGCC-TCA-CCTG 7390 A T CT	
	TGACAGCAGCC TTA CCTG	
	IIIIIIII III IIII	
	ACTGTCGTCGG AGT GGAC	
	_ _ II	
GAM468 MLC1	TGACAGCAGCC--TCTCCT-CTCC 7394 ATTA G	
	TGACAGCAGCC TCCT CTCC	
	IIIIIIII IIIII IIII	
	ACTGTCGTCGG AGGA GAGG	
	AG____ _	
GAM468 MS4A8B	TGCCAGCAGCCACGTATCTCTTGATCC7388 TGA _ _ GC_ III	
	CAGCAGCCAT TATC CT TCC	
	IIIIIIII IIIII II III	
	GTCGTCGGTG ATAG GA AGG	
	ACG C A ACT III	
GAM468 NUDT1	CAGCAGCCACGTCTCCTGC 7383 TGACAG TA_	
	CAGCCAT TCCTGCTC	
	IIIIII IIIIIII	
	GTCGGTG AGGACGGG	
	____ CAG	
GAM468 PPP2R2B	TGACAGCAGGC-TTA-CTTGC 7391 CCA CC TC	
	TGACAGCAG TTAT TGC	
	IIIIIIII IIIII III	

ACTGTCGTC AATG ACG
 CG_ A_ II
 GAM468 RAG1 TGACAGCAG--ATGA-CCTCCT 7392 CCATTA GCTC
 TGACAGCAG TCCT
 ||||| |||
 ACTGTCGTC AGGA
 TACTGG IIIC
 GAM468 RAG1 CATCAGCCATTATCACTGGTCC 7384 TGACAG _ C
 CAGCCATTATC CTG TCC
 ||||| ||| |||
 GTCGGTAATAG GAC AGG
 T C
 GAM469 AKR1B1 TGACAGGGCTCTTGAGATCCAACA 7422 CCAT__ C AGGI
 TGACAGGGC GTCC ACA
 ||||| ||| |||
 ACTGTCCCG TAGG TGT
 AGAACTC T IIIG
 GAM469 APOBEC2 GACAGG---CATGTCCCAGATGG 7412 TG GCC CAA
 ACAGG CATGTCCCA G
 ||| ||||| |
 TGTCC GTACAGGGT C
 CTA
 GAM469 ATP5J GGGGCCTTTTCCCCACAAGG 7417 TGACAGGGCCCATG
 TCCCACAAGG
 |||||
 GGGGTGTTCC
 GAAAAG_____
 GAM469 CDX1 TGA CTGTCCACCATGTCCCAGAAGG 7420 AGGGC_ C II
 TGAC CCATGTCCCA AAGG
 ||| ||||| |||
 ACTG GGTACAGGGT TTCC
 ACAGGT C II
 GAM469 CYP4F3 TGTCAGGAGCACCTTGTCCCACA 7418 TGA _ _ A AGGI
 CAGG GC CC TGTCCCACA
 ||| || |||||
 GTCC CG GG ACAGGGTGT
 ACA T T A IIIG
 GAM469 DTX1 GACAGGGCC--TGTCACCCA 7410 TG CA _ A A
 ACAGGGCC TGTC CC CA
 ||||| ||| |||
 TGTCCCGG ACAG GG GT
 T C
 GAM469 FUT3 CAGGGCCCAGGGCCCTCCAGG 7408 TGA_ ATG CACA
 CAGGGCCC TCC AGG
 ||||| ||| |||
 GTCCCGGG AGG TCC
 CCGG _____
 GAM469 FUT5 CAGGGCCCA-GTGCCTCCAGG 7407 TGACAG _ _ CAAG
 GGCCCA TGTC CCA
 ||||| ||| |||

	CCGGGT ACGG GGT		
	_____ C A CCCA		
GAM469 FUT6	CAGGGCCCA-GTGCCTCCAGG 7407 TGACAG	_ _	CAAG
	GGCCCA TGTC CCA		
	CCGGGT ACGG GGT		
	_____ C A CCCA		
GAM469 GASC1	TGACAGGGCCCTAAGCCGCACAAGG 7421	AT_ C	II
	TGACAGGGGCC GTG CACAAGG		
	ACTGTCCCGGG CGG GTGTTCC		
	ATT C II		
GAM469 GJA4	TGACAGGG-CCAAATCCGGCACAAG 7424	CAT _	GI
	TGACAGGGCC GTCC CACAAG		
	ACTGTCCCGG TAGG GTGTTC		
	TT_ CC II		
GAM469 GLTSCR1	TGACAGGGCAGCCACGTTCAAGAA 7419	_	CCCA I
	TGACAGGGC CCATGT CAAGG		
	ACTGTCCCG GGTGCA GTTCT		
	TC A_ T		
GAM469 HIF1A	TGTCAGGGCCCA-GCCCGACA 7427 TGA	T C	AG
	CAGGGCCCA GTCC ACA		
	GTCCCGGGT CGGG TGT		
	ACA _ C II		
GAM469 IL8RA	GACAGGGCCC-TGTTCTCCAAGG 7413 TG	A	CCCA
	ACAGGGCCC TGT CAAGG		
	TGTCCCGGG ACA GTTCC		
	_ _ AGAG		
GAM469 LAPTM5	TGGCAGGGTCAGTG-CCCACAAGG 7428 A	CC T _	I
	TG CAGGG CA GT CCCACAAGG		
	AC GTCCC GT CA GGGTGTTC		
	C A_ C I		
GAM469 M6PR	CAGAGCCCTCGATGTCCCAC 7402 TGACAG	_	AAG
	GGCCC ATGTCCCAC		
	TCGGG TACAGGGTG		
	_____ AGC AAG		
GAM469 MAD1L1	ACAGAGAC--TGTCACCAA 7398 TGAC	CCCA	
	AGGG TGTCCACAA		
	TCTC ACAGGGTGTT		
	_____ TG_		
GAM469 MAT1A	CAGGAGCCCAGG-CCCACAAGG 7401 TGACA	T T	
	GGGCCCA G CCCACAAGG		

	CTCGGGT C GGGTGTTC	
	_____ C _	
GAM469 MUCDHL	CAGGGCCCAGTTGTTCTCCAG 7403 TGACAG	___ _ CA AGG
	GGCCCA TGT CC CA	
	CCGGGT ACA GG GT	
	_____ CA A AG CGG	
GAM469 NAP1L4	ACAGGGCCC---TCCCACAGGG 7399 TGAC	ATG A
	AGGGCCC TCCCACA G	
	TCCCGGG AGGGTGT C	
	_____ C	
GAM469 NFRKB	TGACAGGG-CTGTGTCACCACA 7423	CCA _ AGG
	TGACAGGGC TGTC CCACA	
	ACTGTCCCG ACAG GGTGT	
	AC_ T	
GAM469 PAX5	GGGCCTCAGTTTCCCACAAGG 7414 TGA	GGCCCATG
	CAG TCCCACAAGG	
	GTC AGGGTGTTC	
	A_ AA_____	
GAM469 PRG2	TGACTCGTGCCATGTCCCAC 7426	AGG_ C AAG
	TGAC GCC ATGTCCCAC	
	ACTG CGG TACAGGGTG	
	AGCA _	
GAM469 RALBP1	CAGGGCCCAGCCTCCCAGAAG 7404 TGACAG	TG_ C G
	GGCCCA TCCCA AAG	
	CCGGGT AGGGT TTC	
	_____ CGG C G	
GAM469 RHO	GGGCCCATGAACATCCC-CAAGG 7416 TGACA	CCAT A
	GGGC GTCCC CAAGG	
	CTTG TAGGG GTTCC	
	GTA_ _ _	
GAM469 SH2D2A	CAGGGCCCA-GACTCAAAAGG 7406 TGACAG	TG CC C
	GGCCCA T CA AAG	
	CCGGGT G GT TTC	
	_____ CT A_ T	
GAM469 SH3GL1	CAGGGCCCATCACCAGCACCAGG 7405 TGACAG	GT _ A I
	GGCCCAT CC CAC AGG	
	CCGGGTA GG GTG TCC	
	_____ GT TC G G	
GAM469 SPOCK	GACAGGGCCCAT---CACAGAGG 7411 TG	GTCC _
	ACAGGGCCCAT CACA AG	

		TGTCCCGGGTA	GTGT TC	
		_____ C		
GAM469 STX1A		AGGGCCCATGGCAGAGAAGG	7400 TGACAGGG	TCCCAC
		CCCATG AAG		
		GGGTAC TTC		
		_____ CGTCTC		
GAM469 TAF1C		TGCCAGA-CCCATGTCCCA	7425 ACA	CAA
		TG GGGCCCATGTCCCA		
		AC TCTGGGTACAGGGT		
		GG_		
GAM469 UBE2G2		ACAGGGCCCCATTTCTTCAGAAGG	7397 TGAC	ATG_ C_ C I
		AGGGCCC TC CA AAGG		
		TCCCGGG AG GT TTCC		
		_____ GTAA AA C T		
GAM469 WBP2		GGGCCCTAATGTCCCACAA	7415 TGACAGGGCCC	G
		ATGTCCCACAA		
		TACAGGGTGTT		
		GAT_____ A		
GAM469 ZNF278		CAGGGCCCAGGTCCCCCAGGG	7409 TGACAG	T ACA
		GGCCCA GTCCC AGG		
		CCGGGT CAGGG TCC		
		_____ C GG_		
GAM470 ARHG		TGCAGTTGCTGTAG-TGGAGGCAG	7451 CT	AT_ GA I
		GCAG CTG GGTGGAGGCAG		
		CGTC GAC TCACCTCCGTC		
		__ AAC A_ A		
GAM470 AXIN1		CTGCACAGCCGCGGCTGGAGGCAG	7440	GAT A _ II
		CTGCA CTGG GG TGGAGGCAG		
		GACGT GGCC CC ACCTCCGTC		
		GTC G G II		
GAM470 DDX26		AGATGGTAGAGGTGGAGGC	7431 CTGCAGATC	A
		TGGAGGTGGAGGC		
		ATCTCCACCTCCG		
		CC_____ C		
GAM470 FGFR1		TGGAGA---GGAGGTGGAGGGAG	7456 CTGCAGATCT	C
		GGAGGTGGAGG A		
		CCTCCACCTCC T		
		CCTCT_____ C		
GAM470 FUT3		CTGAAGATCTGGA---GAGGCAG	7443 C	GGTG
		CTG AGATCTGGA GAGGCA		

GAC TCTAGACCT CTCCGT
 T _____
 GAM470 GBF1 CAGAGCTGCCGGGCTGGAGGCAG 7434 __ AGAT TG CAGI
 CTGC CTGGAGG GAGG
 ||| ||||| |||
 GACG GACCTCC CTCC
 TC GCCC GT ||G
 GAM470 GPR4 CTGGAGAGCCCAGGAGGTGGAGGC 7439 C _ _ AGI
 CTG AGA TCT GGAGGTGGAGGC
 ||| ||| ||| |||||
 GAC TCT GGG CCTCCACCTCCG
 C C T |||
 GAM470 GRIA2 CTGCTAAACCTGAAG-TGGAGGCAG 7436 __ G II
 CTGC AGATCTG AGGTGGAGGCAG
 ||| ||||| |||||
 GACG TTTGGAC TTCACCTCCGTC
 AT _ II
 GAM470 HSF4 CTGCAGAGTCCGCAGAGGGGTGGAGGCA7437 _ G ____ GIII
 CTGCAGA TCTG A GGTGGAGGCA
 ||||| ||| | |||||
 GACGTCT AGGC T CCACCTCCGT
 C G CTCC ||G
 GAM470 LAG3 CTGCAGAGAGGGAGGTGGAGGAAG 7444 TCT C I
 CTGCAGA GGAGGTGGAGG AG
 ||||| ||||| |||
 GACGTCT CCTCCACCTCC TC
 CTC T I
 GAM470 MSN CAGAGAAGGAGGTGGATGC 7435 CTGCAGATCT G A
 GGAGGTGGA GC
 ||||| ||
 CCTCCACCT CG
 TCTT_____ A A
 GAM470 MUC5B CAGAGCATGGGGATGGAGGCAG 7433 CT GATC A
 GCA TGG GGTGGAGGCAG
 ||| ||| |||||
 CGT ACC CTACCTCCGTC
 T_ ____ C
 GAM470 PABPN1 GCA-ATCTGGAGGGGCAGGGAG 7450 CTGCA T _ C
 GATCTGGAGG GG AGG AG
 ||||| || ||| ||
 TTAGACCTCC CC TCC TC
 _____ _ G C
 GAM470 PHEMX TGCTGGTTTGAAGGTGGAGG 7452 CTGCAGATC CA
 TGGAGGTGGAGG
 |||||
 ACTTCCACCTCC
 CGACCA_____ CI
 GAM470 PLN CTGCAGATCTAGAGTTGTAGCAG 7445 GGA I
 CTGCAGATCTGGAGGT GGCAG
 ||||| |||||

	GACGTCTAGATCTCCA TCGTC	
	ACA I	
GAM470 PRG2	TGCAG---GGAGGTGGAGGGAG 7455 CT ATCT C	
	GCAG GGAGGTGGAGG A	
	CGTC CCTCCACCTCC T	
	— — C	
GAM470 RNF4	GATCTCAGGAAAATGGAGGCAG 7446 CTG ATCT	
	CAG GGAGGTGGAGGCAG	
	GTC CTTTACCTCCGTC	
	— —	
GAM470 RNF4	CTGCAGATCAATGATAAGGTGCAGGCAG7438 TG— G	
	CTGCAGATC GAGGTG AGGCAG	
	GACGTCTAG TTCCAC TCCGTC	
	TTACTA G	
GAM470 RPS6KA2	AGA-CTGGAGGTGGACACAG 7432 CTGCAGATC G	
	TGGAGGTGGA GCA	
	ACCTCCACCT TGT	
	— — G	
GAM470 SHANK2	GCAG-TCTGCGAGGTGGAGAGCAG 7447 CTGC A _ _ I	
	AG TCTG GAGGTGGAG GCAG	
	TC AGAC CTCCACCTC CGTC	
	— _ G T G	
GAM470 SPAG8	TGCAGGT--GGCGGTGGAGGCA 7453 CT ATC A	
	GCAG TGG GGTGGAGGCA	
	CGTC ACC CCACCTCCGT	
	— C— G	
GAM470 SPTBN4	CTGCAGATC-GGGGCTGGGGGC 7441 T A _ A AG	
	CTGCAGATC GG GG TGG GGC	
	GACGTCTAG CC CC ACC CCG	
	— _ G C	
GAM470 SRD5A2	TGGACATCTGG---TGGAGGCA 7454 CTGCAG GGA	
	ATCT GGTGGAGGCA	
	TAGA CCACCTCCGT	
	CCTG— —	
GAM470 STAU	GCTGACCTGGGAGGTGGAGG 7449 CTGCA _ CA	
	GATCTGG AGGTGGAGG	
	CTGGACC TCCACCTCC	
	A— C AA	
GAM470 SUV39H1	GCAGGTGGGGGCAGGTGGAGGCAG 7448 CTGCAGATCT _ I	
	GG AGGTGGAGGCAG	

CC TCCACCTCCGTC
 TCCACCC__ G C
 GAM470 UCP1 CTCCAGCCCCGAAGGTGGAGGAAG 7442 G AT C I
 CT CAG CTGGAGGTGGAGG AG
 || ||| ||||| ||
 GA GTC GGCTTCCACCTCC TC
 G GG T I
 GAM471 DIAPH2 CAACC-ACGCCGTTGCCACT 7459 T _ II
 CAACT AC CTGTTGCCAC
 |||| || |||||
 GTTGG TG GGCAACGGTG
 _ C AI
 GAM471 DIAPH2 CAACC-ACGCCGTTGCCACT 7459 TCTCAACT _ T
 TAC CTGTTGCCACT
 ||| |||||
 GTG GGCAACGGTGA
 G__ C T
 GAM471 JAK2 TCACATCTTGTTCTGTTGCC 7461 T A A__ ACTTG
 TC CA CTT CCTGTTGCC
 || ||| |||||
 AG GT GAA GGACAACGG
 T A CAA IIIGT
 GAM471 JAK2 TCACATCTTGTTCTGTTGCC 7461 T A A__ III
 TC CA CTT CCTGTTGC
 || ||| |||||
 AG GT GAA GGACAACG
 T A CAA GII
 GAM471 PRAME TCTCAG-TCACTTGTTGCCAC 7462 AC C TT
 TCTCA TTAC TGTTGCCAC
 |||| ||| |||||
 AGAGT AGTG ACAACGGTG
 C_ A II
 GAM471 PRAME TCTCAG-TCACTTGTTGCCAC 7462 _ AC C I
 CTCA TTAC TGTTGCCA
 |||| ||| |||||
 GAGT AGTG ACAACGGT
 A C_ A I
 GAM471 RAI2 CTCAGCT---CTGATGCCACTTG 7460 TC A TAC T
 TCA CT CTG TGCCACTT
 ||| || |||||
 AGT GA GAC ACGGTGAA
 _ C _ T
 GAM471 RAI2 CTCAGCT---CTGATGCCACTTG 7460 A TAC T I
 CTCA CT CTG TGCCACT
 |||| || |||||
 GAGT GA GAC ACGGTGA
 C _ T A
 GAM472 CELSR2 GTCAAGCCCCCAAGC--CAGGGC 7471 TG G _ AG C
 TCAAGCCCC CA GC CAG GC
 ||||| || || ||| ||

	AGTTCGGGG GT CG GTC CG	
	— — T — C	
GAM472 CNN1	GTCCAGCCAAGAGCAGCAGCAGC 7469 T___ CCCC GCI	
	GTCAAG GCAGCAGCAGC	
	CGGTTC CGTCGTCGTCG	
	AGGT T___ GII	
GAM472 CYB561	TCTAGCCACAGCCAGCAGCAGCG 7472 T_ _ CCGC CI	
	GTCA AGCC AGCAGCAGCG	
	CGGT TCGG TCGTCGTCGC	
	AT G _____ CA	
GAM472 EGR3	AAGCGGCGGCAGCAGCACCGC 7465 TGTCAA CCC G	
	GC GCAGCAGCA CGC	
	CG CGTCGTCGT GCG	
	C_____ C___ G	
GAM472 FGFR4	GTCAAGACGCTGGGGCAGCAGCAGC 7468 TG _ CCC___ CII	
	TCAAG C GCAGCAGCAGCG	
	AGTTC G CGTCGTCGTCGT	
	— T CGACCC III	
GAM472 GJB3	TCAAGCCC--CAGCTGCAGC 7476 TGTC GC A	
	AAGCCCC AGC GCAGC	
	TTCGGGG TCG CGTCG	
	_____ — A	
GAM472 HAS2	TCAAGTCCC--AGCAGCAG 7475 TGTC _ C CAGC	
	AAG CCC GCAGCAG	
	TTC GGG CGTCGTC	
	_____ A T ACII	
GAM472 ICOS	TGTCAAGCCCAGAGGCACCA 7480 CGCA G GCG	
	TGTCAAGCCC GCA CA	
	ACAGTTCGGG CGT GT	
	TCTC G III	
GAM472 LDOC1	TCCAGCCCCGACCCCAGCAGCAG 7474 TGTCA _ AG CI	
	AGCCCCG C CAGCAGCG	
	TCGGGGC G GTCGTCGT	
	G_____ T GG CC	
GAM472 LENG4	GTCTGGCCCCGCAGCAGCAGC 7470 TGTCAA C	
	GCCCCGCAGCAGCAGCG	
	CGGGGCGTCGTCGTCGT	
	AGAC___ I	
GAM472 MASP1	TCAGGAGCAGCAGCAGCAGC 7477 TGTCA CCC	
	AGC GCAGCAGCAGCG	

	TCG CGTCGTCGTCGT	
	TCC__ T__	
GAM472 TCF8	AGCCACAGAGCAGCAGCAGC	7466 TGTCA CCC
	AGC GCAGCAGCAGCG	
	TCG CGTCGTCGTCGT	
	GTC__ T__	
GAM472 TIC	TGTCA-GCCG-GCAGGCAGCAGCG	7479 A CC _ C
	TGTCA GCC GCAG CAGCAGCG	
	ACAGT CGG CGTC GTCGTCGC	
	_ C_ C I	
GAM472 TNFAIP1	AGACCCAGGCAGCAGCAGC	7467 TGTCAAGCCCC
	GCAGCAGCAGCG	
	CGTCGTCGTCGT	
	GTC_____	
GAM472 TNFRSF5	TCACGCCACAGCAGCAGCAGC	7473 TGTCAA C_
	GCC C GCAGCAGCAGCGC	
	CGG G CGTCGTCGTCGTG	
	TG____ T T	
GAM472 WHSC1	TGTCCGAGACCTGCAGCAGCA	7478 A_ C C GCGC
	TGTC AG CC GCAGCAGCA	
	ACAG TC GG CGTCGTCGT	
	GC T A C	
GAM473 ADAM12	CAGAGGCATCATGGCATTTTACC	7487 A ACTG_ I
	GAG GTGGCATTTTGC	
	CTC TACCGTAAAATG	
	_ CGTAG I	
GAM473 ADAM12	CAGAGGCATCATGGCATTTTACC	7487 A__ GAGACTG I
	GCA GTGGCATTTTGCC	
	CGT TACCGTAAAATGG	
	CTC AG_____ A	
GAM473 CHS1	AGCAGAGACT-TTGGAATT	7483 GG CATI
	AGCAGAGACT TGG	
	TCGTCTCTGA ACC	
	A_ TTAA	
GAM473 CHS1	AGCAGAGACT-TTGGAATT	7483 GG CATTTTG
	AGCAGAGACT TGG	
	TCGTCTCTGA ACC	
	A_ TTA	
GAM473 FMN2	CAGAGACT--TGGCATTTT	7488 GG I
	CAGAGACT TGGCATTT	

	GTCTCTGA ACCGTAAA			
	— A			
GAM473 FMN2	CAGAGACT--TGGCATT TT 7488 AGCA	GG	G	
	GAGACT TGGCATT TT			
	CTCTGA ACCGTAAAA			
	— — —			
GAM473 GALR1	AGCAGAGACTGGACGGATT 7484	_	CATII	
	AGCAGAGACTGG TGG			
	TCGTCTCTGACC GCC			
	T TAAII			
GAM473 GALR1	AGCAGAGACTGGACGGATT 7484	_	CATTTTGC	
	AGCAGAGACTGG TGG			
	TCGTCTCTGACC GCC			
	T TAAIIICC			
GAM473 KAL1	GCAGAGACTCCCAGCATT TT 7491	GG	I	
	CAGAGACT TGGCATT T			
	GTCTCTGA GTCGTAAA			
	GG I			
GAM473 KAL1	GCAGAGACTCCCAGCATT TT 7491 AG	GG	GC	
	CAGAGACT TGGCATT TT			
	GTCTCTGA GTCGTAAAA			
	— GG AI			
GAM473 LDB3	GAGACTGGTGGCTTCGTGC 7490	ATTTTGII		
	GAGACTGGTGGC			
	CTCTGACCACCG			
	AAGCACGI			
GAM473 LDB3	GAGACTGGTGGCTTCGTGC 7490 AGCAGAGA	A T		
	CTGGTGGC TT TGC			
	GACCACCG AG ACG			
	— A C			
GAM473 NDRG3	AGCAGAGGCC--TGGCATT TTG 7486	A GG	C	
	AGCAGAG CT TGGCATT TTG			
	TCGTCTC GG ACCGTAAAAC			
	C _ I			
GAM473 NDRG3	AGCAGAGGCC--TGGCATT TTG 7486 _	A GG	I	
	GCAGAG CT TGGCATT TT			
	CGTCTC GG ACCGTAAAA			
	T C _ I			
GAM473 PRKY	AGCAG-GCC-GGTGGCATT T 7485	AGA	TG	
	AGCAG CTGGTGGCATT T			

	TCGTC GGCCACCGTAAA		
	C__ II		
GAM473 PRKY	AGCAG-GCC-GGTGGCATT 7485	AGA	I
	GCAG CTGGTGGCATT		
	CGTC GGCCACCGTAA		
	T C__ I		
GAM473 SIRPB2	GAGGCTGGGACAGGCATTTTG 7489	A T__	III
	GAG CTGG GGCATTTT		
	CTC GACC CCGTAAAA		
	C CTGT CII		
GAM473 SLC10A1	GCA-AGACTGGTG--TTTTTGC 7492	G	GCATTTI
	GCA AGACTGGTG		
	CGT TCTGACCAC		
	_ AAAACG		
GAM473 SLC10A1	GCA-AGACTGGTG--TTTTTGC 7492	AGCA	GCA
	GAGACTGGTG TTTTGC		
	TTCTGACCAC AAAACG		
	G__ A__		
GAM474 BIG1	TGACAAAATATTATGGGTA 7509	GT	TII
	TGACAAAATAT TGTG		
	ACTGTTTTATA ATAC		
	_ CCA		
GAM474 BIG1	TGACAAAATATTATGGGTA 7509	GT T	GAGT
	TGACAAAATAT TG GTA		
	ACTGTTTTATA AC CAT		
	AT C IIIT		
GAM474 CCNT2	AAAATATGTAGTGTAATAATT 7496	T	I
	AAATATGT GTGTAGAGT		
	TTTATACA CACATTTTA		
	T I		
GAM474 CCNT2	AAAATATGTAGTGTAATAATT 7496	TGACAAAA	T
	TATGT GTGTAGAGT		
	ATACA CACATTTTA		
	_____ T		
GAM474 CDKN2A	TGACGGAAGGAAGCTTGTGTAGAG 7506	AAAATAT__ _	TTII
	TGAC GTT GTGTAGAG		
	ACTG CGA CACATCTC		
	CCTTTCCTT A IIIT		
GAM474 CDKN2A	TGACGGAAGGAAGCTTGTGTAGAG 7506	GACAAAATATG	I
	TTGTGTAGA		

		AACACATCT			
		CCTTTCCTTCG	I		
GAM474 CLDN14		TGAGAGAAAAT--TGTGTAGA	7510	CAAAATAT	GT
		TGA GTTGTGTAGA			
		ACT TAACACATCT			
		CTCTTT__	II		
GAM474 EYA4		GACAATTTATAT-GTGTAGAG	7505	_ AA T I	
		ACAA TATGT GTGTAGA			
		TGTT ATATA CACATCT			
		C AA _ I			
GAM474 EYA4		GACAATTTATAT-GTGTAGAG	7505	TG AA T	
		ACAA TATGT GTGTAGAGT			
		TGTT ATATA CACATCTCG			
		_ AA _			
GAM474 HMMR		TGAAGAAATA-GTTACATGTAGAGTT	7508	CA T _ II	
		TGA AAATA GTT GTGTAGAGTT			
		ACT TTTAT CAA TACATCTCAA			
		TC _ TG II			
GAM474 HMMR		TGAAGAAATA-GTTACATGTAGAGTT	7508	GACA T _ I	
		AAATA GTT GTGTAGAGT			
		TTTAT CAA TACATCTCA			
		TTC_ _ TG I			
GAM474 KCND2		AAATATGTTGTGT-GAGTT	7500	A I	
		AAATATGTTGTGT GAGT			
		TTTATACAACACA CTCA			
		_ A			
GAM474 LDHB		AAAAGTTTATGTGTAGAGTT	7495	AAATATGT I	
		TGTGTAGAGT			
		ACACATCTCA			
		TTTCAAAT I			
GAM474 LDHB		AAAAGTTTATGTGTAGAGTT	7495	TGACAAAATATGT	
		TGTGTAGAGT			
		ACACATCTCA			
		CAAAT_____			
GAM474 MIPOL1		AAATATGTTGATTTGGAATT	7499	TGTA_ II	
		AAATATGTTG GAGT			
		TTTATACAAC CTTA			
		TAAAC AI			
GAM474 NR3C1		AAATATGTTAAGTTTTGAGTT	7498	T A_ III	
		AAATATGTTG GT GAGT			

	TTTATACAAT CA CTCA		
	T AAA AII		
GAM474 OSCAR	CAAGATTTATTGTGTAGAG 7504 A A II		
	CAA AT TGTTGTGTAGA		
	GTT TA ATAACACATCT		
	C A CI		
GAM474 OSCAR	CAAGATTTATTGTGTAGAG 7504 TGACAAAATA		
	TGTTGTGTAGAGT		
	ATAACACATCTCG		
	CTAA _____		
GAM474 RBBP9	ACAAAATAT-ATGTCCTAGA 7503 T GTAGII		
	ACAAAATATGT GT		
	TGTTTTATATA CA		
	_ GGATCT		
GAM474 RFXAP	TGACAAAATACTGGAGTGT-TAGTT 7507 GTT_ AG I		
	TGACAAAATAT GTGT AGTT		
	ACTGTTTTATG CACA TCAA		
	ACCT A_ I		
GAM474 RFXAP	TGACAAAATACTGGAGTGT-TAGTT 7507 GTT_ AG I		
	GACAAAATAT GTGT AGT		
	CTGTTTTATG CACA TCA		
	ACCT A_ I		
GAM474 RFXAP	AACAAATTTT-TGTAGAGTT 7497 A T G_ I		
	AATA GTT TGTAGAGT		
	TTGT TAA ACATCTCA		
	_ T AA I		
GAM474 ZNF22	AATATGTTGAATCTAGAGT 7501 _G III		
	AATATGTTG T TAGAG		
	TTATACAAC A ATCTC		
	TT G AII		
GAM474 ZNF8	ACAAAATATGTCGCTAAAGAG 7502 C GT_ I		
	AAAATATGTTGT AGA		
	TTTTATACAGCG TCT		
	_ ATT I		
GAM474 ZNF8	ACAAAATATGTCGCTAAAGAG 7502 TGAC GT_ TT		
	AAAATATGTTGT AGAG		
	TTTTATACAGCG TCTC		
	_____ ATT CC		
GAM475 C18orf1	ACACCACTCCACACGAAG 7514 AGAAIII		
	ACACCACTCCCA		

	TGTGGTGAGGGT			
	GTGCTTC			
GAM475 C18orf1	ACACCACTCCCACACGAAG	7514 TA	A__	AATAA
	CACCACTCCCA GAAG			
	GTGGTGAGGGT CTTC			
	__ GTG A G			
GAM475 CARPX	CCAATCCCAAGAATGAATGAG	7529 CCAC	_	AI
	TCCCAAGAA GAAT			
	AGGGTTCTT CTTA			
	T__ A CT			
GAM475 CARPX	CCAATCCCAAGAATGAATGAG	7529 TACACCAC	_	AAG
	TCCCAAGAA GAAT			
	AGGGTTCTT CTTA			
	_____ A CTC			
GAM475 CDK10	CACCACTCCTCCCAAGAAG	7522 __ CA		
	CAC CTCCCAAGAA			
	GTG GAGGGTTCTT			
	GTG AG C			
GAM475 CDK10	CACCACTCCTCCCAAGAAG	7522 TA CA		AATAA
	CAC CTCCCAAGAAG			
	GTG GAGGGTTCTTC			
	G_ AG GT			
GAM475 DHCR24	CCACTCCCACCAAGACAAAG	7530 AG		ATAAI
	CACTCCCA AAGA			
	GTGAGGGT TTCT			
	GG GTTTI			
GAM475 DHCR24	CCACTCCCACCAAGACAAAG	7530 TACACCA	_	A TAA
	CTC CCAAGA GAA			
	GGG GGTTC TTT			
	A_____ T G CAC			
GAM475 DYRK1A	AGAATTCCAAGTGGTGCTA	7521 C GT		
	AGA TTC GGTGGTGCT			
	TCT AAG TCACCACGA			
	T GT TI			
GAM475 DYRK1A	AGAATTCCAAGTGGTGCTA	7521 TGAGAC GT		AG
	TTC GGTGGTGCTA			
	AAG TCACCACGAT			
	TT_____ GT GT			
GAM475 FZD4	ACAGCAGCAGCCAAGAAGA	7513 C CTC_		
	ACA CA CCAAGAAG			

		TGT GT GGTTC TTC			
		C CGTC TI			
GAM475 FZD4	ACAGCAGCAGCCAAGAAGA	7513 TACACCACTC	ATAA		
	CCAAGAAGA				
	GGTTC TTC				
	GTCGTCGTC_ CIII				
GAM475 GOCAP1	TACACTGCTCCCAAGAACAAT	7536 CA G AAG			
	TACAC CTCCCAAGAA AAT				
	ATGTG GAGGGTTCTT TTA				
	AC G III				
GAM475 GOCAP1	TACACTGCTCCCAAGAACAAT	7536 CA G I			
	ACAC CTCCCAAGAA AA				
	TGTG GAGGGTTCTT TT				
	AC G I				
GAM475 HNF3G	AGAGCTTCGTGGTGTGAGCT	7519 _ GT_ III			
	AGA CTTCGTGGTG GC				
	TCT GAAGCACCAC CG				
	C ACT AII				
GAM475 HNF3G	AGAGCTTCGTGGTGTGAGCT	7519 TG A GT_ AAG			
	AG CTTCGTGGTG GCT				
	TC GAAGCACCAC CGA				
	_ _ ACT GGI				
GAM475 MAT1A	TGAGACTTCCTGG-GCTGC	7539 G TGG TAA			
	TGAGACTTC TGG TGC				
	ACTCTGAAG ACC ACG				
	G CG_ III				
GAM475 MAT1A	TGAGACTTCCTGG-GCTGC	7539 G TG_ GI			
	TGAGACTTC TGG GT				
	ACTCTGAAG ACC CG				
	G CGA II				
GAM475 MXI1	GACTTAGACTTGGGTGCTAAG	7533 ___ CGTGGT I			
	GACTT GGTGCTA				
	CTGAA CCACGAT				
	AAT C_____ T				
GAM475 MXI1	GACTTAGACTTGGGTGCTAAG	7533 TG CGTGGT A			
	AGACTT GGTGCTAAG				
	TCTGAA CCACGATTC				
	AA C_____ C				
GAM475 NDN	CATCAGTCCCATATAAAAGAATAAG	7523 ACCAC ___ I			
	TCCCA AGAAGAATAA				

	AGGGT TTTTCTTATT		
	TC__ ATA I		
GAM475 NDN	CATCAGTCCCATATAAAAAGAATAAG 7523 TACAC C __		II
	CA TCCCA AGAAGAATAAG		
	II IIII IIIIIIIII		
	GT AGGGT TTTTCTTATTC		
	A__ C ATA TA		
GAM475 OLFM1	CTTAGTGAAATGGTGCTAAG 7531 C __		III
	CTT GTG GTGGTGCTAA		
	III III IIIIIIIII		
	GAA CAC TACCACGATT		
	T TT CII		
GAM475 OLFM1	CTTAGTGAAATGGTGCTAAG 7531 TGAGACTTCGT		
	GGTGGTGCTAAG		
	IIIIIIIIII		
	TTACCACGATTC		
	ACT_____		
GAM475 OTOF	CACCACTCCAAGAAAAGAAAAA 7524 A C ATAI		
	CCACTCC AAGAAGA		
	IIIIII IIIII		
	GGTGAGG TTCTTTT		
	_ _ CTTT		
GAM475 OTOF	CACCACTCCAAGAAAAGAAAAA 7524 TACA C ATAAG		
	CCACTCC AAGAAGA		
	IIIIII IIIII		
	GGTGAGG TTCTTTT		
	_ _ CTTT		
GAM475 PKNOX1	CACCACTCCTAAGTAAACAAT 7525 C A AIII		
	CACCACTCC AAG AGA		
	IIIIII III III		
	GTGGTGAGG TTC TTT		
	A A GTTA		
GAM475 PKNOX1	CACCACTCCTAAGTAAACAAT 7525 TACA C AA G		
	CCACTCC AAG GAATAA		
	IIIIII III IIIII		
	GGTGAGG TTC TTTGTT		
	_ _ A A_ A		
GAM475 PLOD2	ACC-CTCCCCCAGAAAAGAATAAG 7517 CCA _ I		
	CTCCCAAGAA GAATAA		
	IIIIIIII IIIII		
	GGGGGTTTTT CTTATT		
	AG_ T I		
GAM475 PLOD2	ACC-CTCCCCCAGAAAAGAATAAG 7517 TACACCA _ I		
	CTCCCAAGAA GAATAAG		
	IIIIIIII IIIII		
	GGGGGTTTTT CTTATTC		
	GAG__ T C		
GAM475 PON1	ACAACACTCCCAAGAATTTTAAG 7516 C GAATAAI		
	CA CACTCCCAAGAA		
	II IIIIIIIII		

	GT GTGAGGGTTCTT			
	T AAAATTI			
GAM475 PON1	ACAACACTCCCAAGAATTTTAAG	7516	TA C	GAA I
	CA CACTCCCAAGAA TAAG			
	GT GTGAGGGTTCTT ATTC			
	__ T AAA T			
GAM475 PPIH	ACACCAC---CAAGAAGAA	7515	CTC	
	ACACCA CCAAGAAGA			
	TGTGGT GGTTCCTCT			

GAM475 PPIH	ACACCAC---CAAGAAGAA	7515	TA CTC	T
	CACCA CCAAGAAGAA			
	GTGGT GGTTCCTCT			
	_____ C			
GAM475 RAB18	CTTCCCCGTGGTGCTAGGA	7532	GTG	AGII
	CTTC GTGGTGCTA			
	GAAG CACCACGAT			
	GGG CCTI			
GAM475 RCN1	TACACCACTTACAGTAAGTAATAA	7534	CC AG _	GI
	TACACCACT CA AAG AATAA			
	ATGTGGTGA GT TTC TTATT			
	AT CA A II			
GAM475 RCN1	TACACCACTTACAGTAAGTAATAA	7534	A CC AG _	I
	CACCACT CA AAG AATA			
	GTGGTGA GT TTC TTAT			
	AT CA A I			
GAM475 RRM2B	TGATAATTAGTAGTGGTGCTAA	7540	GACTTC	GA
	TGA GTGGTGGTGCTAA			
	ACT CATCACCACGATT			
	ATTAAT II			
GAM475 RRM2B	TGATAATTAGTAGTGGTGCTAA	7540	GAGACTTC	I
	GTGGTGGTGCTA			
	CATCACCACGAT			
	CTATTAAT I			
GAM475 SCA7	TGAGACA-CGATCCTGGTGCTAA	7538	TT TGG_	GA
	TGAGAC CG TGGTGCTAA			
	ACTCTG GC ACCACGATT			
	T_ TAGG II			
GAM475 SCA7	TGAGACA-CGATCCTGGTGCTAA	7538	TT TGG_	I
	GAGAC CG TGGTGCTA			

	CTCTG GC ACCACGAT			
	T_ TAGG I			
GAM475 SEDL	CACTCCCAACTGCAGAATA	7526	GA__	III
	CACTCCCAA AGAAT			
	GTGAGGGTT TCTTA			
	GACG TII			
GAM475 SMARCC1	CCACTCCCAAGAGTCCAGAACAA	7528	_____	IIIT
	CCACTCCCAAGA AGAATA			
	GGTGAGGGTTCT TCTTGT			
	CAGG TIII			
GAM475 SPOCK	ACTATTTCCAAGAAGAAGAA	7518	ACCACTC	TI
	CCAAGAAGAA			
	GGTTCTTCTT			
	ATAAA__ CT			
GAM475 SPOCK	ACTATTTCCAAGAAGAAGAA	7518	TACACCACTC	TAA
	CCAAGAAGAA			
	GGTTCTTCTT			
	TAAA_____ CTT			
GAM475 TBX3	TAAACCACGC-CAAGAAGA	7535	TAC TC	ATA
	ACCAC CCAAGAAGA			
	TGGTG GGTTCCTTCT			
	ATT C_ III			
GAM475 TBX3	TAAACCACGC-CAAGAAGA	7535	TAC TC	I
	ACCAC CCAAGAAG			
	TGGTG GGTTCCTC			
	ATT C_ T			
GAM475 TP63	CCACTATCCCAAGAAGAAAAA	7527	__	TAIII
	CCAC TCCCAAGAAGAA			
	GGTG AGGGTTCTTCTT			
	AT TTTII			
GAM475 TP63	CCACTATCCCAAGAAGAAAAA	7527	TACACCAC	TAAG
	TCCCAAGAAGAA			
	AGGGTTCTTCTT			
	AT_____ TTTT			
GAM475 WHSC1	TATACCTTTTTCAAGAAGAAT	7537	AC ACTCC	I
	ACC CAAGAAGAA			
	TGG GTTCTTCTT			
	TA AAAAA I			
GAM475 WHSC1	TATACCTTTTTCAAGAAGAAT	7537	TAC ACTCC	AAG
	ACC CAAGAAGAAT			

	TGG GTTCTTCTTA		
	ATA AAAAA III		
GAM475 ZNF80	AGACCTTCGTGGTGAGTGTTA	7520	_ _ CTIII
	AGAC TTCGTGGTG GTG		
	TCTG AAGCACCAC CAC		
	G T AATII		
GAM475 ZNF80	AGACCTTCGTGGTGAGTGTTA	7520	TGAGA _ CTAAGA
	CTTCGTGGTG GTG		
	GAAGCACCAC CAC		
	TG_ _ _ T AATGTI		
GAM476 ADORA2B	GGTGGCCGGGACCCACGGGTC	7557	_ A T AG I
	GGT GG GGC CCACGGG		
	CCG CC CTG GGTGCCC		
	A G _ _ _ A		
GAM476 ADORA2B	GGTGGCCGGGACCCACGGGTC	7557	TAG A T AG
	GGT GG GGC CCACGGGTC		
	CCG CC CTG GGTGCCCAG		
	_ _ G _ _		
GAM476 APPBP2	AGGGGCGGTGGCAGCCACG	7545	TA II
	AGGG GGTGGCAGCCAC		
	TCCC CCACCGTCGGTG		
	CG CI		
GAM476 APPBP2	AGGGGCGGTGGCAGCCACG	7545	TA A GGT
	GGGT GGTGGCAGCCACG		
	CCCG CCACCGTCGGTGC		
	C_ _ _ GII		
GAM476 BAI2	AGGGTAGGTAGCTGCAGCCGCG	7544	_ _ ACIII
	AGGGTAGGTGGC AGCC		
	TCCCATCCATCG TCGG		
	ACG CGCII		
GAM476 BAI2	AGGGTAGGTAGCTGCAGCCGCG	7544	TA _ _ A GGTC
	GGGTAGGTGGC AGCC CG		
	CCCATCCATCG TCGG GC		
	_ _ _ ACG C GIII		
GAM476 BLK	AGGTGGCAGCACCCCCGGTC	7549	CA_ _ GTIII
	AGGTGGCAGC CGG		
	TCCACCGTCG GCC		
	TGGGG AGIII		
GAM476 BLK	AGGTGGCAGCACCCCCGGTC	7549	TAGGGTAGGT G A GT
	GGCA CC CGG		

	TCGT GG GCC			
	G_____ G G AG			
GAM476 CXorf6	GGCAGGTGGCAGCTCAGGGG 7555	_ C II		
	GGTAGGTGGCAGC CA GG			
	CCGTCCACCGTCG GT CC			
	A C CI			
GAM476 CXorf6	GGCAGGTGGCAGCTCAGGGG 7555 TAGGGT	_ C T		
	AGGTGGCAGC CA GGG			
	TCCACCGTCG GT CCC			
	_____ A C C			
GAM476 CYP24	TAGGGCTTGCTGG-AGCCACGGG 7559	AG_ C TC		
	TAGGGT G TGG AGCCACGGG			
	ATCCCG C ACC TCGGTGCC			
	AA G _ II			
GAM476 CYP24	TAGGGCTTGCTGG-AGCCACGGG 7559	AG_ C I		
	AGGGT G TGG AGCCACGG			
	TCCCG C ACC TCGGTGCC			
	AA G _ I			
GAM476 DCK	AGGGCTGGGAGGCGGCCACGGT 7543	____ T AGC I		
	GGG AGGTGGC CACGGG			
	CCC TCCGCCG GTGCC			
	CCGA _ _ I			
GAM476 DCK	AGGGCTGGGAGGCGGCCACGGT 7543	TA A_ T A CI		
	GGGT GG GGC GCCACGGGT			
	CCCG CC CCG CGGTGCCCA			
	_ AC T C CI			
GAM476 EPHX1	GGGGAGGTGGCAGGCGGGGG 7552	_ T CCA I		
	GG AGGTGGCAG CGG			
	CC TCCACCGTC GCC			
	C _ C_ C			
GAM476 EPHX1	GGGGAGGTGGCAGGCGGGGG 7552	TAG T CCA T		
	GG AGGTGGCAG CGGG			
	CC TCCACCGTC GCCC			
	_____ C_ C			
GAM476 FOXM1	GGGGAGGTGGCAGGGAGGGG 7553	_ T CCAC I		
	GG AGGTGGCAG GG			
	CC TCCACCGTC CC			
	C _ CCTC I			
GAM476 FOXM1	GGGGAGGTGGCAGGGAGGGG 7553	TAG T CCAC		
	GG AGGTGGCAG GGGT			

	CC TCCACCGTC CCGG	
	____ CCTC	
GAM476 GRIK3	GGCAGGTGGCAG-CTCTGGTC 7556 _ CACG I	
	GTAGGTGGCAGC GGT	
	CGTCCACCGTCG CCA	
	C AGA_ I	
GAM476 GRIK3	GGCAGGTGGCAG-CTCTGGTC 7556 TAGGGT CACG	
	AGGTGGCAGC GGT	
	TCCACCGTCG CCA	
	_____ AGA_	
GAM476 KCNA7	AGGGTAGGTGACAGGCCTGGTTC 7548 _ AC GTI	
	GGGTAGGTGGCAG CC GG	
	CCCATCCACTGTC GG CC	
	C A_ AAI	
GAM476 KCNA7	AGGGTAGGTGACAGGCCTGGTTC 7548 TA _ ACG CI	
	GGGTAGGTGGCAG CC GGT	
	CCCATCCACTGTC GG CCA	
	_____ C A__ AG	
GAM476 LZTS1	GGGCTGGTGGCAGCCCAGGG 7551 A A I	
	GGT GGTGGCAGCC CGG	
	CCG CCACCGTCGG GTC	
	A _ C	
GAM476 LZTS1	GGGCTGGTGGCAGCCCAGGG 7551 TAGGGTA A T	
	GGTGGCAGCC CGGG	
	CCACCGTCGG GTCC	
	CGA_____ C	
GAM476 MBP	GGGTGTGTGGGCAGCCACGG 7550 AG _ II	
	GGGT GTGG CAGCCACG	
	CCCA CACC GTCGGTGC	
	CA C CI	
GAM476 MBP	GGGTGTGTGGGCAGCCACGG 7550 TAGGGTAG _ GT	
	GTGG CAGCCACGG	
	CACC GTCGGTGCC	
	CACA_____ C GG	
GAM476 PARK2	GGGTAGGTGGCGGCTGCGGG 7554 A CA I	
	GGTAGGTGGC GC CGG	
	CCATCCACCG CG GCC	
	C AC I	
GAM476 PARK2	GGGTAGGTGGCGGCTGCGGG 7554 TAGG A CA	
	GTAGGTGGC GC CGGGT	

	CATCCACCG CG GCCCG		
	_____ C AC		
GAM476 PLXNB3	AGGGGAGGTGGCAGGCAGGG	7546 _ T	C CGI
	GGG AGGTGGCAG CA		
	CCC TCCACCGTC GT		
	C _ C CCI		
GAM476 PLXNB3	AGGGGAGGTGGCAGGCAGGG	7546 TA T	C C T
	GGG AGGTGGCAG CA GGG		
	CCC TCCACCGTC GT CCC		
	C _ C _ T		
GAM476 SGCD	TAGCTGGCAGCCA-GTGTC	7560 G	CGGGTI
	TAG TGGCAGCCA		
	ATC ACCGTCGGT		
	G CACAGI		
GAM476 SOX12	TAGGCTGTAGA-GGCAGCCACG	7558 _ T	GGTC
	TAGG GTAGG GGCAGCCACG		
	ATCC CATCT CCGTCGGTGC		
	GA _ C		
GAM476 SOX12	TAGGCTGTAGA-GGCAGCCACG	7558 AGG_ T	I
	GTAGG GGCAGCCAC		
	CATCT CCGTCGGTG		
	CCGA _ I		
GAM476 UMOD	AGGTGAGATGGCAGCCATGG	7547 G _	CGI
	GGT AGGTGGCAGCCA		
	CCA TCTACCGTCGGT		
	_ C ACI		
GAM476 UMOD	AGGTGAGATGGCAGCCATGG	7547 TAG _	C T
	GGT AGGTGGCAGCCA GGG		
	CCA TCTACCGTCGGT CCT		
	_ C A I		
GAM477 ACTN2	AGCAGTATGAGCAAAAAGAA	7564	AATGAI
	AGCAGTATGAG		
	TCGTCATACTC		
	GTTTTTCT		
GAM477 ACTN2	AGCAGTATGAGCAAAAAGAA	7564 TA	AAT CTAAC
	GCAGTATGAG GAA		
	CGTCATACTC TTT		
	_ GTT CTTTI		
GAM477 AGL	AGCAATGAAAGAGAATGAA	7563 AT_	
	AGCAGT GAGAATGA		

		TCGTTA CTCTTACT			
		CTTT TII			
GAM477 AGL		AGCAATGAAAGAGAATGAA	7563 TA	AT__	CTAAC
		GCAGT GAGAATGAA			
		CGTTA CTCTTACTT			
		_ CTTT AIIIA			
GAM477 COL17A1		TAG-AGAATGCAGAATGAAC	7576 C T _		II
		TAG AG ATG AGAATGAA			
		ATC TC TAC TCTTACTT			
		_ T G GI			
GAM477 COL17A1		TAG-AGAATGCAGAATGAAC	7576 C T _		TAAC
		TAG AG ATG AGAATGAA			
		ATC TC TAC TCTTACTTG			
		_ T G IIIA			
GAM477 GABRA3		AGAAGGATGA--ATGAACTGAAACA	7565 CAGTATGA		AI
		GAATGAACT			
		CTTACTTGA			
		TCCTA__ CT			
GAM477 GABRA3		AGAAGGATGA--ATGAACTGAAACA	7565 TAGCAGTATGA		_ I
		GAATGAACT AACA			
		CTTACTTGA TTGT			
		CTTCCTA__ CT T			
GAM477 HS3ST4		TAGCAGAAGATAAGAATGAAC	7573 T__		TAACA
		TAGCAG ATGAGAATGAAC			
		ATCGTC TATTCTTACTTG			
		TTC IIIAC			
GAM477 HS3ST4		TAGCAGAAGATAAGAATGAAC	7573 T__		III
		TAGCAG ATGAGAATGAA			
		ATCGTC TATTCTTACTT			
		TTC GII			
GAM477 IGFBP3		AGCATGAGAATGACTCTAA	7568	A AII	
		AGTATGAGAATGA CT			
		TCGTACTCTTACT GA			
		_ GAT			
GAM477 IGFBP3		AGCATGAGAATGACTCTAA	7568 TAGCAGTA	A_ C	
		TGAGAATGA CTAA			
		ACTCTTACT GATT			
		_____ GA C			
GAM477 IMPG2		GTTTGAGAATGAACAACCA	7572 GTA	T II	
		TGAGAATGAAC AAC			

	ACTCTTACTTG TTG			
	CAA _ GT			
GAM477 ITSN1	TAGGATTATGAGAAT--ATTAACA 7577	CAG	__	TAAI
	TAG TATGAGAATG AAC			
	ATC ATACTCTTAT TTG			
	CTA AA TIII			
GAM477 ITSN1	TAGGATTATGAGAAT--ATTAACA 7577	CAG		AAC
	TAG TATGAGAATG TAACA			
	ATC ATACTCTTAT ATTGT			
	CTA A__			
GAM477 KLRD1	TAGCAAAAATAGAGAATGAA 7574	TAT__		CTAAC
	TAGCAG GAGAATGAA			
	ATCGTT CTCTTACTT			
	TTTAT IIIAC			
GAM477 KLRD1	TAGCAAAAATAGAGAATGAA 7574	TAT__		III
	TAGCAG GAGAATGA			
	ATCGTT CTCTTACT			
	TTTAT TII			
GAM477 MAN2A2	GCAGTCTCTGTGAATGAACT 7571	A__ A		III
	GCAGT TG GAATGAAC			
	CGTCA AC CTTACTTG			
	GAG A AII			
GAM477 MAN2A2	GCAGTCTCTGTGAATGAACT 7571	TAGCAGTA A		AAC
	TG GAATGAAC			
	AC CTTACTTGA			
	TCAGAG__ A AAI			
GAM477 PIM2	AGTAAGAGCATATGAACTAA 7566	T A__		III
	AGTA GAG ATGAACTA			
	TCAT CTC TACTTGAT			
	T GTA TII			
GAM477 PIM2	AGTAAGAGCATATGAACTAA 7566	T C	GAGA	C
	AG AGTAT ATGAACTAA			
	TC TCGTA TACTTGATT			
	_ _ _ C			
GAM477 RFXAP	AGTATGAGAATAAACTAACA 7569			I
	GTATGAGAATGAACTAAC			
	CATACTCTTATTTGATTG			
	I			
GAM477 RFXAP	AGTATGAGAATAAACTAACA 7569	TAGCAGTA		
	TGAGAATGAACTAAC			

ACTCTTATTTGATTG

GAM477 SLC4A10	AGTATGAGAATACTAACTA	7567	___	III
	AGTATGAGAAT GAACT			
	TCATACTCTTA TTTGA			
	TG TII			
GAM477 SNX6	TACCAGGATACATGAATGAACTAA	7575	G ___ A	CAI
	TA CAG TATG GAATGAACTAA			
	AT GTC ATGT CTTACTTGATT			
	G CT A III			
GAM477 SNX6	TACCAGGATACATGAATGAACTAA	7575	AGCA A	I
	GTATG GAATGAACTA			
	TATGT CTTACTTGAT			
	GTCC A I			
GAM477 WNT5A	CATTCTGCAGAATGAACTAA	7570	GTA _	II
	CA TG AGAATGAACTA			
	GT AC TCTTACTTGAT			
	AAG G TI			
GAM477 WNT5A	CATTCTGCAGAATGAACTAA	7570	TAGCAGTA _	C
	TG AGAATGAACTAA			
	AC TCTTACTTGATT			
	AG___ G C			
GAM478 ABCC1	TGAGAGGGAAAGAAAAGAGGT	7595	A ___	CCAGAG
	TGAGAG GAAA AAGAGGT			
	ACTCTC CTTT TTCTCCA			
	C CTT IIIGAG			
GAM478 ABCC1	TGAGAGGGAAAGAAAAGAGGT	7595	A ___	III
	TGAGAG GAAA AAGAGG			
	ACTCTC CTTT TTCTCC			
	C CTT AII			
GAM478 APBA1	GAGAGAGTAAA-GAGGTCC	7591	AA	I
	GAGAGAG AAAGAGGTC			
	CTCTCTC TTTCTCCAG			
	A_ G			
GAM478 APBA1	GAGAGAGTAAA-GAGGTCC	7591	TG AA	AG
	AGAGAG AAAGAGGTCC			
	TCTCTC TTTCTCCAGG			
	_ A_ AI			
GAM478 BECN1	TGAGAGAGATAAAAA--TCCAG	7601	AAA	A
	TGAGAGAGA AGAGGTCCAG			

	ACTCTCTCT TTTTAGGTC		
	A__ I		
GAM478 BECN1	TGAGAGAGATAAAAA--TCCAG 7601_ AAA I		
	GAGAGAGA AGAGGTCCA		
	CTCTCTCT TTTTAGGT		
	A A__ I		
GAM478 CENTD2	GAGAGAGAAAGACAGAGGGAGAGAG 7588 AAA TCC I		
	AGAGAGA AGAGG AGA		
	TCTCTTT TCTCC TCT		
	CTG CTC I		
GAM478 CENTD2	GAGAGAGAAAGACAGAGGGAGAGAG 7588 T AAA TCC II		
	GAGAGAGA AGAGG AGAG		
	CTCTCTTT TCTCC TCTC		
	T CTG CTC TI		
GAM478 CYP4A11	TGAGAGAGAGAAGGGCAGG--CAGA 7597 AA A C__ GI		
	TGAGAGAGA AAG GGT CAGA		
	ACTCTCTCT TTC CCG GTCT		
	C_ _ TCC II		
GAM478 CYP4A11	TGAGAGAGAGAAGGGCAGG--CAGA 7597_ AAAG CCAI		
	GAGAGAGAA AGGT		
	CTCTCTCTT TCCG		
	T CCCG TCII		
GAM478 CYP4A11	TGAGAGAGAAAGTG-GGTCCAG 7600 AAGA AG		
	TGAGAGAGAAA GGTCCAG		
	ACTCTCTCTTT CCAGGTC		
	CAC_ II		
GAM478 CYP4A11	TGAGAGAGAAAGTG-GGTCCAG 7600_ AAGA I		
	GAGAGAGAAA GGTCCA		
	CTCTCTCTTT CCAGGT		
	A CAC_ I		
GAM478 DPYSL2	GAGAGAGAAAGAGAGAGT-GAGAG 7590 A TCC I		
	AGAGAGAAA AGAGG AGA		
	TCTCTCTTT TCTCT TCT		
	C CAC I		
GAM478 DPYSL2	GAGAGAGAAAGAGAGAGT-GAGAG 7590 TG A TCC I		
	AGAGAGAAA AGAGG AGAG		
	TCTCTCTTT TCTCT TCTC		
	_ C CAC G		
GAM478 FSTL1	GAG-GAAACTGAGGTCCAGA 7585_ A AA I		
	AG GAAA GAGGTCCAG		

	TC CTTT CTCCAGGTC	
	C _ GA I	
GAM478 FSTL1	GAG-GAAACTGAGGTCCAGA 7585 TGAGAGA AA	
	GAAA GAGGTCCAGA	
	CTTT CTCCAGGTCT	
	_____ GA	
GAM478 HSPA2	GAGAGAGAAAGGCAAAGAGGT 7587 _____ IIIA	
	GAGAGAGAAA AAGAGG	
	CTCTCTCTTT TTCTCC	
	CCGT AIII	
GAM478 HSPA2	GAGAGAGAAAGGCAAAGAGGT 7587 T__ AA CCAGAG	
	GAGAGAG AAAGAGGT	
	CTCTTTC TTTCTCCA	
	TCT CG AIIIGA	
GAM478 IL18R1	GAGGGAGAAAAAGAATAGCTCCA 7589 AGA ____ G I	
	GAGAAAAAGA G TCC	
	CTCTTTTCT C AGG	
	_____ TAT G I	
GAM478 IL18R1	GAGGGAGAAAAAGAATAGCTCCA 7589 TG A ____ G GAGI	
	AG GAGAAAAAGA G TCCA	
	TC CTCTTTTCT C AGGT	
	__ C TAT G AIII	
GAM478 KCND2	AGTGAGAAAC-GTGGTCCAGAG 7584 GA_ AAGA I	
	GAGAAA GGTCCAGA	
	CTCTTT CCAGGTCT	
	TCA GCA_ I	
GAM478 KCND2	AGTGAGAAAC-GTGGTCCAGAG 7584 TGAGA AAGA	
	GAGAAA GGTCCAGAG	
	CTCTTT CCAGGTCTC	
	A_____ GCA_	
GAM478 LYZ	TGAGAGAGACAAAATGAGCTGAAGA 7594 G A GTCCAGI	
	GAGAGA AAAA GAG	
	CTCTCT TTTT CTC	
	G A GACTTCI	
GAM478 LYZ	TGAGAGAGACAAAATGAGCTGAAGA 7594 _ _ GTCC GII	
	TGAGAGAGA AAAA GAG AGA	
	ACTCTCTCT TTTT CTC TCT	
	G A GACT III	
GAM478 NDP	TGAGAGCTAGAAAGAGGTCC 7599 AGAA AGA	
	TGAGAG AAAGAGGTCC	

	ACTCTC TTTCTCCAGG			
	GATC III			
GAM478 NDP	TGAGAGCTAGAAAGAGGTCC	7599	AGAA	I
	GAGAG AAAGAGGTC			
	CTCTC TTTCTCCAG			
	GATC I			
GAM478 PLSCR1	GAGCGAGACAA---GGTCCAGAG	7593	A AAAA	I
	GAG GAGA GAGGTCCAG			
	CTC CTCT TTCCAGGTC			
	G G___ T			
GAM478 PLSCR1	GAGCGAGACAA---GGTCCAGAG	7593	TG A AAAA	
	AG GAGA GAGGTCCAGA			
	TC CTCT TTCCAGGTCT			
	___ G G___			
GAM478 SERPINA5	AGAGGGAAACTGAGGTCCAGAG	7583	A AA	I
	GAG GAAA GAGGTCCAGA			
	CTC CTTT CTCCAGGTCT			
	C GA I			
GAM478 SERPINA5	AGAGGGAAACTGAGGTCCAGAG	7583	TGAG A AA	
	AG GAAA GAGGTCCAGAG			
	TC CTTT CTCCAGGTCTC			
	___ C GA			
GAM478 SFRS2IP	GAGAGAGAAAA--TGGTCAAG	7592	AGA CI	
	GAGAGAGAAAA GGTC			
	CTCTCTCTTTT CCAG			
	A___ TT			
GAM478 SFRS2IP	GAGAGAGAAAA--TGGTCAAG	7592	TG AGA C A	
	AGAGAGAAAA GGTC AG			
	TCTCTCTTTT CCAG TC			
	___ A___ T A			
GAM478 SH3BP4	AGGGAGTGAAAGAGGTCCA	7582	A AA	II
	AG GAG AAAGAGGTCC			
	TC CTC TTTCTCCAGG			
	C AC TI			
GAM478 SH3BP4	AGGGAGTGAAAGAGGTCCA	7582	TGAGA AA	A
	GAG AAAGAGGTCCAG			
	CTC TTTCTCCAGGTT			
	C___ AC G			
GAM478 SIRT6	GAGAGAAAAAGA-ATCCACAG	7586	G GI	
	AGAGAAAAAGAG TCCA			

	TCTCTTTTCTT AGGT		
	— GT		
GAM478 SIRT6	GAGAGAAAAAGA-ATCCACAG 7586 TGAGAG	G G	
	AGAAAAAGAG TCCA A		
	TCTTTTCTT AGGT T		
	— — G		
GAM478 SOX10	TGAGAGAGAAAAACAGGAGTC 7596	— AG CAGA	
	TGAGAGAGAAAA AG GTC		
	ACTCTCTCTTTT TC CAG		
	G CT G		
GAM478 SOX10	TGAGAGAGAAAAACAGGAGTC 7596	AG T	
	TGAGAGAGAAAA AGG		
	ACTCTCTCTTTT TCC		
	G_ TCA		
GAM478 TG	AGAGAAAAAGATGACCATAG 7580	GGT GAI	
	GAGAAAAAGA CCA		
	CTCTTTTCT GGT		
	ACT ATI		
GAM478 TIMM17B	TGAGAGAGAAAAAGGGGACC 7598	A T AGA	
	TGAGAGAGAAAAAG GG CC		
	ACTCTCTCTTTTTC CC GG		
	C T		
GAM478 TIMM17B	TGAGAGAGAAAAAGGGGACC 7598	A TCI	
	GAGAGAGAAAAAG GG		
	CTCTCTCTTTTTC CC		
	— CTG		
GAM478 WNT10B	AGAAGGAAAAAGAGGCTCCAAGAG 7581	A — AI	
	AG GAAAAAGAGG TCCAG		
	TC CTTTTTCTCC AGGTT		
	— G CI		
GAM478 WNT10B	AGAAGGAAAAAGAGGCTCCAAGAG 7581	TGA A — — I	
	GAG GAAAAAGAGG TCCA GAG		
	TTC CTTTTTCTCC AGGT CTC		
	— — G T A		
GAM479 CALM1	GCGGGGTACCT-CCG-ATGC 7610	TAGC GTGG C	
	GGGGGTAC CG ATGC		
	CCCCCATG GC TACG		
	— — GAG_ —		
GAM479 CBFA2T2	GGGCGTG-GTGGCGCATGC 7611	TAGCGGGGGTAC	
	GTGGCGCATG		

		CACCGCGTAC			
		CAC_____			
GAM479	DMD	TGCTGCTTCCCAAACCTTAGAAA	7619	GT	_G CC
		GCTGTT T CAAACTTAGGAA			
		I			
		CGACGA G GTTTGAATCTTT			
		_ A G TI			
GAM479	DMP1	GTGCT-TTTGCAAACCTAAG	7612	G	T GAA
		GTGCT TTTGCAAACCT AG			
		II			
		CACGA AAACGTTTGA TC			
		_ T III			
GAM479	GATA6	TGCAGTCTTGCAAACCTGAGTAA	7618	GT	TG_ T GAACC
		GC TTTGCAAACCT AG			
		II II			
		CG GAACGTTTGA TC			
		_ TCA C ATTAI			
GAM479	GDF2	TGCTGTTTGC--TCTGAAGGAACC	7620	GT	AAACTT
		GCTGTTTGC AGGAACC			
		CGACAAACG TCCTTGG			
		_ AGACT_			
GAM479	GOT2	GTGCTGTTT-CTCAC-GAGGAACC	7614		G_ AACTT
		GTGCTGTTT CA AGGAACC			
		II			
		CACGACAAA GT TCCTTGG			
		GA GC__			
GAM479	HCS	AGCTGGGCATGGTGGCGCATGC	7606	TA	GG C_ G
		GC GGGTA GTGGCGCATGC			
		II			
		CG CCCGT CACCGCGTACG			
		_ A_ AC G			
GAM479	LTB4R	GTGCTGTTTGCTAAATCAG	7613		A C GAAC
		GTGCTGTTTGC AA TTAG			
		II			
		CACGACAAACG TT AGTC			
		A T IIIC			
GAM479	MCM4	TAGCTGGGATTACA-GGCGCATGC	7616	_	GG T GI
		TAGC GGG TACG GGCGCATGC			
		ATCG CCC ATGT CCGCGTACG			
		A TA _ II			
GAM479	MYBPH	AGCGGGGGGT-CTTGG-GCAT	7605	TA	ACG C G
		GCGGGGGT TGG GCAT			
		CGCCCCCA ACC CGTA			
		_ GA_ _ G			
GAM479	NCOA6	TAGCAGGGCATGGTGGCGCATGC	7617		GTAC GI
		TAGCGGGG GTGGCGCATGC			

	ATCGTCCC CACCGCGTACG	
	GTAC II	
GAM479 PTGIS	GCTGGAGTGCCGTGGCGCA 7609 TAGCG A_ TGC	
	GGGGT CGTGGCGCA	
	CCTCA GCACCGCGT	
	A___ CG CAI	
GAM479 PTPN2	CGGGGAGAGCGCTGGCGC-TGCG 7607 TAGCG TA _ A	
	GGGG CG TGGCGC TGCG	
	CCTC GC ACCGCG ACGC	
	_____ TC G _	
GAM479 PTPN2	AGCGCTGGCGCTGCGGCGCATGCG 7604 TA G G AC I	
	GC GG GT GTGGCGCATGCG	
	CG CC CG CGCCGCGTACGC	
	CG A G A_ G	
GAM479 RP2	TAGCCAGGTGTA-GTGGCGCATGC 7615 G _ C GI	
	TAGC GGG GTA GTGGCGCATGC	
	ATCG TCC CAT CACCGCGTACG	
	G A _ II	
GAM479 SORCS1	TGCTGTTTG-GAACTTCTGAA 7621 GT CA AG C	
	GCTGTTTG AACTT GAA	
	CGACAAAC TTGAA CTT	
	_ C_ GA T	
GAM479 SPON1	CTGATTTGCAAACCTT-GAAC 7608 GTGCT AG	
	GTTTGCAAACCTT GAAC	
	TAAACGTTTGAA CTTG	

GAM480 DMD	GCTGCCCAATGCCATCCTG 7626 GG GGAAG_ CATA	
	CTGCCCAA CCTG	
	GACGGGTT GGAC	
	_ ACGGTA C	
GAM480 EIF2B5	CTTCCGCAAGGAAG-CTGC 7624 GGCTG _ C AT	
	CC CAAGGAAGC TGC	
	GG GTTCCTTCG ACG	
	A___ C _ GT	
GAM480 MBNL	GGCTTTGCAAGGAAGCCGGCA 7627 GCC T TAG	
	GGCT CAAGGAAGCC GCA	
	CCGA GTTCCTTCGG CGT	
	AAC C	
GAM480 ROM1	CTGCCCAAGGGAG--TGCAGAG 7625 GGCT A CC TA	
	GCCCAAGG AG TGCA	

		CGGGTTCC TC ACGT	
		_____ C _ CT	
GAM481 AMD1		AAAGGACTAATAAAATTTTC 7630 TAGCAAAG GAT_	
		GACTAA ATTTTC	
		CTGATT TAAAAG	
		_____ ATTT	
GAM481 BAT1		AGCAAAGGAAAACAAAGATACTATTTCT7631 TA CT___ _ III	
		GCAAAGGA AAGATAT TTTCT	
		CGTTTCCT TTCTATG AAAGA	
		_____ TTTGT AT TII	
GAM481 GLRA3		AGCAAAGG---AAGA-ATGTTC 7632 TA CTA TATT	
		GCAAAGGA AGA TT	
		CGTTTCCT TCT AA	
		_____ TAC_	
GAM481 KCNMB3		AGCAAAGGA-TGAGATACATTCT 7633 TA CTA T	
		GCAAAGGA AGATAT TTCT	
		CGTTTCCT TCTATG AAGA	
		_____ AC_ T	
GAM482 IFNW1		TAGAA--GCAAATTTTAAAC 7636 AT G AT	
		TAGA AG AAAATTTTAAAC	
		ATCT TC TTTTAAAATTG	
		_____ G	
GAM483 ALPL		CCTCTGGGTCTGGAGAAATA 7640 G TGCTATI	
		CT TGGGTCTGG	
		GA ACCCAGACC	
		G TCTTTAI	
GAM483 ATRN		CTGTGGGTCTCATGGTGCATGATAT 7643 TGT _ TATAI	
		GGGTC TGGTGC	
		CCCAG ACCACG	
		_____ T TACTA	
GAM483 CYP8B1		CTCCCATGTGGGTCTGGGGATA 7641 T _ TGCTI	
		CC TGTGGGTCTGG	
		GG ACACCCAGACC	
		_ T CCTAI	
GAM483 HPCA		CTCC-GTGGGTCTGTGTG-TAT 7642 TC _ CTI	
		CTGTGGGTCTG GTG	
		GGCACCCAGAC CAC	
		A_ A ATI	
GAM483 KCNA7		TCCTTTGGGTCTGGTGCTA 7646 G _ II	
		TCCT TGGGTC TGGTGCT	

	AGGA ACCCAG ACCACGA		
	A G TI		
GAM483 MHC2TA	TCCTGTGGGCACTGGGGCT 7645	_ T II	
	TCCTGTGGGT CTGG GC		
	II		
	AGGACACCCG GACC CG		
	T C AI		
GAM483 TGM4	TGTGGGTCTGGCTGCT-TAT 7648	_ ATAI	
	TGTGGGTCTGG TGCT		
	ACACCCAGACC ACGA		
	G ATAI		
GAM483 TRO	CCTGTGGGTCCTG--GCTAT 7639	GGT I	
	CCTGTGGGTCT GCTA		
	GGACACCCAGG CGAT		
	AC_ A		
GAM483 VASP	TCCTGTGGGGTTCATTGGTGC 7644	_ _ IIIG	
	TCCTGTGGG TC TGGTG		
	II		
	AGGACACCC AG ACCAC		
	CA TA GIII		
GAM483 WHSC1	TCTCCTGTGTTTCTCGGGCT 7647	GG _ T I	
	CTCCTGTG TCT GG GC		
	II II		
	GAGGACAC AGA CC CG		
	AA G _ I		
GAM484 COLQ	GGGAGCCAGCCAAGGCTGTCCT 7658	GA A T_ I	
	AGCCA CC GGCTGTCC		
	II		
	TCGGT GG CCGACAGG		
	C_ C TT I		
GAM484 COLQ	GGGAGCCAGCCAAGGCTGTCCT 7658	T A A T_ GA	
	GGA GCCA CC GGCTGTCCT		
	II		
	CCT CGGT GG CCGACAGGA		
	_ _ C TT AI		
GAM484 FCN2	GGAGGCCAACCT-GTTCTCCT 7661	_ A GCTG I	
	GA GCCAACCTG TCC		
	CT CGGTTGGAC AGG		
	C C AAG_ I		
GAM484 FCN2	GGAGGCCAACCT-GTTCTCCT 7661	TG A GCTG G	
	GA GCCAACCTG TCCT		
	CT CGGTTGGAC AGGA		
	_ C AAG_ G		
GAM484 GAS7	GCCAACCTGAGCTACCCTG 7655	_ GT II	
	GCCAACCTG GCT CCT		

		CGGTTGGAC CGA GGA			
		T TG CI			
GAM484 GJB1		GCCACACCTGGCTGCTGCTG	7654	_	CCTIII
		GCCA ACCTGGCTGT			
		CGGT TGGACCGACG			
		G ACGACI			
GAM484 HLCS		GGAAGCC---CTGGCTGTCC	7660	AAC	I
		GGAAGCC CTGGCTGT			
		CCTTCGG GACCGACA			
		G			
GAM484 HLCS		GGAAGCC---CTGGCTGTCC	7660	TG AAC	
		GAAGCC CTGGCTGTCCT			
		CTTCGG GACCGACAGGG			
GAM484 MEN1		GCCAACCTGGGCATACTGA	7656		CT C II
		GCCAACCTGG GT CTG			
		CGGTTGGACC TA GAC			
		CG T TI			
GAM484 OTX1		GGCAGCCAACCT---TGTC	7659	A	GGCTGT
		GG AGCCAACCT			
		CC TCGGTTGGA			
		G ACAGII			
GAM484 OTX1		GGCAGCCAACCT---TGTC	7659	TGGA	GGC C
		AGCCAACCT TGTC			
		TCGGTTGGA ACAG			
		CG_ _ C			
GAM484 PLXNA1		TGGAAGCCACCCAGG-AGT-CTGA	7666		A TG CT C
		TGGAAGCCA CC G GTC TGA			
		ACCTTCGGT GG C CAG ACT			
		_ GT CT _			
GAM484 PLXNA1		TGGAAGCCACCCAGG-AGT-CTGA	7666		A TG CT CTI
		TGGAAGCCA CC G GTC			
		ACCTTCGGT GG C CAG			
		_ GT CT ACT			
GAM484 PMM2		TGAAAGC--ACCTGGCTGT	7664	CA	CCT
		TGAAAGC ACCTGGCTGT			
		ACTTTCG TGGACCGACA			
		III			
GAM484 PMM2		TGAAAGC--ACCTGGCTGT	7664	CA	I
		TGAAAGC ACCTGGCTG			

	ACTTTCG TGGACCGAC			
	— A			
GAM484 RANBP17	AGCCAACATCACTGTCCTGA 7652 CTG I			
	GCCAAC GCTGTCCTG			
	CGGTTG TGACAGGAC			
	TAG I			
GAM484 SERPINA4	GCCAGCACCTG-CTGTCCTG 7653 — G II			
	GCCA ACCTG CTGTCCT			
	CGGT TGGAC GACAGGA			
	CG — CI			
GAM484 SLC12A7	GGAGGGCAGTCCTGGCTGTCTGTG 7657 AA CAA CI			
	GC CCTGGCTGTC			
	CG GGACCGACAG			
	CC TCA CI			
GAM484 SLC12A7	GGAGGGCAGTCCTGGCTGTCTGTG 7657 T_ AA CAA C AI			
	GG GC CCTGGCTGTC TG			
	CC CG GGACCGACAG AC			
	CT — TCA C CI			
GAM484 TCF7	TGAAAGACAGGCTCTGGCTGTCTATGA 7663 C AC_ C II			
	TGGAAG CA CTGGCTGTC TGA			
	ACTTTC GT GACCGACAG ACT			
	T CCGA T II			
GAM484 TCF7	TGAAAGACAGGCTCTGGCTGTCTATGA 7663 AGCCAAC CTI			
	GGA CTGGCTGTC			
	TCT GACCGACAG			
	GTCCGA_ TAC			
GAM484 TK2	TGGAAGCCAGGGCTGGCTGCCC 7662 AC_ TGA			
	TGGAAGCCA CTGGCTGTCC			
	ACCTTCGGT GACCGACGGG			
	CCC			
GAM484 TK2	TGGAAGCCAGGGCTGGCTGCCC 7662 G AC_ I			
	GAAGCCA CTGGCTGTC			
	CTTCGGT GACCGACGG			
	— CCC I			
GAM484 TMEPAI	AGACAACCTGCTGGCTGTCTTG 7651 C — CTIII			
	AG CAACCT GGCTGTC			
	TC GTTGGA CCGACAG			
	T CGA AACII			
GAM484 TMEPAI	AGACAACCTGCTGGCTGTCTTG 7651 TGGA AAC C A			
	AGCC CTGGCTGTC TG			

	TTGG GACCGACAG AC	
	____ AC_ A C	
GAM484 ZNF142	TGGAAGCCACTCTCTCT-TCCT 7665	AC GG G GA
	TGGAAGCCA CT CT TCCT	
	ACCTTCGGT GA GA AGGA	
	GA GA _	
GAM484 ZNF142	TGGAAGCCACTCTCTCT-TCCT 7665_	AC GG G I
	GGAAGCCA CT CT TCC	
	CCTTCGGT GA GA AGG	
	A GA GA _ I	
GAM485 ATP7B	TGAAATGCACACTCCAGAGCA 7675	T CGT GCA
	TGAAATGCAC TTCC GCA	
	ACTTTACGTG GAGG CGT	
	T TCT	
GAM485 BCLG	TGTAACGCACTTTTCCC-TACAGCA 7676 A	G I
	TG AATGCACTTTTCCC TGCAGCA	
	AC TTGCGTGAAAGGG ATGTCGT	
	A _ I	
GAM485 DIAPH2	GAAATGCACTTATTTCTTTCCAGC 7674 TG	____ CGTG All
	AAATGCACTT TCC CAGC	
	TTTACGTGAA AGG GTCG	
	____ TAA AAAG G	
GAM485 JAG2	AAATGCACTTTTACGAGGAG 7670 TGAA	C TGC C
	ATGCACTTTC CG AG	
	TACGTGAAAG GC TC	
	____ T TCC C	
GAM485 NRIP1	ATGCACTTT-TCATGCAGCA 7672 TGAAATGC	CC
	ACTTT CGTGCAGC	
	TGAAA GTACGTCG	
	____ A_	
GAM485 RIMS2	GAAGATTCAGTA-CCCGTGCAGC 7673 TGAAATG CTTT	A
	CA CCCGTGCAGC	
	GT GGGCACGTCG	
	TTCTAA_ CAT_ A	
GAM485 UBQLN2	AAAAGCACTTTTCTG-GCA 7669 TGAAAT	CGT G
	GCACTTTCC GCA	
	CGTGAAAGG CGT	
	TT____ AC_ A	
GAM485 ZNF131	AATGCACTTTTTCATCATGCAGC 7671 TGAAAT	_C_ A
	GCACTTT C CGTGCAGC	

	CGTGAAA G GTACGTCG		
	_____ A TA G		
GAM486 BCRP2	TGAGAACACC----ACAGCCTC 7688	GTGT	A
	TGAGAACACC ACAGC		
	ACTCTTGTGG TGTCG		
	_____ G		
GAM486 BCRP2	TGAGAACACC----ACAGCCTC 7688	GTGT	A
	TGAGAACACC ACAGC TC		
	ACTCTTGTGG TGTCG AG		
	_____ G		
GAM486 FABP2	TGAGAACACG CAGTATTCAGC 7685	--	A III
	TGAGAACAC C GTGT CAG		
	ACTCTTGTG G CATA GTC		
	C T A GII		
GAM486 FABP2	TGAGAACACG CAGTATTCAGC 7685	--	A ATCGG
	TGAGAACAC C GTGT CAGC		
	ACTCTTGTG G CATA GTCG		
	C T A IIIGG		
GAM486 FOSB	GAGAACCACAAGTACAGCATGGG 7683	AC T	CGI
	AGAAC CG GTACAGCAT		
	TCTTG GT CATGTCGTA		
	GT T CCI		
GAM486 FOSB	GAGAACCACAAGTACAGCATGGG 7683	TG AC T	C I
	AGAAC CG GTACAGCAT GG		
	TCTTG GT CATGTCGTA CC		
	_____ GT T C C		
GAM486 GAD1	TGAGAACACCAGACGTACAGC 7686	___	ATCGG
	TGAGAACACCG TGTACAGC		
	ACTCTTGTGGT GCATGTCG		
	CT IIIGG		
GAM486 GAD1	TGAGAACACCAGACGTACAGC 7686	___	III
	TGAGAACACCG TGTACAG		
	ACTCTTGTGGT GCATGTC		
	CT GII		
GAM486 HEPH	TGAGGCACGCTGGGT-CAGCATCGG 7684	AA C ___ A	I
	TGAG CAC GT GT CAGCATCGG		
	ACTC GTG CG CA GTCGTAGCC		
	C_ _ ACC _ I		
GAM486 HEPH	TGAGGCACGCTGGGT-CAGCATCGG 7684	AA C ___ A	I
	GAG CAC GT GT CAGCATCG		

	CTC GTG CG CA GTCGTAGC		
	C_ _ ACC _ I		
GAM486 INMT	AGAGCCCC-TGTACAGCAT 7679	ACA G I	
	AGA CC TGTACAGCA		
	TCT GG ACATGTCGT		
	CG_ G A		
GAM486 INMT	AGAGCCCC-TGTACAGCAT 7679	TGAGAACA G C	
	CC TGTACAGCAT		
	GG ACATGTCGTA		
	TCG_____ G A		
GAM486 ITS1	GAGAACACCATCTAGTACAG 7680	_____	
	GAGAACACCGT GTACA		
	CTCTTGTGGTA CATGT		
	GAT CII		
GAM486 ITS1	GAGAACACCATCTAGTACAG 7680	TG _____ CATCG	
	AGAACACCGT GTACAG		
	TCTTGTGGTA CATGTC		
	_____ GAT CIIIG		
GAM486 KCNJ15	TGAGAACACTGTCCAGAGCA 7687	C G C TCG	
	TGAGAACAC GT TA AGCA		
	ACTCTTGTG CA GT TCGT		
	A G C III		
GAM486 KCNJ15	TGAGAACACTGTCCAGAGCA 7687	C G C I	
	GAGAACAC GT TA AGC		
	CTCTTGTG CA GT TCG		
	A G C I		
GAM486 RBM8A	GAGAACACC-TGGACAACA 7681	G T I	
	GAGAACACC TG ACAGC		
	CTCTTGTGG AC TGTTG		
	_ C T		
GAM486 RBM8A	GAGAACACC-TGGACAACA 7681	TG G T TC	
	AGAACACC TG ACAGCA		
	TCTTGTGG AC TGTTGT		
	_____ _ C CI		
GAM486 SCAMP1	GAGTACA---TGTACAGCA 7682	GAGAACAC	
	CGTGTACAGC		
	GTACATGTCG		
	CTCAT_____		
GAM486 SCAMP1	GAGTACA---TGTACAGCA 7682	TGAGAACAC T	
	CGTGTACAGCA		

	GTACATGTCGT	
	TCAT_____T	
GAM487 ACCN2	TGCGCGTGTCGTCTCCTTGTG	7696 _ TT C _ I
	GC GTG CG CTCCTTGT	
	CG CAC GC GAGGAACA	
	G _ A A I	
GAM487 ACCN2	TGCGCGTGTCGTCTCCTTGTG	7696 TGGTGCTT C _ G
	GTG CG CTCCTTGTG	
	CAC GC GAGGAACAC	
	CG_____A A G	
GAM487 BCL7A	TGGTGCTTGGGGCGTGCCT	7701 T_ C_ T_____TTGT
	TGGTGCTTG GC GC CC G	
	I	
	ACCACGAAC CG CG GG C	
	CC CA GAI TGTT	
GAM487 BCL7A	TGGTGCTTGGGGCGTGCCT	7701 _____ GCTCC
	TGGTGCTT GTGCC	
	ACCACGAA CACGG	
	CCCCG A CCT	
GAM487 DDX19	CTTGTGCCGTTGTCCTTGGGG	7692 C_ TG
	CTTGTGCCG TCCTTG	
	GAACACGGC AGGAAC	
	AAC CCC	
GAM487 GALR1	TGTTGCTCGGAGCCGCTCCTT	7698 G T_ GTGG
	TG TGCTTG GCCGCTCCTT	
	AC ACGAGC CGGCGAGGAA	
	A CT G	
GAM487 GALR1	TGTTGCTCGGAGCCGCTCCTT	7698 GG T_ I
	TGCTTG GCCGCTCCT	
	ACGAGC CGGCGAGGA	
	A_ CT I	
GAM487 GPR86	TGGTGCTTGTGC--CTCCT	7702 G CCI
	TGGTGCTTGTGCC CT	
	ACCACGAACACGG GG	
	A A	
GAM487 GPR86	TGGTGCTTGTGC--CTCCT	7702 GC TGT
	TGGTGCTTGTGCC TCCT	
	ACCACGAACACGG AGGA	
	_	
GAM487 IL19	TGGTGCTTGC GGGCTGCTCCTTGTG	7699 _ C G
	TGGTGCTTGT GC GCTCCTTGTG	

	ACCACGAACG CG CGAGGAACAC		
	CC A III		
GAM487 IL19	TGGTGCTTGC GGGCTGCTCCTTGTG 7699 GG	___ C	I
	TGCTTGT GC GCTCCTTGT		
	ACGAACG CG CGAGGAACA		
	___ CC A I		
GAM487 LNK	TGGTGCTTGT AATCCCAGCTACTTG 7697	___ _ C	TGGII
	TGGTGCTTGTG CC GCT CTTG		
	ACCACGAACAT GG CGA GAAC		
	TAG T T IIIGG		
GAM487 M11S1	CTTGCTGCCGCTCCCGCTGTGG 7691	_ _	III
	CTTG TGCCGCTCCT TGTG		
	GAAC ACGGCGAGGG ACAC		
	G CG CII		
GAM487 MAN2A2	GTGCAGG-GCCAGCTCCTTGT 7694 TTGT	_	I
	TGC GCC GCTCCTTG		
	ACG CGG CGAGGAAC		
	TCC_ T I		
GAM487 MAN2A2	GTGCAGG-GCCAGCTCCTTGT 7694 TGGT TTGT	_	G
	GC GCC GCTCCTTGT		
	CG CGG CGAGGAACA		
	___ TCC_ T A		
GAM487 MBNL	TGGAAC TTGT-CAGCTCCTTGT 7703	T GCC	GG
	TGG GCTTGT GCTCCTTGT		
	ACC TGAACA CGAGGAACA		
	T GT_ II		
GAM487 MBNL	TGGAAC TTGT-CAGCTCCTTGT 7703	_ T GCC	I
	GG GCTTGT GCTCCTTG		
	CC TGAACA CGAGGAAC		
	A T GT_ I		
GAM487 MYO1C	TGATGCCCCTGCCGCTCCT 7700	G	TGTG
	TGGTGCTT TGCCGCTCCT		
	ACTACGGG ACGGCGAGGA		
	G IIIG		
GAM487 MYO1C	TGATGCCCCTGCCGCTCCT 7700	G	II
	TGGTGCTT TGCCGCTCC		
	ACTACGGG ACGGCGAGG		
	G AI		
GAM487 SPTBN2	TGCTCCTGTGCTCCGCTCTCCTTGTGG7695	___ G CG	I
	GCTT TGC CTCCTTGTG		

	CGAG GCG GAGGAACAC	
	CA _ A_ I	
GAM487 SPTBN2	TGCTCCTGTGCTCCGCTCTCCTTGTGG7695 TG__ G CG III	
	GTGCTT TGC CTCCTTGTGG	
	CACGAG GCG GAGGAACACC	
	AGGA _ A_ GGT	
GAM487 TCF7	GTGCTTGTGACCATGCTCACATGT 7693 C TG _ TCCTTI	
	GTG T TGC CGC	
	CAC G ACG GTG	
	T GT A TACAII	
GAM487 TCF7	GTGCTTGTGACCATGCTCACATGT 7693 TGGT _ _ CT_ GGI	
	GCTTGTG CC GCTC TGT	
	CGAACAC GG CGAG ACA	
	_ _ T TA TGT ACI	
GAM488 CDH10	GACATGTACCTAACA-GAAGCG 7718 A _ ACCI	
	CATGTAC AACAGGA	
	GTACATG TTGTCTT	
	_ GA CGII	
GAM488 CDH10	GACATGTACCTAACA-GAAGCG 7718 AG _ ACC T	
	ACATGTAC AACAGGA GTG	
	TGTACATG TTGTCTT CGC	
	_ GA _ C	
GAM488 CYP1B1	AGAC--GT-CAACAGGAACC 7712 AT A GT	
	AGAC GT CAACAGGAACC	
	TCTG CA GTTGTCTTGG	
	_ _ II	
GAM488 CYP1B1	AGAC--GT-CAACAGGAACC 7712 _ AT A	
	GAC GT CAACAGGAAC	
	CTG CA GTTGTCTTGG	
	T _ _	
GAM488 DCTN1	AGACTTGT---CAGGAACCGTG 7716 A ACAA	
	AGAC TGT CAGGAACCGTG	
	TCTG ACA GTCCTTGGCAC	
	A _ _	
GAM488 DCTN1	AGACTTGT---CAGGAACCGTG 7716 _ A ACAA	
	GAC TGT CAGGAACCGT	
	CTG ACA GTCCTTGGCA	
	T A _ _	
GAM488 DIA1	AGAC-TGTACA---GGAACC 7713 A ACA G	
	AGAC TGT ACAGGAACC	

	TCTG ACA TGTCCTTGG		
	— — — — — I		
GAM488 DIA1	AGAC-TGTACA---GGAACC 7713_ A ACA		
	GAC TGT ACAGGAAC		
	CTG ACA TGTCCTTG		
	T — — — — —		
GAM488 FUT8	AGAAACGGA-AACAGGAACCG 7714 C TAC TG		
	AGA ATG AACAGGAACCG		
	TCT TGC TTGTCCTTGGC		
	T CT_ II		
GAM488 FUT8	AGAAACGGA-AACAGGAACCG 7714_ C TAC I		
	GA ATG AACAGGAACC		
	CT TGC TTGTCCTTGG		
	T T CT_ I		
GAM488 GOCAP1	ACATGAACACATGACAGGAACCG 7706 AG_____ TACA GTI		
	ACATG ACAGGAACCGT		
	TGTAC TGTCCTTGGCG		
	TACTTG _____ AII		
GAM488 GOCAP1	ACATGAACACATGACAGGAACCG 7706 T _____ IIIC		
	ACATG ACA ACAGGAACC		
	TGTAC TGT TGTCCTTGG		
	T GTAC CII		
GAM488 GRLF1	AGACA-GACCAACAGGAA--GTGT 7717 TGTA CC		
	AGACA CAACAGGAA GTGT		
	TCTGT GTTGTCTT CACA		
	CTG_ —		
GAM488 GRLF1	AGACA-GACCAACAGGAA--GTGT 7717 TGTA CCGI		
	AGACA CAACAGGAA		
	TCTGT GTTGTCTT		
	CTG_ CACA		
GAM488 IL17R	AGACATGTACACACAGATGAATACGTG7711 — — C_ TIII		
	AGACATGTACA ACAG GAA CGTG		
	TCTGTACATGT TGTC CTT GCAC		
	G TA AT IIIT		
GAM488 IL17R	AGACATGTACACACAGATGAATACGTG7711 A — AACCGTI		
	TGTACA ACAGG		
	ACATGT TGTCT		
	_ G ACTTATI		
GAM488 PIGA	AGA-ATGCATACAACAGGAAC 7710 C — CGTG		
	AGA ATGT ACAACAGGAAC		

	TCT TACG TGTTGTCCTTG			
	_ TA IIIT			
GAM488 PIGA	AGA-ATGCATACAACAGGAAC 7710 C _ II			
	AGA ATGT ACAACAGGAA			
	TCT TACG TGTTGTCCTT			
	_ TA GI			
GAM488 PTPRF	AGACTGTGTACAACAGTGAAC 7709 A_ _ CGTGT			
	AGAC TGTACAACAG GAAC			
	TCTG ACATGTTGTC CTTG			
	AC A IIITG			
GAM488 PTPRF	AGACTGTGTACAACAGTGAAC 7709 A_ _ III			
	AGAC TGTACAACAG GAA			
	TCTG ACATGTTGTC CTT			
	AC A GII			
GAM488 RET	AGGCATG--CAAAAGGAACCGT 7715 A CAAC G			
	AG CATGTA AGGAACCGT			
	TC GTACGT TCCTTGGCA			
	C TT_ I			
GAM488 RET	AGGCATG--CAAAAGGAACCGT 7715 GA_ CAAC I			
	CATGTA AGGAACCG			
	GTACGT TCCTTGGC			
	TCC TT_ I			
GAM488 WHSC1	ACATGTAC-ACAGACACTGTGT 7707 _ A GA C I			
	CATGTACA CAG AC GTG			
	GTACATGT GTC TG CAC			
	T _ TG A I			
GAM488 WHSC1	ACATGTAC-ACAGACACTGTGT 7707 AGAC A GA C			
	ATGTACA CAG AC GTGT			
	TACATGT GTC TG CACA			
	_ _ TG A			
GAM488 XRCC5	ACATGTACAA---AACTGTGT 7708 _ ACAG C			
	CATGTACA GAAC GTG			
	GTACATGT TTTG CAC			
	T _ _ A			
GAM488 XRCC5	ACATGTACAA---AACTGTGT 7708 AGAC ACAG C			
	ATGTACA GAAC GT			
	TACATGT TTTG CA			
	_ _ A			
GAM489 AKAP2	CACACAGGCAGGGGAAAGAGGA 7724 AC TCA I			
	CAGGT GGAAAGAGG			

	GTCCG CCTTTCTCC		
	GT TCC I		
GAM489 AKAP2	CACACAGGCAGGGGAAAGAGGA	7724	TGACAC TCA
	CAGGT GGAAAGAGGA		
	GTCCG CCTTTCTCCT		
	T_____ TCC		
GAM489 AMD1	GACACCAGGGAGAGGGAAGA	7730	TTCA_ AGI
	ACACCAGG GGAA		
	TGTGGTCC CCTT		
	CTCTC CII		
GAM489 AMD1	GACACCAGGGAGAGGGAAGA	7730	TG TTC A G
	ACACCAGG AGG AAGAG		
	TGTGGTCC TCC TTCTT		
	___ CTC C I		
GAM489 ARHC	CCAGAT-CGGGAAAGAGGA	7727	CA I
	CCAGGTT GGAAAGAGG		
	GGTCTAG CCTTTCTCC		
	C_ T		
GAM489 CNGB3	GACATCA---TCAGGAAAGA	7731	ACAC GGT
	CA TCAGGAAAG		
	GT AGTCCTTTC		
	CT_ AGT		
GAM489 CNGB3	GACATCA---TCAGGAAAGA	7731	TGACAC GGT
	CA TCAGGAAAGAG		
	GT AGTCCTTTCTT		
	T_____ AGT		
GAM489 FMOD	ACCCACCTACAGGAAAGAAGA	7723	___ AGGTT I
	CACC CAGGAAAGAGG		
	GTGG GTCCTTTCTTC		
	GGG AT_____ I		
GAM489 FMOD	ACCCACCTACAGGAAAGAAGA	7723	TGA AGGTT
	CACC CAGGAAAGAGGA		
	GTGG GTCCTTTCTTCT		
	GG_ AT_____		
GAM489 GLRA3	CAACAG---CCGGAAAGAGGA	7725	AC_ GTTCA
	CAG GGAAAGAGG		
	GTC CCTTTCTCC		
	GTT GG_____		
GAM489 GLRA3	CAACAG---CCGGAAAGAGGA	7725	TGACACCA CA
	GGTT GGAAAGAG		

	TCGG CCTTTCTC			
	G_____			
GAM489 HAP1	CCAGGTTTCATGAACACAGAGG 7726	G	___	III
	CCAGGTTCA GAA AGAG			
	III			
	GGTCCAAGT CTT TCTC			
	A GTG CII			
GAM489 KCNA7	TGACAGGCCTGGTTCAGGA 7733	___	A	AAGAGG
	TGACA CC GGTTTCAGGA			
	ACTGT GG CCAAGTCCT			
	CC A IIIAGG			
GAM489 KCNA7	TGACAGGCCTGGTTCAGGA 7733	___	A	III
	TGACA CC GGTTTCAGG			
	ACTGT GG CCAAGTCC			
	CC A TII			
GAM489 KCNK4	GACTACCGGGTG-AGGAAAGAG 7728	AC_	A	TC I
	ACC GGT AGGAAAGA			
	TGG CCA TCCTTTCT			
	TGA C C_ I			
GAM489 KCNK4	GACTACCGGGTG-AGGAAAGAG 7728	TGAC	A	TC A
	ACC GGT AGGAAAGAGG			
	TGG CCA TCCTTTCTCT			
	TGA_ C C_ I			
GAM489 MCC	TGA-AGCAGG---AGGAAAGAGGA 7735	CAC	TTC	
	TGA CAGG AGGAAAGAGG			
	ACT GTCC TCCTTTCTCC			
	TC_			
GAM489 MCC	TGA-AGCAGG---AGGAAAGAGGA 7735	_	CAC	TTC
	GA CAGG AGGAAAGAGG			
	CT GTCC TCCTTTCTCC			
	A TC_			
GAM489 PRG2	ACACCAGGTGCCAGGCAAAG 7721	_	AAAI	
	ACACCAGGT TCAGG			
	TGTGGTCCA GGTCC			
	C GTTTCI			
GAM489 PRG2	ACACCAGGTGCCAGGCAAAG 7721	TGAC	_	_ AGG
	ACCAGGT TCAGG AAAG			
	TGGTCCA GGTCC TTTC			
	_____ C G GCI			
GAM489 RAB23	TGAC-CCAATTTTCAGGAAA 7734	A	G	GAG
	TGAC CCAG TTCAGGAAA			

		ACTG GGTT AAGTCCTTT			
		_ A III			
GAM489 RAB23		TGAC-CCAATTTTCAGGAAA	7734	A G I	
		TGAC CCAG TTCAGGAA			
		ACTG GGTT AAGTCCTT			
		_ A T			
GAM489 SCD		ACAACAGCTCAAGGAAAGAG	7722	CACCA _ I	
		GGTTCA GGAAAGA			
		TCGAGT CCTTTCT			
		GTTG_ T I			
GAM489 SCD		ACAACAGCTCAAGGAAAGAG	7722	TGACACCA _	
		GGTTCA GGAAAGAGG			
		TCGAGT CCTTTCTCT			
		TTG_____ T			
GAM489 STARD4		GACATCCAG-TTCAGGAAA	7729	_ G II	
		GACA CCAG TTCAGGAA			
		CTGT GGTC AAGTCCTT			
		A _ TI			
GAM489 STARD4		GACATCCAG-TTCAGGAAA	7729	TG _ G GAG	
		ACA CCAG TTCAGGAAA			
		TGT GGTC AAGTCCTTT			
		_ A _ AII			
GAM489 TCL1B		GACACCAGG-CCAG--AAGAGG	7732	T A AI	
		GACACCAGGT CAGGA AG			
		CTGTGGTCCG GTCTT TC			
		_ C CI			
GAM489 TCL1B		GACACCAGG-CCAG--AAGAGG	7732	TG T AA	
		ACACCAGGT CAGG AGAGG			
		TGTGGTCCG GTCT TCTCC			

GAM490 ABCC3		AGGATGCGGAACAGGCAAAG	7741	_ T T I	
		GGT TGG AACAGGCAAA			
		CTA GCC TTGTCCGTTT			
		C C _ I			
GAM490 ABCC3		AGGATGCGGAACAGGCAAAG	7741	TGA T T T	
		GGT TGG AACAGGCAAAG			
		CTA GCC TTGTCCGTTTC			
		_____ C _ C			
GAM490 ALPP		AGGTTTGGTGTTCATGGGCTCAGTC	7740	GG AA _ AA I	
		TTTGGT CA GGC AGT			

	AAACCA GT CCG TCA		
	___ CA AC AG I		
GAM490 ALPP	AGGTTTGGTGTTCATGGGCTCAGTC 7740 TGAG	AA ___ AA I	
	GTTTGGT CA GGC AGTC		
	II III		
	CAAACCA GT CCG TCAG		
	___ CA AC AG G		
GAM490 ARF3	TGAGGCAGGAGAAGAGGCCAAAGTC 7748	TT T_ C I	
	TGAGGT GG AA AGGCAAAGTC		
	II		
	ACTCCG CC TT TCCGTTTCAG		
	T_ TC C I		
GAM490 ARF3	TGAGGCAGGAGAAGAGGCCAAAGTC 7748	TT T_ C I	
	GAGGT GG AA AGGCAAAGT		
	II		
	CTCCG CC TT TCCGTTTCA		
	T_ TC C I		
GAM490 ARHA	TTTGGTAACATACATTAAGT 7750	G AAGIII	
	TTTGGTAACA GCA		
	III		
	AAACCATTGT TGT		
	A AATTCA		
GAM490 CAPN10	GGTGGGGTATGAGGCCAAAGT 7744 GTTT	AC I	
	GGTA AGGCAAAG		
	CCAT TCCGTTTC		
	CACC AC I		
GAM490 CAPN10	GGTGGGGTATGAGGCCAAAGT 7744 TGAGGTTT	AC	
	GGTA AGGCAAAGT		
	CCAT TCCGTTTCA		
	CC_____ AC		
GAM490 CYP1B1	TTGGGGACCTGGCAAAGTC 7751 T TA A_	II	
	TTGG AC GGCAAAGT		
	II		
	AACC TG CCGTTTCA		
	_ CC GA GI		
GAM490 GRM4	AGGTTTGGTGAAGTGGGGAAG 7739 G	_ A CAAAI	
	GTTTGGT AAC GG		
	III II		
	CAAACCA TTG CC		
	_ C A CCTTI		
GAM490 GRM4	AGGTTTGGTGAAGTGGGGAAG 7739 TGAG	_ A CA TC	
	GTTTGGT AAC GG AAG		
	III II III		
	CAAACCA TTG CC TTC		
	_____ C A CC CC		
GAM490 HSD3B1	TGAGATTTGGTAACA-GCAAA 7747	G GT	
	TGAGGTTTGGTAACAG CAAA		

	ACTCTAAACCATTGTC GTTT		
	_ II		
GAM490 HSD3B1	TGAGATTTGGTAACA-GCAAA 7747 _	G I	
	GAGGTTTGGTAACAG CAA		
	CTCTAAACCATTGTC GTT		
	A _ I		
GAM490 HSD3B2	TGAGATTTGGTAACA-GCAAA 7747	G GT	
	TGAGGTTTGGTAACAG CAAA		
	ACTCTAAACCATTGTC GTTT		
	_ II		
GAM490 HSD3B2	TGAGATTTGGTAACA-GCAAA 7747 _	G I	
	GAGGTTTGGTAACAG CAA		
	CTCTAAACCATTGTC GTT		
	A _ I		
GAM490 IAPP	TGAGGTTTGCTGAAAGCCA 7746	GTAAC AAAGT	
	TGAGGTTTG AGGC		
	ACTCCAAAC TTCG		
	GACT_ GTIII		
GAM490 IAPP	TGAGGTTTGCTGAAAGCCA 7746	GTAAC II	
	TGAGGTTTG AGGC		
	ACTCCAAAC TTCG		
	GACT_ GT		
GAM490 LOH11CR2A	AGGTTTCAGGTCCCAGGCAAAG 7738 G _ AA I		
	GTTT GGT CAGGCAAA		
	CAAG CCA GTCCGTTT		
	_ T GG I		
GAM490 LOH11CR2A	AGGTTTCAGGTCCCAGGCAAAG 7738 TGAG _ AA C		
	GTTT GGT CAGGCAAAGT		
	CAAG CCA GTCCGTTTCG		
	___ T GG A		
GAM490 NAV2	GGTTTGATTGGAACAGGCAAA 7742 _ III		
	GGTTTGGT AACAGGCAA		
	CCAAACTA TTGTCCGTT		
	ACC TII		
GAM490 NAV2	GGTTTGATTGGAACAGGCAAA 7742 TGA T T C		
	GGTT GG AACAGGCAAAGT		
	CTAA CC TTGTCCGTTTTA		
	AA_ _ _ T		
GAM490 PKIB	TGAGGTTTGGGAA----AAAGTC 7749	T C CAI	
	TGAGGTTTGG AA AGG		

	ACTCCAAACC TT TTC		
	C T AGI		
GAM490 PKIB	TGAGGTTTGGGAA-----AAAGTC 7749	TAACA C	
	TGAGGTTTGG GG AAAGT		
	ACTCCAAACC CT TTTCA		
	_____ T		
GAM490 SLC6A1	GGGTGGGTAACAGGCACAG 7743 _ TT	AAII	
	GGT GGTAACAGGCA		
	CCA CCATTGTCCGT		
	C C_ GTCI		
GAM490 SLC6A1	GGGTGGGTAACAGGCACAG 7743 TGAGGTTT	A T	
	GGTAACAGGCA AG		
	CCATTGTCCGT TC		
	AC_____ G T		
GAM490 SRD5A1	TTTTTTAAATGGCAAAGTC 7752 TTTGGTAACA	II	
	GGCAAAGT		
	CCGTTTCA		
	AAAAAATTTA GI		
GAM490 SREBF1	GTTTGCAAA-AGGCAAAGT 7745 G C I		
	GTTTG TAA AGGCAAAG		
	CAAAC GTT TCCGTTTC		
	_ T A		
GAM490 SREBF1	GTTTGCAAA-AGGCAAAGT 7745 TGAGGTTTG C		
	GTAA AGGCAAAG		
	CGTT TCCGTTTC		
	_____ T		
GAM491 AGM1	AAAACAGATCTAGAGACAAT 7755 TGAGAAAA	AAT	
	CAGATTTAGAGA		
	GTCTAGATCTCT		
	_____ GTT		
GAM491 BRCA1	TGTGAACACAGGGTTTTAGAGAAGTA 7773 TGA A A_	ATAII	
	GAA ACAG TTTAGAGAA		
	CTT TGTC AAATCTCTT		
	ACA G CCA CATII		
GAM491 CBFB	AGAAAAAATGAT-TAGAGAAA 7758 TGAGAAAACA T T		
	GATT AGAGAAA		
	CTAA TCTCTTT		
	TTTTTTA_ _ T		
GAM491 CBFB	AGAAAAAATGATT-AGAGAAA 7759 TGAGAAAACA T T		
	GATT AGAGAAA		

		CTAA TCTCTTT			
		TTTTTTA__ _ T			
GAM491 COL19A1		AAAACAGATTCATAAAAAAT	7756	TGAGAAAA	G
		CAGATTTA AGAAAT			
		GTCTAAGT TTTTTA			
		_____ A			
GAM491 EIF2C1		GAGAAAAAGAACCAGATTTAGAAAAA	7770	T_____ AA	TAII
		GAGAA CAGATTTAGAGAAA			
		TTCTT GTCTAAATCTTTTT			
		TCTTT G_ CIII			
GAM491 EPHA3		TGGGATAACAGATTTGAGAGA	7774	A A _ AATA	
		TG GA AACAGATTT AGAGA			
		AC CT TTGTCTAAA TCTCT			
		C A C IIIA			
GAM491 FGF7		AGAAAACAGTCCACTTAAAGAAAT	7760	TGAG _____	AI
		AAAACAG ATTTAGAGAAAT			
		TTTTGTC TGAATTTCTTTA			
		_____ AGG GA			
GAM491 FPRL1		AGAAAACAGAATCAGAGGAAT	7766	TGAG T A A	
		AAAACAGA TTAGAG AAT			
		TTTTGTCT AGTCTC TTA			
		_____ T C A			
GAM491 HHEX		GAGATAAACAGA-TTACAGAAA	7769	TG _ _ ATA	
		AGA AAACAGATT TAGAGAA			
		TCT TTTGTCTAA GTCTTTT			
		_ A T III			
GAM491 MAPK14		AGTAATCATATTTAGAGAAA	7765	TGAGAAAA G	T
		CA ATTTAGAGAAA			
		GT TAAATCTCTTT			
		ATTA_____ A C			
GAM491 MBL2		AGAAAACAGAGTTCATAGAGAAA	7761	TGAG TT_____	TAI
		AAAACAGA TAGAGAAA			
		TTTTGTCT ATCTCTTT			
		_____ CAAGT CAI			
GAM491 PDE6H		AGATAAACAAAATGTAGAGAAATA	7757	TGAGA TT_	I
		AAACAGA TAGAGAAATA			
		TTTGTTT ATCTCTTTAT			
		TA_____ TAC A			
GAM491 PSA		AGAAAACAG---TAGAGAA	7763	TGAG ATT	
		AAAACAG TAGAGAA			

TTTTGTC ATCTCTT

GAM491 PTEN	TGAGAAAACATATTTA-ATAAAT 7777	G	A	ATA
	TGAGAAAACA ATTTAG GAA			
	ACTCTTTTGT TAAATT TTT			
	A A AII			
GAM491 RAD23B	GAAAACAGATTT-GAAAAA 7768	TGAGAA	A	
	AACAGATTT GAGAAA			
	TTGTCTAAA CTTTTT			
GAM491 RAG1	GAAACCTAGATTTAGAAAAAT 7767	TGAGAAAAC	A	
	AGATTTAGAGAAAT			
	TCTAAATCTTTTTA			
	TGGA_____ A			
GAM491 RIG	TGAGGAAGCA--TTTAGAGAA 7776	AAAAC _	AT	
	TGAG AG ATTTAGAGAA			
	ACTC TC TAAATCTCTT			
	CT__ G II			
GAM491 SFRP1	TGAGAATTCCTATTTAGAGA 7775	AACAG	AAT	
	TGAGAA ATTTAGAGA			
	ACTCTT TAAATCTCT			
	AAGGG III			
GAM491 SH3BP4	AGAAAGCAGTTTTAGAGAA 7764	TGAGAAAA A	AT	
	CAG TTTAGAGAA			
	GTC AAATCTCTT			
	TTTC_____ A AC			
GAM491 SRGAP1	GAGAACACAGGGATTTAGAG 7771	TG A _	AAAT	
	AGAA ACA GATTTAGAG			
	TCTT TGT CTAAATCTC			
	_ G CC CII			
GAM491 TIMP4	AGAAAACAGACTAAGCCAGAA 7762	TGAG	T _	ATA
	AAAACAGATT AG AGAA			
	TTTTGTCTGA TC TCTT			
	_____ T GG CTI			
GAM491 UBE2B	TGAAAAAAGTACAGATTTACA-AAAT 7772	_____	G	ATAII
	TGAGAAA ACAGATTTA AGAA			
	ACTTTTT TGTCTAAAT TTTT			
	TCA G AIIIA			
GAM492 ADAM12	TGCCCAAGCCACATCTCATAA 7798	GA _	GAAAI	
	CCA GCCACATCT			

	GGT CGGTGTAGA			
	G_ T GTATI			
GAM492 ADAM12	TGCCCCAAGCCACATCTCATAA	7798 TGA _	GAAAAGGAA	
	CCA GCCACATCT			
	GGT CGGTGTAGA			
	ACG T GTATTIIIA			
GAM492 ADSS	CCAGCCACA--TGCAGAGGAA	7790 _	TC AAA I	
	CAGCCACA TG AGGA			
	GTCGGTGT AC TCCT			
	G _ GTC I			
GAM492 ADSS	CCAGCCACA--TGCAGAGGAA	7790 TGACCA	CT_ AA	
	GCCACAT GA AGGA			
	CGGTGTA CT TTCT			
	_____ CGT CC			
GAM492 B3GALT5	TGACCAGCCA-GTCAATAACGGAA	7802	CA TGAAAA I	
	TGACCAGCCA TC GGAA			
	ACTGGTCGGT AG CCTT			
	C_ TTATTG I			
GAM492 B3GALT5	TGACCAGCCA-GTCAATAACGGAA	7802 _	CA TGAAAA I	
	GACCAGCCA TC GGA			
	CTGGTCGGT AG CCT			
	A C_ TTATTG I			
GAM492 BRCA1	TGACCAGCCGACGTTTTTAAAG	7799 _	ATCTGAAAAI	
	ACCAGCC AC			
	TGGTCGG TG			
	C CAAAAATTII			
GAM492 C11orf8	CCACATCTGCAAAAAAGAA	7787 _	III	
	CCACATCTG AAAAGGA			
	GGTGTAGAC TTTTCT			
	GT TII			
GAM492 CANX	TGACCACAGAACAACAGATGAAAAGGAA	7797 _	C TC III	
	TGACCA GC ACA TGAAAAGGAA			
	ACTGGT TG TGT ACTTTTCCTT			
	GTCT T CT III			
GAM492 CANX	TGACCACAGAACAACAGATGAAAAGGAA	7797 GACC	C TC I	
	AGC ACA TGAAAAGGA			
	TTG TGT ACTTTTCCT			
	TGTC T CT I			
GAM492 CHC1L	TGACCTTAGTCACATCTGA	7796 _	C AAAGGA	
	TGACC AG CACATCTGA			

	ACTGG TC GTGTAGACT			
	AA A IIIAAG			
GAM492 CHC1L	TGACCTTAGTCACATCTGA	7796	__ C	III
	TGACC AG CACATCTG			
	ACTGG TC GTGTAGAC			
	AA A TII			
GAM492 DMD	TGACCAGCCTCA-C--AAAAG	7800	A CT AI	
	TGACCAGCC CAT GA			
	ACTGGTCGG GTG TT			
	A TT CI			
GAM492 DMD	TGACCAGCCTCA-C--AAAAG	7800	A CTG G	
	TGACCAGCC CAT AAAAG			
	ACTGGTCGG GTG TTTTC			
	A __ I			
GAM492 ED1	CCCCATCTCCTGAAAAGGAA	7786	__ CA_	III
	CCA TCTGAAAAGGA			
	GGT GGACTTTTCCT			
	GG AGA TII			
GAM492 EHD2	CCA-CGACATCCCTGAAAAGGA	7788	CA C __	I
	GC ACATCT GAAAAGG			
	TG TG TAGG CTTTTC			
	__ C GA I			
GAM492 EHD2	CCA-CGACATCCCTGAAAAGGA	7788	T CAG ACAT	A
	GAC CC CTGAAAAGGA			
	CTG GG GACTTTTCCT			
	G TA_ __ C			
GAM492 FCRH3	ACCAGCCACA-CAAAAAGG	7780	_ CT	I
	CCAGCCACAT GAAAAG			
	GGTCGGTGTG TTTTTC			
	T T_ I			
GAM492 FCRH3	ACCAGCCACA-CAAAAAGG	7780	TGAC CT	A
	CAGCCACAT GAAAAGG			
	GTCGGTGTG TTTTTC			
	__ T_ C			
GAM492 FEN1	GACTAGC-ACTACTGAAAAGG	7795	_ C C AT	I
	AC AGC AC CTGAAAAG			
	TG TCG TG GACTTTTC			
	C A _ AT I			
GAM492 FEN1	GACTAGC-ACTACTGAAAAGG	7795	TG C C AT	A
	AC AGC AC CTGAAAAGG			

	TG TCG TG GACTTTTCC	
	__ A _ AT C	
GAM492 FLRT2	GAACATCCACGATG-GAAAAGGAA 7794 AC G ATCT I	
	CA CCAC GAAAAGGA	
	GT GGTG CTTTTCCT	
	TT A CTAC I	
GAM492 FLRT2	GAACATCCACGATG-GAAAAGGAA 7794 T CAG ATCT I	
	GAC CCAC GAAAAGGAA	
	TTG GGTG CTTTTCCTT	
	_ TA_ CTAC G	
GAM492 FVT1	CAGCCACATTCCTGAAGAG 7783 _ AAI	
	CAGCCACAT CTGAA	
	GTCGGTGTA GACTT	
	AG CTC	
GAM492 GLUD1	GACCATGCCACCTTCTGAAAAGG 7791 ACCA A_ I	
	GCCAC TCTGAAAAG	
	CGGTG AGACTTTTC	
	GTA_ GA I	
GAM492 GLUD1	GACCATGCCACCTTCTGAAAAGG 7791 TG _ A_ AAI	
	ACCA GCCAC TCTGAAAAGG	
	TGGT CGGTG AGACTTTTCC	
	_ A GA G	
GAM492 LZTS1	CCAGCCACA---GAAAAGG 7789 TCT	
	CCAGCCACA GAAAAG	
	GGTCGGTGT CTTTTC	

GAM492 LZTS1	CCAGCCACA---GAAAAGG 7789 TGACCA TCT	
	GCCACA GAAAAG	
	CGGTGT CTTTTC	

GAM492 PIP5K1A	GACCAAGCCACATCTGAAAA 7792 _	
	GACCA GCCACATCTGAAA	
	CTGGT CGGTGTAGACTTT	
	T TI	
GAM492 PIP5K1A	GACCAAGCCACATCTGAAAA 7792 TG _ GA	
	ACCA GCCACATCTGAAAAG	
	TGGT CGGTGTAGACTTTT	
	_ T	
GAM492 POLG	ACCAGCCA-AGAAGAAAAGGAA 7781 _ CATCT I	
	CCAGCCA GAAAAGGA	

	GGTCGGT CTTTTCCT	
	T TCTT_ I	
GAM492 POLG	ACCAGCCA-AGAAGAAAAGGAA 7781 TGAC CATCT	
	CAGCCA GAAAAGGAA	
	GTTCGGT CTTTTCCTT	
	____ TCTT_	
GAM492 RB1CC1	CAGGCAC-TGTGAAAAGGA 7785 C ATC I	
	CAG CAC TGAAAAGG	
	GTC GTG ACTTTTCC	
	C AC_ T	
GAM492 RB1CC1	CAGGCAC-TGTGAAAAGGA 7785 TGACCAGC ATC	
	CAC TGAAAAGG	
	GTG ACTTTTCC	
	____ AC_	
GAM492 SWAP70	CAGC-ACATACTCGGAAAAGGAA 7784 AGC _ _ I	
	CACAT CT GAAAAGGA	
	GTGTA GA CTTTTCCT	
	____ T GC I	
GAM492 SWAP70	CAGC-ACATACTCGGAAAAGGAA 7784 TGACCAGCC A T	
	AC TC GAAAAGGAA	
	TG AG CTTTTCCTT	
	TGTA_____ C	
GAM492 TSSC4	TGACCAGCCCCA-CTGGGAAGG 7801 A T AA AA	
	TGACCAGCC CA CTG AAGG	
	ACTGGTCGG GT GAC TTCC	
	G _ CC	
GAM492 TSSC4	TGACCAGCCCCA-CTGGGAAGG 7801 _ A T AA I	
	GACCAGCC CA CTG AAG	
	CTGGTCGG GT GAC TTC	
	A G _ CC I	
GAM492 VCL	AGCTCACTTCTGAAAAGGA 7782 _ A II	
	AGC CAC TCTGAAAAGG	
	TCG GTG AGACTTTTCC	
	A A TI	
GAM492 VCL	AGCTCACTTCTGAAAAGGA 7782 TGACCAGCC A	
	AC TCTGAAAAGGA	
	TG AGACTTTTCCCT	
	____ A	
GAM492 ZNF132	GACCAGCCAAGCAACAGAATAAGG 7793 TG _ TCT _ AAI	
	ACCAGCCA CA GAA AAGG	

	TGGTCGGT GT CTT TTCC	
	___ TC TGT A CII	
GAM493 ABCA1	AATGTT-GTGTTCCTTCA 7807 GTAGA GGC	
	AATG GTTTCCTTCA	
	TTAC CAAAAGAAGT	
	AACA_ III	
GAM493 ABCA1	AATGTT-GTGTTCCTTCA 7807 GTAGA I	
	AATG GTTTCCTTCA	
	TTAC CAAAAGAAG	
	AACA_ T	
GAM493 BHMT2	TGGTAGAGTCTGTTGCAGTGCTT 7818 AATG TCTT _ I	
	GTAGAGTTT CAG GCTT	
	CATCTCAGA GTC CGAA	
	___ CAAC A T	
GAM493 BHMT2	TGGTAGAGTCTGTTGCAGTGCTT 7818 G TCTT _ I	
	GTAGAGTTT CAG GCT	
	CATCTCAGA GTC CGA	
	_ CAAC A I	
GAM493 C8A	ATGGATTGAGTTTTC-TCAG 7811 TA_ CAII	
	ATGG GAGTTTCTT	
	TACC CTCAAAAGAG	
	TAA TCII	
GAM493 C8A	ATGGATTGAGTTTTC-TCAG 7811 AA TA_ T GCT	
	TGG GAGTTTCT CAG	
	ACC CTCAAAAGA GTC	
	_ TAA _ AII	
GAM493 CAPN10	TGGTAGAGT---TTCAGGTCTT 7819 _ TTCT _	
	GGTAGAGTT TCAGG CT	
	CCATCTCAA AGTCC GA	
	A _ A	
GAM493 CAPN10	TGGTAGAGT---TTCAGGTCTT 7819 AATG TTCT _	
	GTAGAGTT TCAGG CT	
	CATCTCAA AGTCC GA	
	___ A	
GAM493 CDH7	TACAGTTTCTT--GCTT 7816 G CAG	
	TA AGTTTCTT GCT	
	AT TCAAAGAA CGA	
	G _	
GAM493 CENTD1	AATGTTA---TTTCTTCA 7808 GTAGA GG	
	AATG GTTTCCTTCA	

	TTAC TAAAAGAAGT		
	AA__ II		
GAM493 EGFL5	AATGGTAGA---ACCTTCAGG 7809	TT	TTCI
	AATGGTAGAG TTC		
	III		
	TTACCATCTT AAG		
	GG TCCI		
GAM493 EGFL5	AATGGTAGA---ACCTTCAGG 7809	TTT	C
	AATGGTAGAG TCTTCAGG		
	TTACCATCTT GGAAGTCC		
	__ I		
GAM493 FBXL11	TGGGAAAGCCTTCTTCAGGC 7820	T	I
	GG AGAGTTTTCTTCAGG		
	II		
	CC TTTCGGAAGAAGTCC		
	C _ I		
GAM493 FBXL11	TGGGAAAGCCTTCTTCAGGC 7820	AAT T	T
	GG AGAGTTTTCTTCAGGC		
	II		
	CC TTTCGGAAGAAGTCCG		
	__ _ T		
GAM493 KCNJ16	AATGGTAGAGAATGCTCTTTAG 7806	TT__	C GCTT
	AATGGTAGAG TTCTT AG		
	TTACCATCTC GAGAA TC		
	TTAC A IIIT		
GAM493 KCNJ16	AATGGTAGAGAATGCTCTTTAG 7806	AT TT__	CAI
	GGTAGAG TTCTT		
	CCATCTC GAGAA		
	__ TTAC ATI		
GAM493 LNK	ATGG--GAGTTTTCTGTCAG 7813	TA _	I
	ATGG GAGTTTTCT TCA		
	TACC CTCAAAAGA AGT		
	__ C C		
GAM493 LNK	ATGG--GAGTTTTCTGTCAG 7813	AA TA _	GC
	TGG GAGTTTTCT TCAG		
	ACC CTCAAAAGA AGTC		
	__ _ C GI		
GAM493 MEN1	ATGGTAGAG--ATGTTTCAG 7814	TT_	TTCAI
	ATGGTAGAG TTC		
	TACCATCTC AAG		
	TAC TCIII		
GAM493 MEN1	ATGGTAGAG--ATGTTTCAG 7814	AA TTTTC	GC
	TGGTAGAG TTCAG		

	ACCATCTC AAGTC		
	___ TAC___ AI		
GAM493 POLK	AGAGTCTCGCTCTTCAGGCT	7810	___ III
	AGAGTTT TCTTCAGGC		
	TCTCAGA AGAAGTCCG		
	GCG AII		
GAM493 POLK	AGAGTCTCGCTCTTCAGGCT	7810	AATGGTAGAGTT
	TTCTTCAGGCT		
	GAGAAGTCCGA		
	AGC_____		
GAM493 RERE	AATGGTAGATGTTGTGTTC	7805	_ TTC AGGCT
	AATGGTAGA GTT TTC		
	III III		
	TTACCATCT CAA AAG		
	A CAC IIIT		
GAM493 RERE	AATGGTAGATGTTGTGTTC	7805	_ TTCTTII
	AATGGTAGA GTT		
	III		
	TTACCATCT CAA		
	A CACAAGI		
GAM493 SYNGR1	TGGTACAGGTTTCACTCTTCAGGC	7817	___ AGAGTT I
	GGT TTCTTCAGG		
	III		
	CCA GAGAAGTCC		
	GT AAGT___ I		
GAM493 SYNGR1	TGGTACAGGTTTCACTCTTCAGGC	7817	AAT___ AGAGTT TI
	GGT TTCTTCAGGCT		
	III		
	CCA GAGAAGTCCGG		
	CATGT AAGT___ TI		
GAM493 VCAM1	ATGGCAGTTACTGTTCTTCAGGC	7812	AA AGTT___ TTI
	TGGTAG TTCTTCAGGC		
	ACCGTC AAGAAGTCCG		
	___ AATGAC TII		
GAM493 VCAM1	ATGGCAGTTACTGTTCTTCAGGC	7812	TG AGTT___ I
	GTAG TTCTTCAGG		
	III		
	CGTC AAGAAGTCC		
	___ AATGAC I		
GAM493 ZNFN2A1	GGGAGAATTCCCTTCAGGCT	7815	AATGGT TT
	AGAGTT CTTCAGGCT		
	TCTTAA GAAGTCCGA		
	_____ GG		
GAM493 ZNFN2A1	GGGAGAATTCCCTTCAGGCT	7815	GT TT I
	AGAGTT CTTCAGGC		

	TCTTAA GAAGTCCG	
	CC GG I	
GAM494 ADCY2	AGGAGCA-CAGTGAGTTGG 7826 _ T II	
	AGGA CA CAGTGAGTTG	
	TCCT GT GTCACTCAAC	
	C _ CI	
GAM494 ADCY2	AGGAGCA-CAGTGAGTTGG 7826 TACCAGGA T	
	CA CAGTGAGTTGG	
	GT GTCACTCAACC	
	C _ _	
GAM494 ARF1	CAGCACTGAACAGTGAGTTG 7828 G AT_ III	
	CAG AC CAGTGAGTT	
	GTC TG GTCACTCAA	
	G ACTT CII	
GAM494 ARF1	CAGCACTGAACAGTGAGTTG 7828 TACCA TCA	
	GGACA GTGAGTTGGT	
	CTTGT CACTCAACTA	
	GTGA_ _	
GAM494 CISH	TACCAGGACATCCAGGATTGCCTTGGT7833 AG_ AG AIII	
	TACCAGGACATC TG TTGGT	
	ATGGTCCTGTAG AC AACCA	
	GTCCTA GG IIIA	
GAM494 CISH	TACCAGGACATCCAGGATTGCCTTGGT7833 ACCA AG_ AG I	
	GGACATC TG TTGG	
	CCTGTAG AC AACC	
	_ GTCCTA GG I	
GAM494 COL8A1	GACTTCAAGGGTGAGTTGGT 7830 A _ III	
	GAC TCA GTGAGTTGG	
	CTG AGT CACTCAACC	
	A TCC AII	
GAM494 COL8A1	GACTTCAAGGGTGAGTTGGT 7830 TACCAGGACATCA	
	GTGAGTTGGT	
	CACTCAACCA	
	TTCC_	
GAM494 FN14	CAGGACATCTGAGTGAGTGGG 7829 _ TGIII	
	CAGGACATC AGTGAGT	
	GTCCTGTAG TCACTCA	
	AC CCCII	
GAM494 FN14	CAGGACATCTGAGTGAGTGGG 7829 TACCAG _ T_ A	
	GACATC AGTGAGT GGT	

		CTGTAG TCACTCA CCG		
		_____ AC CC G		
GAM494 GK		GGA-ATCCATGAGTTGGTA 7831 C A I		
		GGA ATC GTGAGTTGGT		
		CCT TAG TACTCAACCA		
		_ G T		
GAM494 GNB1		ACCAGGACAATCTGTGTGT 7823 _ A AGII		
		ACCAGGACA TC GTG		
		TGGTCCTGT AG CAC		
		T A ACAI		
GAM494 GNB1		ACCAGGACAATCTGTGTGT 7823 TA _ A A TGGT		
		CCAGGACA TC GTG GT		
		GGTCCTGT AG CAC CA		
		_ T A A CIII		
GAM494 HAP1		TACCAGGACAGCACTAGAG 7834 T G AII		
		TACCAGGACA CA TG		
		ATGGTCCTGT GT AT		
		C G CTC		
GAM494 HAP1		TACCAGGACAGCACTAGAG 7834 T G _ TTGGT		
		TACCAGGACA CA T GAG		
		ATGGTCCTGT GT A CTC		
		C G T IIIAT		
GAM494 MME		GGACATCAGCAAACCTGGTA 7832 TG GT II		
		GGACATCAG A TGGT		
		CCTGTAGTC T ACCA		
		GT TG TI		
GAM494 PXF		ACCAGGACAGCCAGCTGAGCTG 7824 CC _ _ I		
		AGGACA TCAG TGAGTT		
		TCCTGT GGTC ACTCGA		
		_ C G I		
GAM494 PXF		ACCAGGACAGCCAGCTGAGCTG 7824 TA _ _ TA		
		CCAGGACA TCAG TGAGTTGG		
		GGTCCTGT GGTC ACTCGACT		
		_ C G II		
GAM494 SFRP4		AGCACTGCAGTGAGTTGTTA 7827 G AT GTI		
		G AC CAGTGAGTTG		
		C TG GTCACCTAAC		
		G AC AAI		
GAM494 SFRP4		AGCACTGCAGTGAGTTGTTA 7827 TACCAGGACAT GT		
		CAGTGAGTTG		

			GTC	ACT	CAAC		
			GAC		AA		
GAM494	VCL	ACCAGGACA-CAGTGTGTT	7825	T	A	I	
		ACCAGGACA CAGTG GT					
		TGGTCCTGT GTCAC CA					
				A	A		
GAM494	VCL	ACCAGGACA-CAGTGTGTT	7825 TA	T	A	GG	
		CCAGGACA CAGTG GTT					
		GGTCCTGT GTCAC CAA					
					A	GI	
GAM495	CACNG8	GACTCCAGTTTGACCACGGGCAG	7838	A		C	AAGGI
		GACTC TTGACCACG GG AG					
		CTGAG AACTGGTGC CC TC					
		GTCA			G	IIIGG	
GAM495	SNX9	CATGTGACTCCCCGGAGAAGG	7837		ATTGA	ACG	
		GACTC CC CGGAGAAGG					
		CTGAG GG GCCTCTTCC					
		A					
GAM496	ABCC3	GGCAGCATCTCCA-GGTCAGCT	7851		A	T	CAACI
		GCAGCATCT CA GTT					
		CGTCGTAGA GT CAG					
		C			G	C	TCGII
GAM496	ABCC3	GGCAGCATCTCCA-GGTCAGCT	7851 TG		A	T	T A
		GCAGCATCT CA GT CA CTG					
		CGTCGTAGA GT CA GT GAT					
					G	C	C
GAM496	ADAMTS1	CAGCATCTA-ATGCTTC-ACTG	7843		C	CA	I
		AGCATCTA ATGTT ACT					
		TCGTAGAT TACGA TGA					
		G				AG	I
GAM496	ADAMTS1	CAGCATCTA-ATGCTTC-ACTG	7843 TGGCAG		C	CA	
		CATCTA ATGTT ACT					
		GTAGAT TACGA TGA					
						AG	
GAM496	CCNDBP1	TGGCAGCATGGACTTGTTCA	7854		CT	A	ACT
		TGGCAGCAT AC TGTTCA					
		ACCGTCGTA TG ACAAGT					
					CC	A	
GAM496	CCNDBP1	TGGCAGCATGGACTTGTTCA	7854		CT	A	I
		GGCAGCAT AC TGTTCA					

	CCGTCGTA TG ACAAG		
	CC A I		
GAM496 CR1	GGCAGCATCTTCAAGTGCA 7850	A T TCII	
	GGCAGCATCT CA GT		
	CCGTCGTAGA GT CA		
	A T CGTI		
GAM496 CR1	GGCAGCATCTTCAAGTGCA 7850 TG	A T T ACT	
	GCAGCATCT CA GT CA		
	CGTCGTAGA GT CA GT		
	— A T C GII		
GAM496 CSNK1A1	GCAACATACATACATGTTCA 7846	C__ III	
	GCAGCAT TACATGTTT		
	CGTTGTA ATGTACAAG		
	TGT TII		
GAM496 CSNK1A1	GCAACATACATACATGTTCA 7846 T	_ TC ACT	
	GGCA GCA TACATGTTCA		
	TTGT TGT ATGTACAAGT		
	_ A _ CAI		
GAM496 DLG5	GCAGCATCT-C-TGATCAGCTG 7848	ACA T ACI	
	GCAGCATCT TG TCA		
	CGTCGTAGA AC AGT		
	G__ T CGA		
GAM496 DLG5	GCAGCATCT-C-TGATCAGCTG 7848 TGGC	ACA T A	
	AGCATCT TG TCA CT		
	TCGTAGA AC AGT GA		
	___ G__ T C		
GAM496 GALNT7	GCAACAGGT-CATGTTCAA 7847	TCTA I	
	GCAGCA CATGTTCA		
	CGTTGT GTACAAGT		
	CCA_ T		
GAM496 GALNT7	GCAACAGGT-CATGTTCAA 7847 T	CATCTA C	
	GGCAG CATGTTCAA		
	TTGTC GTACAAGTT		
	_ CA___ C		
GAM496 HTLF	TGGCAGCATCAACAGCTTCA 7853	T TG ACT	
	TGGCAGCATC ACA TTCA		
	ACCGTCGTAG TGT AAGT		
	T CG III		
GAM496 HTLF	TGGCAGCATCAACAGCTTCA 7853	T T CI	
	GGCAGCATC ACA GTT		

	CCGTCGTAG TGT CGA			
	T _ AG			
GAM496 MAML1	GGCAACAT--ACATGTTCA 7849	TC	I	
	GGCAGCA TACATGTTCA			
	CCGTTGT ATGTACAAG			
	_ T			
GAM496 MAML1	GGCAACAT--ACATGTTCA 7849	TG	TC	AC
	GCAGCA TACATGTTCA			
	CGTTGT ATGTACAAGT			
	_ _ CI			
GAM496 NPC1	TGGCACCATCCGG-TGTTCAACT 7857	G	ACA	G
	TGGCA CATCT TGTTCAACT			
	ACCGT GTAGG ACAAGTTGA			
	G CC_ I			
GAM496 NPC1	TGGCACCATCCGG-TGTTCAACT 7857	_ G	ACA	I
	GGCA CATCT TGTTCAAC			
	CCGT GTAGG ACAAGTTG			
	A G CC_ I			
GAM496 NRCAM	AGCATCTACAT-TTTAAGTG 7841	_	GTTCAACTI	
	GCATCTACAT			
	CGTAGATGTA			
	T AAATTCAlI			
GAM496 SOX11	TGGCTGCATTAGTCTACATGTT 7852	A	_____	CAACTG
	TGGC GCA TCTACATGTT			
	ACCG CGT AGATGTACAA			
	A AATC IIIGTC			
GAM496 SOX11	TGGCTGCATTAGTCTACATGTT 7852	A	_____	IIIA
	TGGC GCA TCTACATGT			
	ACCG CGT AGATGTACA			
	A AATC AIII			
GAM496 STMN1	CAGCATCTAACA-GTTCAA 7842	_ T	II	
	CAGCATCTA CA GTTCA			
	GTCGTAGAT GT CAAGT			
	T _ TI			
GAM496 STMN1	CAGCATCTAACA-GTTCAA 7842	TGGCAG	_ T	C
	CATCTA CA GTTCAA			
	GTAGAT GT CAAGTT			
	_ _ T _ T			
GAM496 TBX1	CAGTATCTACATGTATCTAC 7844	C	_	AAII
	CAG ATCTACATGT TC			

	GTC TAGATGTACA AG			
	A T ATGI			
GAM496 TBX1	CAGTATCTACATGTATCTAC	7844	TGGCAGC	_ A T
	ATCTACATGT TC AC			
	TAGATGTACA AG TG			
	A_____ T A T			
GAM496 TCP10	TGGGGGCATCTACAT-TTCA	7855	CA G ACT	
	TGG GCATCTACAT TTCA			
	ACC CGTAGATGTA AAGT			
	CC _			
GAM496 TCP10	TGGGGGCATCTACAT-TTCA	7855	_ CA GTTCI	
	GG GCATCTACAT			
	CC CGTAGATGTA			
	A CC AAGII			
GAM496 TMEM1	TGACAGTATTTACATGTTCCAC	7856	C C A TG	
	TGGCAG AT TACATGTTT AC			
	ACTGTC TA ATGTACAAG TG			
	A A G II			
GAM496 TMEM1	TGACAGTATTTACATGTTCCAC	7856	C C AAI	
	GGCAG AT TACATGTTT			
	CTGTC TA ATGTACAAG			
	A A GTI			
GAM496 TRPM7	CAGCAT-T-CATGTTCAAATG	7845	CTA CI	
	CAGCAT CATGTTCAA			
	GTCGTA GTACAAGTT			
	A_ TA			
GAM496 TRPM7	CAGCAT-T-CATGTTCAAATG	7845	TGGCAGCATCTA C	
	CATGTTCAA T			
	GTACAAGTT A			
	GTAA_____ T			
GAM497 AP1M1	GCTGGCTGGCTGGCAAGCGT	7860	G GCG CA	
	TGGC GGCT GGCAAGCGT			
	ACCG CCGA CCGTTCGCA			
	A _ AC			
GAM497 AP1M1	GCTGGCTGGCTGGCAAGCGT	7860	G _ G II	
	GC GGCTG C GGCAAGCG			
	CG CCGAC G CCGTTCGC			
	A C A AI			
GAM497 BRF1	TGGCCTGCTGCGGGCCAAG	7874	GG _ CGTCA	
	TGGC GCTGCGGGC AAG			

	ACCG CGACGCCCG TTC			
	GA G IIICA			
GAM497 BRF1	TGGCCTGCTGCGGGCCAAG	7874	GG	AAII
	TGGC GCTGCGGGC			
	IIII IIIIIII			
	ACCG CGACGCCCG			
	GA GTTC			
GAM497 CDH23	GCGGGCTGCCAGGGCCAAGC	7861	— _ III	
	GCGGGCTGC GGGC AAG			
	IIIIIIII III III			
	CGCCCGACG CCCG TTC			
	GT G GII			
GAM497 CDH23	GCGGGCTGCCAGGGCCAAGC	7861	TGGC — _ GTCA	
	GGGCTGC GGGC AAGC			
	IIIIII III III			
	CCCGACG CCCG TTCG			
	— GT G GTII			
GAM497 CMAR	GGGCGGTCGTGCAAGCGTC	7870	TG_ G II	
	GGGC CG GCAAGCGT			
	IIII II IIIIIII			
	CCCG GC CGTTCCGA			
	CCA A GI			
GAM497 G6PD	GGCTGGCGGGCAAG-GCCAC	7869	T— _ TG AGCGTCA	
	GGCG GGC CGGGCA			
	IIII III IIIII			
	CCGT CCG GTCCGT			
	CGC T GT IIICACT			
GAM497 G6PD	GGCTGGCGGGCAAG-GCCAC	7869	_ C II	
	GGCTG CGGGCAAG GTCA			
	IIII IIIIIII III			
	CCGAC GCCCGTTC CGGT			
	C _ GI			
GAM497 GRB7	GGCGGGCTG-AGGCATGAGCCA	7867	_ C _ GTCI	
	GCGGGCTG GGGCA AGC			
	IIIIII III III			
	CGCCCGAC TCCGT TCG			
	C _ AC GIII			
GAM497 GRB7	GGCGGGCTG-AGGCATGAGCCA	7867	TG C AGC C	
	GCGGGCTG GGGCA GTCA			
	IIIIII III III			
	CGCCCGAC TCCGT CGGT			
	_ _ ACT C			
GAM497 GRM4	GGCGGGGCAGGCGGGCAAG	7863	_ T_ III	
	GGCGGG C GCGGGCAA			
	IIII I IIIIIII			
	CCGCCC G CGCCCGTT			
	C TC CII			
GAM497 GRM4	GGCGGGGCAGGCGGGCAAG	7863	TG _ T_ CGTCA	
	GCGGG C GCGGGCAA			
	IIII I IIIIIII			

	CGCCC G CGCCCGTTC		
	___ C TC TIIIC		
GAM497 GRM4	GGCAGGCTGCGGGCCACAGGGACAC 7865 G_ TG CAA GI		
	GCGGGC CGGG GC		
	II		
	CGCCCG GTCC TG		
	GA GT CTG II		
GAM497 GRM4	GGCAGGCTGCGGGCCACAGGGACAC 7865 TG AA TCACII		
	GCGGGCTGCGGGC GCG		
	CGTCCGACGCCCG TGT		
	___ G_ CCCTGT		
GAM497 LHB	TGGAAGGCTGCGGG-GAGGGTC 7875 C CA C AC		
	TGG GGGCTGCGGG AG GTC		
	ACC TCCGACGCCC TC CAG		
	T C_ C II		
GAM497 LHB	TGGAAGGCTGCGGG-GAGGGTC 7875_ C CA C I		
	GG GGGCTGCGGG AG GT		
	CC TCCGACGCCC TC CA		
	A T C_ C I		
GAM497 POU3F1	GGCGGGCTGCGCGCCCGCG 7866 G AA II		
	GGCGGGCTGCG GC GC		
	CCGCCGACGC CG CG		
	G GG CI		
GAM497 POU3F1	GGCGGGCTGCGCGCCCGCG 7866 TG G AA CA		
	GCGGGCTGCG GC GCGT		
	CGCCCGACGC CG CGCG		
	___ G GG II		
GAM497 PTTG1IP	GGCTGGGCTGCGG---AGCGTGCAC 7862_ _ GCA _ I		
	GC GGGCTGCGG AGCGT CA		
	CG CCCGACGCC TCGCA GT		
	C A _ C I		
GAM497 PTTG1IP	GGCTGGGCTGCGG---AGCGTGCAC 7862 TG _ GCA _		
	GC GGGCTGCGG AGCGT CAC		
	CG CCCGACGCC TCGCA GTG		
	_ A _ C		
GAM497 RTN2	GGCGTCCTGCGGGC-AGAGACAC 7868_ GG AGCGTCAI		
	GCG CTGCGGGCA		
	CGC GACGCCCGT		
	C AG CTCTGTII		
GAM497 RTN2	GGCGTCCTGCGGGC-AGAGACAC 7868 TG GG _ _ GT AC		
	GCG CTGCGGGCA AG C C		

	CGC GACGCCCGT TC G G		
	__ AG C T TG II		
GAM497 S100B	TGGCGGGCTGCACGGTGCACGC 7873	__ _ A GTCAC	
	TGGCGGGCTGC GG GCA GC		
	ACCGCCCGACG CC CGT CG		
	TG A G IIICA		
GAM497 S100B	TGGCGGGCTGCACGGTGCACGC 7873	__ _ AGIII	
	TGGCGGGCTGC GG GCA		
	ACCGCCCGACG CC CGT		
	TG A GCGII		
GAM497 SOD3	GGGCTGCGGGGAGACTTCA 7871	CAA GTCII	
	GGGCTGCGGG GC		
	CCCGACGCC TG		
	CTC AAGTI		
GAM497 SOD3	GGGCTGCGGGGAGACTTCA 7871 TG	CTGC A__ TCA	
	GCGGG GGGC AGCG		
	CGCCC TCTG TCGT		
	A_ C__ AAG CII		
GAM497 SPG7	GGGCGGTCTGTGCAAGCGTC 7870	TG_ G II	
	GGGC CG GCAAGCGT		
	CCCG GC CGTTCGCA		
	CCA A GI		
GAM497 TEM7	GGGATACAGGCAAGCGTCAC 7872 C	I	
	GG TCGGGCAAGCGTCA		
	CC ATGTCCGTTTCGCAGT		
	T I		
GAM497 TEM7	GGGATACAGGCAAGCGTCAC 7872	TGGCGGGC	
	TGCGGGCAAGCGTCA		
	ATGTCCGTTTCGCAGT		
GAM497 TNFRSF11A	GGCGGGCTGCTGAGCATCCGT 7864 G	_ AGCGI	
	CGGGCTGC GGGCA		
	GCCCGACG CTCGT		
	_ A AGGCI		
GAM497 TNFRSF11A	GGCGGGCTGCTGAGCATCCGT 7864 TG	_ AG CAC	
	GCGGGCTGC GGGCA CGT		
	CGCCCGACG CTCGT GCA		
	_ A AG CII		
GAM498 ADPRT	CACCGGGTGTGACTCGGCTAC 7881	TCACA _ _ ACTA	
	GGGTGTGACT GGC CC		

CCCACACTGA CCG GG
 TGG__ G AT IIIA
 GAM498 ENC1 TCACAGGGTGAGAATGGTCAAGTA 7888 T C CCCACTAI
 TCACAGGGTG GA TGG
 ||||| || ||
 AGTGTCCCAC CT ACC
 T T AGTTCATI
 GAM498 FEN1 CACAGAGGAGGGGATGACTGGCC 7878 TCAC__ T CACTA
 AGGG GTGACTGGCC
 ||| |||||
 TCCC TACTGACCGG
 TGTCTCC _ AIIIA
 GAM498 GNA15 TCCCAGGGTGTGCGTCACCCAC 7886 A ACTG TA
 TC CAGGGTGTG GCCAC
 || ||||| ||||
 AG GTCCCACAC TGGGTG
 G GCAG II
 GAM498 ICA1 CAGTGTGAGAACTGGCCAC 7883 TCACAGG T ____
 GTG GA CTGGCCCACTA
 ||| || |||||
 CAC CT GACCGGGTGGT
 A_____ T TGT
 GAM498 POU2AF1 CAGAGGGTGTGAGTGACCC 7879 TCAC C ACT
 AGGGTGTGA TGGCCC
 ||||| ||||
 TCCCACACT ACTGGG
 TC__ C AII
 GAM498 PRX CAGAGGGCAAGGCTGGCCAC 7882 TCAC TGA TA
 AGGGTG CTGGCCAC
 |||| |||||
 TCCCGT GACCGGGTG
 TC__ TCC CI
 GAM498 RASSF1 TCTCAGGGCAGCCCTGGCCCACTA 7889 A _ GA I
 TC CAGGGT GT CTGGCCCACTA
 || ||||| || |||||
 AG GTCCCG CG GACCGGGTGAT
 A T G_ I
 GAM498 SFTP2 TCACAGGGT-TGGCTTGGGCACCAC 7885 G A _ _ TAI
 TCACAGGGT TG CT GGC CCAC
 ||||| || || ||||
 AGTGTCCCA AC GA CCG GGTG
 _ C AC T III
 GAM498 SH3BP2 TCACAGG-GTCACTGCCCTCT 7887 GTG G A A
 TCACAGGGT ACTG CCC CT
 ||||| ||| ||| ||
 AGTGTCCCA TGAC GGG GA
 G__ G A I
 GAM498 SLC14A2 CAGGGTGTG-GTGGCACAC 7884 TCACAG AC C
 GGTGTG TGGC CAC
 |||| ||| |||

	CCACAC ACCG GTG			
	_____ C_ T			
GAM498 SYN3	CAGAGGGTGTGA-T-GCCCA	7880 TCAC	CTG	C
	AGGGTGTGA GCCCA			
	TCCCACACT CGGGT			
	TC__ A__ A			
GAM499 CELL	TCAC-TGTGGGCAGCGCCA	7895 C	CA_ TCGA	
	TCAC TGTGGGCA CCA			
	AGTG ACACCCGT GGT			
	_ CGC IIIA			
GAM499 CELL	TCAC-TGTGGGCAGCGCCA	7895 C	CACCII	
	TCAC TGTGGGCA			
	AGTG ACACCCGT			
	_ CGCGGT			
GAM499 CFTR	CAGCTGTGGGCAACAAC-TCGA	7892 AC	_ CCA I	
	CTGTGGGCA CA TCG			
	GACACCCGT GT AGC			
	TC T TG_ I			
GAM499 CFTR	CAGCTGTGGGCAACAAC-TCGA	7892 TCAC	_ CCA GA	
	CTGTGGGCA CA TCGA			
	GACACCCGT GT AGCT			
	TC__ T TG_ AI			
GAM499 SELE	CCTGTGGGCATTCAACATC	7894	_ C III	
	CCTGTGGGCA CA CAT			
	GGACACCCGT GT GTA			
	AA T GII			
GAM499 SELE	CCTGTGGGCATTCAACATC	7894 TCACCT	_ C GAG	
	GTGGGCA CA CATC			
	CACCCGT GT GTAG			
	_____ AA T ACA			
GAM499 SLC19A1	CACCTGTGGGCAAGGCACTAGCG	7893 ACC	___ CATCI	
	TGTGGGCA CAC			
	ACACCCGT GTG			
	_____ TCC ATCGI			
GAM499 SLC19A1	CACCTGTGGGCAAGGCACTAGCG	7893 TC	___ CAT AGAI	
	ACCTGTGGGCA CAC CG			
	TGGACACCCGT GTG GC			
	_____ TCC ATC GIII			
GAM500 ABCD4	CATGCTTTGTGCTTTCTGGGT	7899 AG	___ III	
	CATGCT GT TTCTGGGT			

	GTACGA CA AAGACCCA	
	AA CGA AII	
GAM500 ABCD4	CATGCTTTGTGCTTTCTGGGT 7899 TGGCA_ AGGT CT	
	TGCT TTCTGGGT	
	ACGA AAGACCCAA	
	CGAAAC ____ AA	
GAM500 BLTR2	GGCATGGTGCTAGGTTCCAGG 7904 ____ TGIII	
	GGCA TGCTAGGTTTC	
	CCGT ACGATCCAAGG	
	ACC TCCII	
GAM500 BLTR2	GGCATGGTGCTAGGTTCCAGG 7904 ____ CA T TTCT	
	TGG TGCTAGGTTTC GGG	
	ACC ACGATCCAAGG CCT	
	CGT ____ T IIIT	
GAM500 CD1C	GGC-TCCTGGGTTGCTGGGTTCT 7907 _ ATG A T I	
	GC CT GGTT CTGGGTTC	
	CG GA CCAA GACCCAAG	
	C AG_ C C I	
GAM500 CD1C	GGC-TCCTGGGTTGCTGGGTTCT 7907 TGGCATG A T	
	CT GGTT CTGGGTTC	
	GA CCAA GACCCAAGA	
	CGAG____ C C	
GAM500 ERBB2	GGCAGTACTAGGTTTCAGGG 7903 _ T II	
	GGCA TGCTAGGTTTC GG	
	CCGT ATGATCCAAAG CC	
	C T CI	
GAM500 ERBB2	GGCAGTACTAGGTTTCAGGG 7903 TG _ T TTC	
	GCA TGCTAGGTTTC GGG	
	CGT ATGATCCAAAG CCC	
	__ C T TII	
GAM500 HPS4	GCATGCTAG--AGCTGGTGTCT 7902 _ TTT _ I	
	CATGCTAGG CTGG GTTC	
	GTACGATCT GACC CAAG	
	C C__ A I	
GAM500 HPS4	GCATGCTAG--AGCTGGTGTCT 7902 TGGC TTT _	
	ATGCTAGG CTGG GTTCT	
	TACGATCT GACC CAAGA	
	____ C__ A	
GAM500 MARS	CTAGGGTTGCTCTGGGTTCT 7900 T__ III	
	CTAGG TTCTGGGTTC	

	GATCC GAGACCCAAG		
	CAAC AII		
GAM500 MMP19	TGGCATG---GGA--CTGGGTTCT 7908	CTA TTT	
	TGGCATG GG CTGGGTTT		
	ACCGTAC CC GACCCAAG		
	___ T__		
GAM500 MMP19	TGGCATG---GGA--CTGGGTTCT 7908_	CTA TTT	
	GGCATG GG CTGGGTT		
	CCGTAC CC GACCCAA		
	A ___ T__		
GAM500 PON2	CATGCCATACATTTCTGGGT 7898	G___ III	
	CATGCTA GTTTCTGGG		
	GTACGGT TAAAGACCC		
	ATG AII		
GAM500 PON2	CATGCCATACATTTCTGGGT 7898 T G	TAG C	
	G CATGC GTTTCTGGGTT		
	C GTATG TAAAGACCCAG		
	_ G ___ T		
GAM500 SLC10A1	GGCAGATTCGGTTTCTGGTTTC 7906	TGCTA GTTI	
	GCA GGTTCCTGG		
	CGT CCAAAGACC		
	CTAAG AAI		
GAM500 SLC10A1	GGCAGATTCGGTTTCTGGTTTC 7906 TG	TGCTA G T	
	GCA GGTTCCTGG TTC		
	CGT CCAAAGACC AAG		
	___ CTAAG A T		
GAM500 SLC39A4	GGCTT-CTGGGTTTCTGGG 7905	ATG A I	
	GGC CT GGTTCCTGG		
	CCG GA CCAAAGACC		
	AA_ C C		
GAM500 SLC39A4	GGCTT-CTGGGTTTCTGGG 7905 TG	ATG A T	
	GC CT GGTTCCTGGGT		
	CG GA CCAAAGACCCG		
	___ AA_ C I		
GAM500 THBD	GCATACTCGGATTGCTGGGTTCT 7901 C	A T _ I	
	ATGCT GG TT CTGGGTTT		
	TATGA CC AA GACCCAAG		
	_ G T C I		
GAM500 THBD	GCATACTCGGATTGCTGGGTTCT 7901 TGGC	A T _ I	
	ATGCT GG TT CTGGGTTT		

	TATGA CC AA GACCCAAGA		
	_____ G T C G		
GAM501 AK1	TGGGAATACAGGCACATGCCACC 7916	_____	TTTTAI
	TGGGAATAC CATA GCCACC		
	ACCCTTATG GTGT CGGTGG		
	TCC A IIIATT		
GAM501 ARSD	TGGGATTAAAGGCATGAGCCACCTT 7915	A C_____	TTAII
	TGGGA TA CAT AGCCACCTT		
	ACCCT AT GTA TCGGTGGAA		
	A TTCC C IIIAT		
GAM501 DACH	AATAACACATAGCCACCCTT 7911	TGGGAAT _	
	AC CATAGCCACCTTTT		
	TG GTATCGGTGGGAAG		
	_____ T		
GAM501 DEDD	GGAATACCACTTCCACTTTCTTTT 7912	TG AG C All	
	GGAATACCAT CCAC TTTT		
	CCTTATGGTG GGTG AAGA		
	_____ AA A AAA		
GAM501 IDH3B	TGGCAAGTAGCATAGCCACC 7914	G _ C	TTTT
	TGG AA TA CATAGCCACC		
	ACC TT AT GTATCGGTGG		
	G C C IIIA		
GAM501 TCF3	TGGGAGGGTCAGAGCCACCTT 7917	ATAC T	TTA
	TGGGA CA AGCCACCTT		
	ACCCT GT TCGGTGGAA		
	CCCA C III		
GAM501 TIC	GGA-ACCTGTCGCCACCTTTTA 7913	T ACCATA	
	GGAAT GCCACCTTTTA		
	CCTTG CGGTGAAAAT		
	_____ ACAG_____		
GAM502 CAPN9	AGTGG-ATGGAAAAGAAAGTG 7920	TTA CAA	TT
	GTGG GGAAGAAAGTG		
	TACC TTTTCTTTCAC		
	ACC _____ TT		
GAM502 HBD	TTA-TGTCA-GAAGAAAGTGT 7923	TTA GCAA	T
	GTG GGAAGAAAGTGT		
	TAC TCTTCTTTCACA		
	AA_ AG_____ I		
GAM502 SCGB2A2	GTGGCAAGGATCAAGGAAG 7921	TTAGTG _____	A GTT
	GCAAGGA AG AAGT		

	CGTTCCT TC TTCG	
	_____ AGT C GCI	
GAM502 ZNFN2A1	TGGTAATGAAAGAAAGTGGTC 7922 TTAGTGGCAA	T
	GGAAGAAAGTG TC	
	CTTCTTTTCAC AG	
	TTA_____ C	
GAM503 APBA2	AACAGTAATAATAGCATCTA-AAT 7927 TA	_ CAATI
	ACAGTA TAATAGCATTTA	
	TGTCAT ATTATCGTAGAT	
	_____ T TTATI	
GAM503 ATP6V1C1	AACAGTATAAATG--TTTACA 7929 TA	TAGCA A
	ACAGTATAA TTTACA	
	TGTCATATT AAATGT	
	_____ TAC_____ G	
GAM503 BCRP2	TATAAAACCAGCATTTACAAT 7951 TAACAGTATAA	
	TAGCATTTACAAT	
	GTCGTAAATGTTA	
	TG_____	
GAM503 BRCA1	TAACAGCACAA---CATTTACAA 7949	ATA
	TAACAGTATA GCATTTACAA	
	ATTGTCGTGT TGTAATGTT	

GAM503 CASP3	AACAGTATAA-AACA-TTACTAT 7931 TA	T T AAT
	ACAGTATAA AGCATT AC	
	TGTCATATT TTGTAA TG	
	_____ _ _ ATA	
GAM503 CCNT2	AAAAGTGAATACATAGCATTTCAAAT 7926 TAAC_____	A A TII
	AGTATA TAGCATTT CAA	
	TTATGT ATCGTAAA GTT	
	TTTCAC _ _ TAA	
GAM503 DISC1	ACAGTATAATATCACACTTACA 7932 TAAC	_____ AT
	AGTATAATA GCATTTACA	
	TCATATTAT TGTGAATGT	
	_____ AG AA	
GAM503 DKK1	TAAAAGTTTCATTGCATTTACA 7947 C ATA A	AT
	TAA AGT AT GCATTTACA	
	ATT TCA TA CGTAAATGT	
	T AAG A	
GAM503 DSCR5	TAACAATACTTGAACATTTACAAT 7950	AAT I
	TAACAGTAT AGCATTTACAAT	

	ATTGTTATG TTGTAAATGTTA			
	AAC I			
GAM503 FPRL1	TAACAGTATATAAACATAAACA 7948	AT	TT	AT
	TAACAGTATA AGCAT ACA			
	ATTGTCATAT TTGTA TGT			
	AT TT II			
GAM503 GM2A	ACATTGTAATAGCATCTTTAAT 7939	TAACAGTA		ACAAT
	TAATAGCATTT			
	ATTATCGTAGA			
	TAAC_____ AATTA			
GAM503 KLK3	ACAGTATAACAGCTCTTTA 7934	TAAC	A_	CAA
	AGTATAATAGC TTTA			
	TCATATTGTCTG AAAT			
	_____ AG AAI			
GAM503 MEN1	ACAATATAG--GCATTTACAA 7937	TAAC	ATA	
	AGTATA GCATTTACAA			
	TTATAT CGTAAATGTT			
	_____ C_			
GAM503 MYB	TAACCATA-AATGAGCATTTACAAT 7943	A	TAAT	I
	TAAC GTA AGCATTTACAAT			
	ATTG TAT TCGTAAATGTTA			
	G TTAC I			
GAM503 NAB1	TAACAGTATAAAAAGTTGTTTAC 7945	T	CA_	AAT
	TAACAGTATAAA AG TTTAC			
	ATTGTCATATT TC AAATG			
	T AAC III			
GAM503 PEX1	ACATAATTATAGCATTTACCAAT 7935	TAACAGTATA		AATI
	ATAGCATTTAC			
	TATCGTAAATG			
	TATTAA_____ GTTA			
GAM503 PLGL	ACAGTATAACAACGATTACA 7936	TAAC	AT	A
	AGTATAATAGC TTACA			
	TCATATTGTTG AATGT			
	_____ CT A			
GAM503 PLGL	TAACAACGATTACATAGCATTTACA 7941	TATA_____		ATII
	TAACAG ATAGCATTTACA			
	ATTGTT TATCGTAAATGT			
	GCTAATG IIIT			
GAM503 PRSS16	TAACATTCAAAAATACCAATATTTACAAT7942	GTAT_	G _____	III
	TAACA AATA CA TTTACAAT			

	ATTGT TTAT GT AAATGTTA	
	AAGTT G TAT III	
GAM503 SCML2	AATATTTTATTGGCATTACAA 7930 TAACAGTATAATA	
	GCATTACAAAT	
	CGTAAATGTTG	
	TATAAAATAAC__	
GAM503 SELE	AGT-TGACAGCATTACAA 7940 TAACAGTATA	
	ATAGCATTACAA	
	TGTCGTAAATGT	
	C_____	
GAM503 SON	ACAGTATAAAAGCGTTATTTA 7933 TAAC T ATTTACAAT	
	AGTATAA AGC	
	TCATATT TCG	
	____ T CAATAAATT	
GAM503 TAF5	TAA-ATTAAAATAGCATTT 7946 TAACAG T ACA	
	TA AATAGCATTT	
	AT TTATCGTAAA	
	ATTTA_ T III	
GAM503 TM4SF6	ACAGTATTACTTCATTACAAAT 7938 TAAC A AG	
	AGTAT AT CATTACAAAT	
	TCATA TG GTAAATGTTA	
	____ A AA	
GAM503 TSG	TAAAA-TATGGTAAGCATTTAC 7944 TAAC AAT_ AAT	
	AGTAT AGCATTTAC	
	TTATA TCGTAAATG	
	ATT_ CCAT III	
GAM503 UBE2A	AACATTAGACAAAACATTACAA 7928 TAAC_ T T TI	
	AG ATAA AGCATTTACAA	
	TC TGTT TTGTAAATGTT	
	TGTAA _ _ CI	
GAM504 ADARB1	GACACACACGG--AACACAAT 7986 TG AGT_ CACCATC	
	ACACACAC CAC	
	TGTGTGTG GTG	
	____ CCTT TTACIII	
GAM504 ADRB3	GACACACACACACACACAC 7983 TG GT _ CATC	
	ACACACACA CAC CAC	
	TGTGTGTGT GTG GTG	
	____ GT T TIII	
GAM504 ADRB3	ACACACACACACACACCAT 7966 TG GT _ CA	
	ACACACACA CAC CACCAT	

		TGTGTGTGT GTG GTGGTA		
		— — T CA		
GAM504 AMPD3		ACACACACACACAACCTAACA 7980 TG	GT	C CATCA
		ACACACACA CAC AC		
		TGTGTGTGT GTG TG		
		— — T ATTGT		
GAM504 AOA		TGACACACACA--CCCCACCCTC 7991	G A	A A
		TGACACACACA TC CCACC TC		
		ACTGTGTGTGT GG GGTGG AG		
		— — G I		
GAM504 BCL7A		ACACACACACACACACACAT 7963 TG	GT	_ _ CA
		ACACACACA CAC CAC CAT		
		TGTGTGTGT GTG GTG GTA		
		— — T T TG		
GAM504 CHC1L		GACAAAGACCACTCACCACCATC 7981 T	A	ACAG AI
		GAC CAC TCACCACCATC		
		CTG GTG AGTGGTGGTAG		
		TGTTT _ _ GI		
GAM504 DCX		ACACACACACACACATGCACCA 7958 TG	GT	ATCA
		ACACACACA CACCACC		
		TGTGTGTGT GTGGTGG		
		TGTG AC A		
GAM504 DMC1		ACACACACACACACAAACAT 7976 TG	T	CCACCATC
		ACACACACAG CA		
		TGTGTGTGTT GT		
		TGTG T ATG AC		
GAM504 EPHB3		ACACACACACACACACTCACACATC 7957 TG	GT	_ _ A
		ACACACACA CAC CAC CATC		
		TGTGTGTGT GTG GTG GTAG		
		— GT A T GGI		
GAM504 EPHB3		ACACACACACTCACACATCCCATC 7961 TGAC	G	_ _ AI
		ACACACA TCAC CA CCATC		
		TGTGTGT AGTG GT GGTAG		
		— G T AG AG		
GAM504 FAT2		ACACACACAGCCACAAACCACTCA 7965 TGAC	C	_ CAI
		ACACACAGTCAC ACCAT		
		TGTGTGTCGGTG TGGTG		
		— TT AGT		
GAM504 FLT1		ACACACACAGTTACACCAC 7956 TGAC	_	CATC
		ACACACAGT CACCAC		

		TGTGTGTCA GTGGTG		
		_____ AT ACII		
GAM504 FXYD6		ACACACACACACACACA-CATCA 7967 TG	GT _ C	
		ACACACACA CAC CAC ATCA		
		TGTGTGTGT GTG GTG TAGT		
		_____ T _		
GAM504 GRM4		GACACACACAGAGGCCACCA 7984 TG	TCA TC	
		ACACACACAG CCACCA		
		TGTGTGTGTC GGTGGT		
		_____ TCC CI		
GAM504 GSTM5		ACACACACACACACACCCATC 7977 TG	GT CA A	
		ACACACACA CAC CCATC		
		TGTGTGTGT GTG GG TAG		
		_____ TG A		
GAM504 HMGB2		ACACACACATTCCACACGCATCA 7969 TGAC	G AC _ I	
		ACACACA TC CAC CATCA		
		TGTGTGT AG GTG GTAGT		
		_____ A GT C A		
GAM504 HSPA4		ACACACACACACACACACCA 7964 TG	GT _ C	
		ACACACACA CAC CACCAT		
		TGTGTGTGT GTG GTGGTA		
		_____ T C		
GAM504 IL21R		ACACACACAGACACTGTAAACATCA 7960 TGAC	T CAC_____ II	
		ACACACAG CAC CATCA		
		TGTGTGTC GTG GTAGT		
		_____ T ACATT CC		
GAM504 IL21R		GACACACACACACACACAC 7983 TG	GT _ CATC	
		ACACACACA CAC CAC		
		TGTGTGTGT GTG GTG		
		_____ GT T TIII		
GAM504 JUND		ACACACACACACACAACCA 7970 TG	GT C TC	
		ACACACACA CAC ACCA		
		TGTGTGTGT GTG TGGT		
		_____ T CC		
GAM504 KCNN4		GACACACACAGACA-CACGAT 7985 TG	T C CATC	
		ACACACACAG CAC AC		
		TGTGTGTGTC GTG TG		
		_____ T _ CTAC		
GAM504 KCNN4		TGACACACACCTCTACTCACCAC 7987	AG _ _ CAI	
		TGACACACAC TC AC CACCAT		

	ACTGTGTGTG AG TG GTGGTG	
	G_ A A III	
GAM504 MAX	ACACACACACTCACTCACTCACTCA 7962 TG	A G _ _ CAII
	ACACAC CA TCAC CAC CAT	
	TGTGTG GT AGTG GTG GTG	
	TG A G A A AIII	
GAM504 MEF2A	ACACACACACTCACACCCA 7973 TGAC	G CA C
	ACACACA TCAC CCAT	
	TGTGTGT AGTG GGTG	
	_____ G TG T	
GAM504 MPP2	TGACACACACACACACAC 7989	GT _ CATC
	TGACACACACA CAC CAC	
	ACTGTGTGTGT GTG GTG	
	GT T IIIA	
GAM504 NOS1	ACACACACAGGCACGCACAACCA 7968 TGAC	T _ C I
	ACACACAG CAC CAC ATCA	
	TGTGTGTC GTG GTG TGGT	
	_____ C C T T	
GAM504 PFKFB2	GAAACACACAGTTACACCACC 7982 TGAC	_ ATCA
	ACACACAGT CACCACC	
	TGTGTGTCA GTGGTGG	
	TT_ AT CIII	
GAM504 PITX1	ACACACACA-CCACCCGCGCCATC 7959 TG	AGT A_ AI
	ACACACAC CACC CCATC	
	TGTGTGTG GTGG GGTAG	
	_ _ GCGC GG	
GAM504 PKD1	ACACACACACACA-CACAGTCA 7979 TG_	ACCATCA
	ACACACACAGTCACC	
	TGTGTGTGTCAGTGG	
	TGTGTG IIIACTA	
GAM504 PTGFRN	ACCCATCACATTTACCACCATC 7954 TGACA _ GTC	A
	CA CACA ACCACCATC	
	GT GTGT TGGTGGTAG	
	G_ A AAA C	
GAM504 SFN	ACACACACACCCATCTCCA 7972 TG	A_ A CCATC
	ACACACAC GTC CCA	
	TGTGTGTG TAG GGT	
	_ GG A CGIII	
GAM504 SFN	ACACACACACACACACCCATC 7977 TG	GT CA A
	ACACACACA CAC CCATC	

		TGTGTGTGT GTG GGTAG		
		— — TG A		
GAM504 SLC25A1		TGTCACACACAG--ACCAC 7990 TGA TC CAT		
		CACACACAG ACCAC		
		GTGTGTGTC TGGTG		
		ACA — III		
GAM504 SLC30A3		ACACACACAGACAAAACCA 7975 TGAC T CC C		
		ACACACAG CA ACCAT		
		TGTGTGTC GT TGGTG		
		— — T TT T		
GAM504 SYNGR1		TGTCAC-CAGAAGTCACCACCTTCA 7988 TGA A C_ A I		
		CAC CA AGTCACCACC TCA		
		GTG GT TCAGTGGTGG AGT		
		ACA _ CT A I		
GAM504 TCF15		ACACACACACCCTGTCACCAACA 7955 TG A_ C TCAI		
		ACACACAC GTCACCA CA		
		TGTGTGTG CAGTGGT GT		
		— GGA T CAII		
GAM504 USF2		ACACACACACACACCCCCA 7971 TG GT A TC		
		ACACACACA CACC CCA		
		TGTGTGTGT GTGG GGT		
		— — G TT		
GAM504 WSX1		ACACACACACTCTCTGCCA 7974 TG AG A_ CCATC		
		ACACACAC TC CCA		
		TGTGTGTG AG GGT		
		— AG AC TTIII		
GAM504 WT1		ACACACACACACACGACCATC 7978 TG GT C A		
		ACACACACA CAC ACCATC		
		TGTGTGTGT GTG TGGTAG		
		— — C A		
GAM505 ATSV		CAGGCATGGGATTGGGGTCTCT 7995 CAG T CI		
		GTGG ATTGGGGTC		
		TACC TAACCCCAG		
		G_ C AG		
GAM505 ATSV		CAGGCATGGGATTGGGGTCTCT 7995 TGGCAG T C C		
		GTGG ATTGGGGTC CT		
		TACC TAACCCCAG GA		
		CG_ C A C		
GAM505 B4GALT1		GGCAG-TGGT-TTGGGGTCC 8010 G A I		
		GGCAG TGGT TTGGGGT		

	CCGTC ACCA AACCCCA				
	— — G				
GAM505 B4GALT1	GGCAG-TGGT-TTGGGGTCC	8010	TG	G A	C
	GCAG TGGT TTGGGGTCC				
	CGTC ACCA AACCCCAGG				
	— — — C				
GAM505 BMP1	GCAGGACGCA--GGGGTCCCTC	8001	TG	TT	I
	GCAGG GTA GGGGTCCC				
	CGTCC CGT CCCCAGGG				
	TG — A				
GAM505 BMP1	GCAGGACGCA--GGGGTCCCTC	8001	TGGC	TG	TT
	AGG GTA GGGGTCCCT				
	TCC CGT CCCCAGGGA				
	— — — TG —				
GAM505 CYP1A2	GGCAGGTGGATAACTTGGGGTTC	8006	TA	—	
	GGCAGGTGG TTGGGGT				
	CGTCCACC AACCCCA				
	TATTG GII				
GAM505 CYP1A2	GGCAGGTGGATAACTTGGGGTTC	8006	TG	TA	— CCTC
	GCAGGTGG TTGGGGTTC				
	CGTCCACC AACCCCAG				
	— TATTG TIII				
GAM505 DLG5	GGCAGGTGGGA--GGAGTCCC	8012	—	TATT	I
	GCAGGTGG GGGGTCC				
	CGTCCACC CCTCAGG				
	C CT — I				
GAM505 DLG5	GGCAGGTGGGA--GGAGTCCC	8012	TG	TATT	
	GCAGGTGG GGGGTCCCT				
	CGTCCACC CCTCAGGGG				
	— CT —				
GAM505 DNASE1L1	TGGCAGGTGGCATGAGTGCAGGGCCCCT8023				CIII
	TGGCAGGTGGTAT TGGGGTCCCT				
	ACCGTCCACCGTA GTCCCGGGGA				
	CTCAC IIIC				
GAM505 DNASE1L1	TGGCAGGTGGCATGAGTGCAGGGCCCCT8023	— —	GTAT		I
	GGCA GGTG TGGGGTCCC				
	CCGT TCAC GTCCCGGGG				
	CA AC — I				
GAM505 EGLN2	TGGCCTCACCACTG-CCACTGCTG	8019	A	AG	— T II
	TG CCTCA TG CCACTGCTG				

	AC GGAGT AC GGTGACGAC	
	C GGTG _ II	
GAM505 FADD	GCAGGTGGTCTGTGGCTCACTC 8002 A _ G C I	
	CAGGTGGT TTG GG TC CT	
	GTCCACCA GAC CC AG GA	
	_ A G T I	
GAM505 FADD	GCAGGTGGTCTGTGGCTCACTC 8002 TGGC A _ G C	
	AGGTGGT TTG GG TC CTC	
	TCCACCA GAC CC AG GAG	
	_____ _ A G T	
GAM505 FGFR1	GCAGTGTGGGGTTTGGGGTCCC 7999 CA__ T A I	
	GG GGT TTGGGGTCC	
	CC CCA AACCCCAGG	
	CACA _ _ I	
GAM505 FGFR1	GCAGTGTGGGGTTTGGGGTCCC 7999 TGGCA T A TC	
	GG GGT TTGGGGTCCC	
	CC CCA AACCCCAGGG	
	TCACA _ _ TG	
GAM505 GALNS	GGCAGGTGGAATTGTGCAGTCCC 8008 GC TAT__ G I	
	AGGTGG TG GGTCC	
	TCCACC AC TCAGG	
	_ TTAAC G I	
GAM505 GALNS	GGCAGGTGGAATTGTGCAGTCCC 8008 TG TAT__ G CI	
	GCAGGTGG TG GGTCCCT	
	CGTCCACC AC TCAGGGG	
	_ TTAAC G II	
GAM505 GRB7	CAGGTGGTAGGAGGGTGTCCC 7996 TT_ _ III	
	CAGGTGGTA GGG GTCC	
	GTCCACCAT CCC CAGG	
	CCT A GII	
GAM505 GRB7	CAGGTGGTAGGAGGGTGTCCC 7996 TGGCAG TT_ _ TC	
	GTGGTA GGG GTCCC	
	CACCAT CCC CAGGG	
	_____ CCT A CT	
GAM505 ITGA7	GGCAGGTCCT--TGGGGTCC 8011 GGTA I	
	GGCAGGT TTGGGGT	
	CCGTCCA AACCCCA	
	GG__ G	
GAM505 ITGA7	GGCAGGTCCT--TGGGGTCC 8011 TG GGTA C	
	GCAGGT TTGGGGTCC	

	CGTCCA AACCCCAGG			
	___ GG___ A			
GAM505 KCNQ1	CATGGGGTATTGGGGCCTCT	7998	CA T	CI
	GG GGTATTGGGGTC			
	II IIIIIIIII			
	CC CCATAACCCCGG			
	A_ _ AG			
GAM505 KCNQ1	CATGGGGTATTGGGGCCTCT	7998	TGGCA T	C
	GG GGTATTGGGGTC CT			
	II IIIIIIIII II			
	CC CCATAACCCCGG GA			
	_____ A			
GAM505 KLK3	GCAGGTGGTAAGCTTGGGG	8000	___ III	
	GCAGGTGGTA TTGGG			
	IIIIIIII IIII			
	CGTCCACCAT AACCC			
	TCG CII			
GAM505 KLK3	GCAGGTGGTAAGCTTGGGG	8000	TGGC ___	CCCT
	AGGTGGTA TTGGGGT			
	IIIIII IIII			
	TCCACCAT AACCCCG			
	_____ TCG AIII			
GAM505 LENG4	CAGGCGCCAGTGGGGTCCC	7997	G T II	
	CAGGTG TA TGGGGTCC			
	IIIIII II IIIIIII			
	GTCCGC GT ACCCCAGG			
	G C GI			
GAM505 LENG4	CAGGCGCCAGTGGGGTCCC	7997	TGGCAG G T	
	GTG TA TGGGGTCCCT			
	III II IIIIIIIII			
	CGC GT ACCCCAGGGG			
	_____ G C			
GAM505 MNT	TGGCAGGTGGCTGTGCTGGGGT	8021	A___	CCCTC
	TGGCAGGTGGT TTGGGGT			
	IIIIIIII IIII			
	ACCGTCCACCG GACCCCA			
	ACAC IIICT			
GAM505 MNT	TGGCAGGTGGCTGTGCTGGGGT	8021	A___	III
	TGGCAGGTGGT TTGGGG			
	IIIIIIII IIII			
	ACCGTCCACCG GACCCC			
	ACAC AII			
GAM505 MYBPC2	TGGGAGGTTGGGGATTGGGGTC	8020	C ___ T	CCTC
	TGG AGGT GG ATTGGGGTC			
	III IIII II IIIIIII			
	ACC TCCA CC TAACCCCAG			
	C AC C IIIC			
GAM505 MYBPC2	TGGGAGGTTGGGGATTGGGGTC	8020	___ CA T T	I
	GG GG GG ATTGGGGT			
	II II II IIIIIII			

		CC CC CC TAACCCCA			
		CT AA _ _ I			
GAM505 NPM3		GGCAGGTGGGAAGGGAGGCC	8013	TG	TATT_ TC
		GCAGGTGG GGGGTCCC			
		CGTCCACC CTCCGGGG			
		_ CTTCC II			
GAM505 NPM3		GGCAGGTGGGAAGGGAGGCC	8013		TATT_ CI
		GCAGGTGG GGGGTC			
		CGTCCACC CTCCGG			
		CTTCC II			
GAM505 OCLN		GGCAGCACGGATGGGGGTCCCT	8015	_ T T I	
		GCAG GTGG AT GGGGTCCC			
		CGTC TGCC TA CCCCAGGG			
		G _ C I			
GAM505 OCLN		GGCAGCACGGATGGGGGTCCCT	8015	T_ GG T T C	
		GGCA TGG AT GGGGTCCCT			
		TCGT GCC TA CCCCAGGGA			
		CG _ _ C C			
GAM505 PCK3		GGAAGCTGGTATTGGGATC	8009	C G II	
		GG AG TGGTATTGGGGT			
		CC TC ACCATAACCCTA			
		T G GI			
GAM505 PCK3		GGAAGCTGGTATTGGGATC	8009	TGGC G CCT	
		AG TGGTATTGGGGTC			
		TC ACCATAACCCTAG			
		CT_ G TII			
GAM505 PDPK1		TGGCAGGTGGTCTGGAAGCGTCCC	8025	A _ TC	
		TGGCAGGTGGT TTGGG GTCCC			
		ACCGTCCACCA GACCT CAGGG			
		_ TCG III			
GAM505 PDPK1		TGGCAGGTGGTCTGGAAGCGTCCC	8025	GG A _ I	
		CAGGTGGT TTGGG GTCC			
		GTCCACCA GACCT CAGG			
		_ _ TCG I			
GAM505 PFKM		GGCTGG-GGTATCTGGGGTCCC	8007	A T _ I	
		GC GG GGTAT TGGGGTCC			
		CG CC CCATA ACCCCAGG			
		A _ G I			
GAM505 PFKM		GGCTGG-GGTATCTGGGGTCCC	8007	TG A T _ C	
		GC GG GGTAT TGGGGTCCCT			

	CG CC CCATA ACCCCAGGGG		
	__ A _ G _ I		
GAM505 PML	GGCAGGTGGAGGGTGGGGGACCCT	8004 GC	TATT__ T I
	AGGTGG GGGG CCC		
	TCCACC CCCC GGG		
	__ TCCCAC T I		
GAM505 PML	GGCAGGTGGAGGGTGGGGGACCCT	8004 TG	TATT__ T CI
	GCAGGTGG GGGG CCCT		
	CGTCCACC CCCC GGGA		
	__ TCCCAC T TI		
GAM505 PML	TGGCAGGTGGGATGGATGGGG	8024	TAT__ TCCCTC
	TGGCAGGTGG TGGG		
	ACCGTCCACC ACCC		
	CTACCT IICTC		
GAM505 PML	TGGCAGGTGGGATGGATGGGG	8024	TAT__ III
	TGGCAGGTGG TGGG		
	ACCGTCCACC ACCC		
	CTACCT CII		
GAM505 PRKR	GGCAGGTGGATTACTTGAGGTC	8005	TA__ III
	GGCAGGTGG TTGGGGT		
	CCGTCCACC AACTCCA		
	TAATG GII		
GAM505 PRKR	GGCAGGTGGATTACTTGAGGTC	8005 TG	TA__ CCTC
	GCAGGTGG TTGGGGTC		
	CGTCCACC AACTCCAG		
	__ TAATG TIII		
GAM505 RS1	GGTGGTGTGTGAGGGGGTCCCT	8017 __ _ ATT	IIIA
	GGTG GT GGGGTCCC		
	CCAC CA CCCCAGGG		
	CCA A CTC AIII		
GAM505 RS1	GGTGGTGTGTGAGGGGGTCCCT	8017 TGGCAG GTATT	C
	GTG GGGGTCCCT		
	CAC CCCCAGGGA		
	A__ ACTC_ T		
GAM505 RS1	GTGGTCATTTGGGGTCCCT	8018 A__	III
	GTGGT TTGGGGTCCC		
	CACCA AACCCCAGGG		
	GTA AII		
GAM505 SCT	GGCAGGTGGTGAGGGGGTTCCT	8016	ATT _ CI
	GCAGGTGGT GGGGT CC		

	CGTCCACCA CCCCA GG			
	CTC A II			
GAM505 SCT	GGCAGGTGGTGAGGGGGTTCCT 8016 TG	ATT	C C	
	GCAGGTGGT GGGGT CCT			
	CGTCCACCA CCCCA GGA			
	CTC A A			
GAM505 TGFB1	GGGAGGCGGTCT-GGGGTCCC 8014 GC_	A	I	
	AGGTGGT TTGGGGTCC			
	TCCGCCA GACCCCAGG			
	CCC _ I			
GAM505 TGFB1	GGGAGGCGGTCT-GGGGTCCC 8014 T C	A		
	GG AGGTGGT TTGGGGTCCCT			
	CC TCCGCCA GACCCCAGGGG			
	- - -			
GAM505 THRA	TGGCAGGTGGGAGGGCTGGGG 8022	TA__	TCCCTC	
	TGGCAGGTGG TTGGGG			
	ACCGTCCACC GACCCC			
	CTCCC II CTC			
GAM505 THRA	TGGCAGGTGGGAGGGCTGGGG 8022	TA__	III	
	TGGCAGGTGG TTGGG			
	ACCGTCCACC GACCC			
	CTCCC CII			
GAM505 TIMM44	GCAGGTGGTGTTGCGGTGCCTC 8003	A G C I		
	CAGGTGGT TTG GGT CCT			
	GTCCACCA AAC CCA GGA			
	C G C I			
GAM505 TIMM44	GCAGGTGGTGTTGCGGTGCCTC 8003 TGGC	A G C		
	AGGTGGT TTG GGT CCTC			
	TCCACCA AAC CCA GGAG			
	C G C			
GAM505 TNXB	ACCACAAATGCAGCCACTGCTG 7994 TGACCT	_	I	
	CAAGTGT CCACTGCTG			
	GTTTACG GGTGACGAC			
	GT__ TC A			
GAM506 ATP7B	CAGACAAGGCCGCGTGCTGCA-GGGC 8035 GC _	_ AT__	GII	
	AGA AAGGCCGCG GC GGGCG			
	TCT TTCCGGCGC CG CCCGT			
	_ G A ACGT III			
GAM506 B3GAT1	AGAAAAGAACAGGCATGGGC 8030 GCA	GC C	G	
	GAAAG CG GGCATGGGC			

	TTTTC GT CCGTACCCG		
	___ TT _ G		
GAM506 BARHL1	CAGAAAGGCGGGCGGAAGGGGC	8036 GC	C_ CAT GG
	AGAAAGGC GCGG GGGC		
	TCTTTCCG CGCC CCCG		
	___ CC TTC GI		
GAM506 C1orf6	GAGAGGCAGGAGGCATGGGC	8041 GCAGAA	CGC_ G
	AGGC GGCATGGGC		
	TCCG CCGTACCCG		
	_____ TCCT G		
GAM506 COL1A1	GCAGAAAGG--GCAGCATTGG	8048	CC _ GCG
	GCAGAAAGG GCGGCAT GG		
	CGTCTTTCC CGTCGTA CC		
	___ A		
GAM506 DUSP7	GCAGAAAGG-AGCGTCCTGG	8047	CC GCA GCG
	GCAGAAAGG GCG TGG		
	CGTCTTTCC CGC ACC		
	T_ AGG		
GAM506 DVL1	CAGGAAGGCCGCGATGTGTGCG	8040 GC A	CA G G
	AG AAGGCCGCGG TG GCG		
	TC TTCCGGCGCT AC CGC		
	___ C AC A G		
GAM506 EVX1	AGAAAGGCCGGGTGCCTGGGAGG	8028 GCAG	CG_ A C I
	AAAGGCCG GC TGGG GG		
	TTTCCGGC CG ACCC CC		
	_____ CCA G T C		
GAM506 FANCC	AGGAAGGAAGGGGCATGGGC	8033 GCAGA	CCGC
	AAGG GGCATGGGCG		
	TTCC CCGTACCCGT		
	C_____ TTCC		
GAM506 GPC1	GCAGAAAGGCAGGCGAGGC	8046	CGC AT G
	GCAGAAAGGC GGC GGGC		
	CGTCTTTCCG CCG TCCG		
	T_ C_ I		
GAM506 HR	GAAAGGCCGAGG--GGCCGG	8043 GCAGAA	C CAT G
	AGGCCG GG GG C		
	TCCGGC CC CC G		
	_____ T _ G		
GAM506 HRB	GGCCGCGGCGCCAAGGGAGG	8050 GCAGAAAG	C CAT_ G
	GCCG GG GG CG		

	CGGT CC CC GC		
	CG_____ T CTCCT G		
GAM506 HUNK	CAGAAAGGCTGGGGC-TGAGC 8038 GC	CGC A G	
	AGAAAGGC GGC TGGGC		
	TCTTTCCG CCG ACTCG		
	___ ACC _ G		
GAM506 IKBKB	GCAGAAAGGACCACAG-ATGG 8045	_ C GCG	
	GCAGAAAGG CCGCGG ATGG		
	CGTCTTTCC GGTGTC TACC		
	T _ III		
GAM506 KCNAB2	GCAGAAAGGGGCCCTCG--ATGGGC 8044	_ G_ GC GGI	
	GCAGAAA GGCC CG ATGGGC		
	CGTCTTT CCGG GC TACCCG		
	CC GA _ III		
GAM506 MAP3K9	AGAAAGGCC-CTGCA-GGGC 8031 GCAG	GCG T	
	AAAGGCC GCA GGGC		
	TTTCCGG CGT CCCG		
	___ GA_ _		
GAM506 MCM5	GCAGAAAGGAGGGTGCCTGGG 8049	CCGCG A CGG	
	GCAGAAAGG GC TGGG		
	CGTCTTTCC CG ACCC		
	TCCCA G III		
GAM506 NR1I2	CAGTAAAGCAGGGGCATGGGC 8039 GC A	CGC GG	
	AG AAGGC GGCATGGGC		
	TC TTTCG CCGTACCCG		
	_ A TCC GI		
GAM506 POU2AF1	AGGCCACCAGGGCATGGGC 8034 GCAGAAAGG C		
	CCG GGCATGGGCG		
	GGT CCGTACCCGT		
	_____ C		
GAM506 RNH	CAGAAAGGCCAC--CATGGGC 8037 GC	GG	
	AGAAAGGCCGC CATGGGCG		
	TCTTTCCGGTG GTACCCGT		

GAM506 SRP46	GAAAGGCCGGGCGGAGAGGCGG 8042 GCAGAA	C AT__	
	AGGCCG GGC GGGCGG		
	TCCGGC CCG TCCGCC		
	_____ CCTC		
GAM506 UBQLN2	AGAAAGGCCTGGGCGTAGGC 8032 GCAG	GC A G	
	AAAGGCC GGC TGGGC		

	TTTCCGG CCG ATCCG	
	____ AC C G	
GAM506 WHSC1	AGAAAGGC--CGGCCTGAGGACGG 8029 GCAG GC AT__	
	AAAGGCC GGC GGGCGG	
	TTTCCGG CCG CCTGCC	
	____ _ GACT	
GAM507 ATP1B2	GGAAAAGGATGTGAGGCTCAGAC 8062 TGGC TT T_ TI	
	AAAG TGT GGCTCAGAC	
	TTTC ACA CCGAGTCTG	
	CT__ CT CT TI	
GAM507 BNC	TGGTAACAGGTTGTTGGCT 8064 CAA_ T CAGAC	
	TGG AG TTGTTGGCT	
	ACC TC AACAACCGA	
	ATTG C IIITC	
GAM507 CIAS1	AAAGTTCTCCTGTTGGCTC 8053 TGGCAAAG A C	
	TTTGTTGGCTC GA	
	GGACAACCGAG CT	
	AAGA____ _ A	
GAM507 COL10A1	GGGAAGGTTTGTGG-TCTGA 8063 T C A C A C	
	GG AA GTTTGTGG TC GA	
	CC TT CAAACAACC AG CT	
	_ _ C _ A A	
GAM507 CREBL2	CACAGTGTGTTTCTGGCTCAGA 8056 TGGCAA G CT	
	GTTT TTGGCTCAGA	
	CAAA GACCGAGTCT	
	TCACA__ _ CG	
GAM507 CRH	TGGCATTCTCT-TTGGCTCAGAC 8070 AAG G T	
	TGGCA TTT TTGGCTCAGAC	
	ACCGT GAG AACCGAGTCTG	
	AA_ A I	
GAM507 FMO1	TGGGAAAGAGGTATGATGGCTCAGA 8065 C TT__ T CTII	
	TGG AAAG TG TGGCTCAGA	
	ACC TTTC AC ACCGAGTCT	
	C TCCAT T IIIT	
GAM507 HR	TGGCACTGTGGTTGTTGGCT 8066 AA _ CAGAC	
	TGGCA GT TTGTTGGCT	
	ACCGT CA AACAACCGA	
	GA CC IIITC	
GAM507 LMO2	GGGAAGGTCTATTTTGGCTCAGGCT 8058 T C A _ ACTII	
	GG AA GTTTGT TGGCTCAG	

	CC TT CAGATA ACCGAGTC	
	_ _ C AA CGAAI	
GAM507 MCL1	CAAAGTTTGTGTTGCTGAACT 8055 TGGCAAA	G C I
	GTTTGTG CT AGACT	
	CAAACAAC GA TTTGA	
	TCAAA_ _ C C	
GAM507 MN1	TGGCAAAGTGTGATGACTCA 8067	_ T GACT
	TGGCAAAGT TTG TGGCTCA	
	ACCGTTTCA AAC ACTGAGT	
	C T IIIT	
GAM507 NR2F2	GCAAAGTTTTGTGCTGATGGCT 8057 TGGC	_ _ CAGAC
	AAAGTTT GT TGGCT	
	TTTCAAA CA ACCGA	
	_ _ A GCT ACII	
GAM507 PTHLH	AAAGTGTGAATGGCTCAGA 8054 TGGCAAA TTGT	C
	GT TGGCTCAGA	
	CA ACCGAGTCT	
	A_ _ CTT_ T	
GAM507 RFC2	GGGACAGTCATGTTGGCTCAGCCT 8060 T AA	_ A I
	GGCA GTT TGTTGGCTCAG CT	
	CTGT CAG ACAACCGAGTC GG	
	C _ T _ A	
GAM507 SIAT8E	GGCAAAGTTTCTGGTTGGC 8061 TG	_ TCAGAC
	GCAAAGTTT GTTGGC	
	CGTTTCAAA CAACCG	
	_ GAC CIITC	
GAM507 SLC16A2	TGGCAA-GTTACTGTTGGCTC 8068 A	_ AGAC
	TGGCAA GTT TGTTGGCTC	
	ACCGTT CAA ACAACCGAG	
	_ TG IIIT	
GAM507 SORBS1	GGGACAGTCTTGGTAGCTCAGACT 8059 T AAG T	I
	GGCA TTTG TGGCTCAGACT	
	CTGT GAAC ATCGAGTCTGA	
	C CA_ C C	
GAM507 ZNF175	TGGCACAGTTTGTGACTC 8069 A	AGAC
	TGGCA AGTTTGTGACTC	
	ACCGT TCAAACAACTGAG	
	G IIIT	
GAM508 ALCAM	TGTGTGTCTATATGCATCTGTGA 8090 TGGCTGTG	_ C I
	GTCTA TGCATCT TGA	

		CAGAT ACGTAGA ACT		
		A_____ AT C A		
GAM508 ATF7	TGGCTGTGG	---ATGCATC 8084	TCT TC	
	TGGCTGTGG	ATGCATC		
	ACCGACACC	TACGTAG		
		_____ II		
GAM508 ATP10C	TGGCTGTGG	--GATGCATATTCCTGA 8086	TCT C__ I	
	TGGCTGTGG	ATGCAT TCTGA		
	ACCGACACC	TACGTA GGA		
		C__ TAA I		
GAM508 CELSR1	TGGCTGTGG	-CTTTGTCCCTCTG 8088	T A CA A	
	TGGCTGTGG	CT TG TCTCTG		
	ACCGACACC	GA AC GGAGAC		
		_ A AG I		
GAM508 CIT	GCTGTGGTCTCT	TTCCAGCTCTG 8077 TGGC	ATG_ T A	
	TGTGGTCT	CA CTCTG		
	ACACCAGA	GT GAGAC		
		_____ GAAG C A		
GAM508 CRAT	TGGCTGTGGT	---GGCATC 8085	CTAT TC	
	TGGCTGTGGT	GCATC		
	ACCGACACCA	CGTAG		
		C__ II		
GAM508 DLG5	GCTG-GGTC-A-GCATCTCTG	8078 TGGC T TAT		
	TG GGTC	GCATCTCT		
	AC CCAG	CGTAGAGA		
		_____ T__		
GAM508 GABRE	TGGCTGTGGT	-TTTG-AACACTGA 8089	CTAT_ TCT	
	TGGCTGTGGT	GCA CTGA		
	ACCGACACCA	TGT GACT		
		AACT _____		
GAM508 GABRP	TGGCCGAGGAATGTGCATCTCTG	8087 T TCTA AI		
	TGGCTG GG	TGCATCTCTG		
	ACCGGC CC	ACGTAGAGAC		
		T TTAC II		
GAM508 INHBC	GCTGTGGTCT	---CAACTCTG 8079 TGGC	ATG T	
	TGTGGTCT	CA CTCT		
	ACACCAGA	GT GAGA		
		_____ T		
GAM508 IRAK4	GGCTGTGGT-TAT-CATCT	8080 TG C G CT		
	GCTGTGGT	TAT CATCT		

	CGACACCA ATA GTAGA		
	— — — CI		
GAM508 KRT16	GGCTGTGGTAGAGGCAGCTC	8081 TG	CTAT T TG
	GCTGTGGT GCA CTC		
	CGACACCA CGT GAG		
	— TCTC C TI		
GAM508 PCDHB11	GGCTGAGGGGAGTGCATCTCT	8082 TG	T TCTA GA
	GCTG GG TGCATCTCT		
	CGAC CC ACGTAGAGA		
	— T CCTC AI		
GAM508 SLC7A7	CTGTGGTCTGATGCTCCTC	8074 TGGCTG	_ AT G
	TGGTCT ATGC CTCT		
	ACCAGA TACG GAGG		
	— C AG A		
GAM508 TRO	CTGTGGTCTCAGTCTGTATATCTGA	8073 _ G	A C CTGAII
	TGG CT TGGTCT TG ATCT		
	ACC GA GTCAGA AT TAGA		
	A _ C A CTTTAI		
GAM508 UBQLN3	GCTGTGGTCCCGTCCTTCTCT	8076 TGGC	ATGCA_ GA
	TGTGGTCT TCTCT		
	ACACCAGG AGAGA		
	— GCAGGA AA		
GAM508 VDR	GGCAGCGGTGGAGGCATCTCTG	8083 T_ T	TCTAT A
	GGC GTGG GCATCTCTG		
	TCG CACC CGTAGAGAC		
	CG C TC_ C		
GAM508 WFDC1	CTGTC-TCTAAGCATCTCTG	8075 TGGCTGTGG	T
	TCTA GCATCTCTG		
	AGAT CGTAGAGAC		
	AG_ T		
GAM509 ADRBK1	TGGGCGGGGGTACACTGATGG	8107 GAGA	AG_ I
	GGCG ACACTGATG		
	CCGC TGTGACTAC		
	C_ CCCC A I		
GAM509 ADRBK1	TGGGCGGGGGTACACTGATGG	8107 TGAGA	AG_ CAC
	GGCG ACACTGATGG		
	CCGC TGTGACTACC		
	AC_ CCCC III		
GAM509 AP2M1	GAGGGAGGAGACACTGATG	8096 GA	C_ II
	GAGG GAGACACTGAT		

	CTCC CTCTGTGACTA			
	___ CTC CI			
GAM509 AP2M1	GAGGGAGGAGACACTGATG	8096	TGA CG	GCA
	GAGG AGACACTGATG			
	CTCC TCTGTGACTAC			
	TCC ___ AII			
GAM509 AVP	GAGGCGAGACGCGGCCGCCAC	8102	ACT A	AI
	AGGCGAGAC G TGGC			
	TCCGCTCTG C GCCG			
	___ GC			
GAM509 AVP	GAGGCGAGACGCGGCCGCCAC	8102	TGAGAG	ACTGA G
	GCGAGAC TG CAC			
	CGCTCTG GC GTG			
	___ CGCCG G			
GAM509 B3GNT3	TGACTGGC-AGACACTGA-GGC	8108	GA G	T A
	TGA GGC AGACACTGA GGC			
	ACT CCG TCTGTGACT CCG			
	GA _ _ I			
GAM509 B3GNT3	TGACTGGC-AGACACTGA-GGC	8108	_ GA G	T I
	GA GGC AGACACTGA GG			
	CT CCG TCTGTGACT CC			
	A GA _ _ I			
GAM509 BTD	AGAGGA-AGACACTGAGGG	8093	C	TGI
	AGAGG GAGACACTGA			
	TCTCC TTCTGTGACT			
	_ CCC			
GAM509 BTD	AGAGGA-AGACACTGAGGG	8093	TGAG C	T C
	AGG GAGACACTGA GG			
	TCC TTCTGTGACT CC			
	___ _ C T			
GAM509 CYP2F1	TGAGCTGCAGGAGACACTG	8103	AG _	ATGGCA
	TGAG GC GAGACACTG			
	ACTC CG CTCTGTGAC			
	GA TC IIICAC			
GAM509 CYP2F1	TGAGCTGCAGGAGACACTG	8103	AG _	
	TGAG GC GAGACACT			
	ACTC CG CTCTGTGA			
	GA TC CII			
GAM509 EIF1A	TGAAAAGAGCAGACACTGAT	8104	_ G	GGCA
	TGAGA GGC AGACACTGAT			

	ACTTT TCG TCTGTGACTA			
	TC _ IIIC			
GAM509 EIF1A	TGAAAAGAGCAGACACTGAT 8104	_ G	II	
	TGAGA GGC AGACACTGA			
	ACTTT TCG TCTGTGACT			
	TC _ AI			
GAM509 FTSJ2	TGGGAGCCCAGACACTGAT 8105	A GCG	GGCA	
	TG GAG AGACACTGAT			
	AC CTC TCTGTGACTA			
	C GGG IIIC			
GAM509 FTSJ2	TGGGAGCCCAGACACTGAT 8105	A GCG	II	
	TG GAG AGACACTGA			
	AC CTC TCTGTGACT			
	C GGG AI			
GAM509 GALR1	TGAGAGGCGA-AAACAGCTCGGC 8106	_ _ GA	AC	
	TGAGAGGCGAGA CA CT TGGC			
	ACTCTCCGCTTT GT GA GCCG			
	T C _ II			
GAM509 GALR1	TGAGAGGCGA-AAACAGCTCGGC 8106	_ _ GATGGI		
	GAGAGGCGAGA CA CT			
	CTCTCCGCTTT GT GA			
	T C GCCII			
GAM509 GRB10	GAGAGATTATACTGATGGGAC 8098	CGAG	CAI	
	AGAGG ACACTGATGG			
	TCTCT TGTGACTACC			
	AATA CTI			
GAM509 GRB10	GAGAGATTATACTGATGGGAC 8098	T GGCGAG	C I	
	GAGA ACACTGATGG AC			
	CTCT TGTGACTACC TG			
	T AATA_ C A			
GAM509 INSM1	GAGGCGAGAC-CAGACCGCA 8099	_ ACT G I		
	AGGCGAGAC GAT GC			
	TCCGCTCTG CTG CG			
	C GT_ G I			
GAM509 INSM1	GAGGCGAGAC-CAGACCGCA 8099	TGAGAG	ACT G	
	GCGAGAC GAT GCA			
	CGCTCTG CTG CGT			
	_ GT_ G			
GAM509 ITPR1	AGGAGATGACACTGATTGGC 8095	C _ _ III		
	AGG GA GACACTGAT GG			

	TCC CT CTGTGACTA CC		
	T A A GII		
GAM509 ITPR1	AGGAGATGACACTGATTGGC	8095 TGAGAGGCGA	_ A
	GACACTGAT GGC		
	CTGTGACTA CCG		
	CTA_____ A G		
GAM509 MAGEB4	GAGTGG-GAGACACTGCTGGACAC	8097 AGA C	A _ I
	GG GAGACACTG TGG CA		
	CC CTCTGTGAC ACC GT		
	TCA _ G T I		
GAM509 MAGEB4	GAGTGG-GAGACACTGCTGGACAC	8097 TGAGA C	A _ I
	GG GAGACACTG TGG CAC		
	CC CTCTGTGAC ACC GTG		
	TCA_ _ G T G		
GAM509 MAN2A1	GAGGCGAGACTC-GCCGGCA	8100_ ACTGA I	
	AGGCGAGAC TGGC		
	TCCGCTCTG GCCG		
	C AGCG_ I		
GAM509 MAN2A1	GAGGCGAGACTC-GCCGGCA	8100 TGAGAG	ACTGA
	GCGAGAC TGGCA		
	CGCTCTG GCCGT		
	_____ AGCG_		
GAM509 PITX2	AGATGTCAGACACTGAGGACA	8094 GAGGCG	T I
	AGACACTGA GGC		
	TCTGTGACT CTG		
	CTACAG C I		
GAM509 PITX2	AGATGTCAGACACTGAGGACA	8094 TGAGAGGCG	T C
	AGACACTGA GGCA		
	TCTGTGACT CTGT		
	TACAG_____ C A		
GAM509 SUFU	GAGGCGA---ACTGATGGCAC	8101 GAC	I
	GAGGCGA ACTGATGGC		
	CTCCGCT TGA CTACCG		
	_____ T		
GAM509 SUFU	GAGGCGA---ACTGATGGCAC	8101 TGAGAG	GAC
	GCGA ACTGATGGC		
	CGCT TGA CTACCG		

GAM510 AIM1	AAGAACC AAAATTACAGGCCT	8115 TATAAAGAAAG	_
	AAAATTACAG CCT		

	TTTTAATGTC GGA		
	TGG_____C		
GAM510 ATP8A2	TATAACAAATGGAAATTACAGACT 8135	A AGA	C I
	TATAA GAA AAATTACAG CT		
	ATATT TTT TTTAATGTC GA		
	G ACC T I		
GAM510 BIG1	AAAGAAAAGAAAATGACAGC 8111 TATAAA	T C	
	GAAAGAAAAT ACAGC		
	TTTTCTTTTA TGTCG		
	C_____C T		
GAM510 CALB1	ATATA-AAAGAAAA-TACAGCCT 8124 TATAAA	T	
	GAAAGAAAAT ACAGCCT		
	TTTTCTTTTA TGTCGGA		
	ATA_____		
GAM510 CD34	TAGAGAAAGAAAA-TACAG 8126 TATAA	T C	
	AGAAAGAAAAT ACAG		
	TCTTTCTTTTA TGTC		
	C_____ _ C		
GAM510 CDY1	TATAAAGGAAAAGAAAATCA-AGC 8130	_____ C CTI	
	TATAAAG AAAGAAAATTA AGC		
	ATATTTC TTTCTTTTAGT TCG		
	CT _		
GAM510 CYP4F3	TATGAAAGAAAGAAACTT-CAG 8127	_ A A CCT	
	TAT AAAGAAAGAAA TT CAG		
	ATA TTTCTTTCTTT AA GTC		
	C G _		
GAM510 DMD	TATAAAGGAAAAAGAAAATAAC 8129	_____ T AGCCT	
	TATAAAG AAAGAAAAT AC		
	ATATTTC TTTCTTTTA TG		
	CTT T TC		
GAM510 DUSP4	AAAGAAAGAAAAT-CAGC 8113 TATAAA	TTA	
	GAAAGAAAA CAGC		
	CTTTCTTTT GTCG		
	_____TA_		
GAM510 EYA4	AAAGAAAGAAAAATTGCATCC 8112 TATAAA	TTA_ G T	
	GAAAGAAAA CA CC		
	CTTTCTTTT GT GG		
	_____TAAC A T		
GAM510 FZD10	AAGAAAGAAAAACACAACC 8116 TATAAAGA	T	
	AAGAAAA TACAGCC		

	TTCTTTT GTGTTGG		
	_____ T		
GAM510 HEPH	ATAAAGAAAGAAATATCCAG 8122 TA	ATTA	CC
	TAAAGAAAGAAA CAG		
	ATTTCTTTCTTT GTC		
	_____ ATAG TI		
GAM510 HHLA1	TAAAG---GAAAATTACAG 8125 TATAAAGAAA		
	GAAAATTACAG		
	CTTTTAATGTC		
	TTC_____		
GAM510 HLF	AAGAAAGAAAGAAACAACC 8118 TATA	ATT	A
	AAGAAAGAAA AC GCC		
	TTCTTTCTTT TG CGG		
	_____ GT_ G		
GAM510 IL11	TATATAGAAAGAAAAACACA 8132 A	T	GCC
	TATA AGAAAGAAAA TACA		
	ATAT TCTTTCTTTT GTGT		
	A T		
GAM510 LEF1	AAAGAAAGAAAAATGAAGC 8114 TATAAA	TTAC	C
	GAAAGAAAA AGC		
	CTTTCTTTT TCG		
	_____ TACT T		
GAM510 LYPLA1	ATAAAGCAA-AAAATTACA 8121 TA	AA	C
	TAAAG AGAAAATTACAG		
	ATTTC TTTTTAATGTT		
	_____ G_ I		
GAM510 MAP2	TATAAAGAATGAATATAACA 8131	A A T	GCC
	TATAAAGAA GAA AT ACA		
	ATATTTCTT CTT TA TGT		
	A A T		
GAM510 MEN1	ATATAGAAAGAACTCCTACA 8120 TATAA	AT__	CCT
	AGAAAGAAA TACAG		
	TCTTTCTTT ATGTT		
	ATA__ GAGG		
GAM510 MEN1	ATAAAGAAAGGTGAGTACAG 8123 TA	AAAAT	CC
	TAAAGAAAG TACAG		
	ATTTCTTTC ATGTC		
	_____ CACTC TI		
GAM510 OGT	TATAAAGAAAAAAAATCCAG 8134	TTA	CCT
	TATAAAGAAAGAAAA CAG		

	ATATTTCTTTTTTTT GTC			
	TAG III			
GAM510 RGR	TAAAAAGTCAAAAAATTACAG	8133	TAT AA	CCT
	AAAG AGAAAATTACAG			
	TTTC TTTTTTAATGTC			
	ATT AG III			
GAM510 TFCP2	TATATAAGAAA-AAAATTACAG	8128	_ A	CCT
	TATA AAGAAAGAAA TTACAG			
	ATAT TTCTTTTTTTT AATGTC			
	A _ III			
GAM510 TYRP1	ATAAAGTGAAAGAAAA-TACAG	8119	TATAAA	T CCT
	GAAAGAAAAT ACAG			
	CTTTCTTTTA TGTC			
	ATTTCA _ AII			
GAM510 ZIC1	AAGAAAGAAAGAAAAAGCC	8117	TATA	TTAC
	AAGAAAGAAAA AGCC			
	TTCTTTCTTTT TCGG			

GAM511 FAAH	CCATGCAGGACATTTCCTT	8143	T _ A	II
	CC TG AG ACATTTCCT			
	GG AC TC TGTAAGGA			
	T G C AI			
GAM511 FAAH	CCATGCAGGACATTTCCTT	8143	TGAGACCTTG A	
	AG ACATTTCCTT			
	TC TGTAAGGAA			
	G_____ C			
GAM511 GABRE	AGAACTTTGGACAACATTTC	8141	C _ G	III
	AGA CTT GA AACATTTC			
	TCT GAA CT TTGTAAAG			
	T AC G GII			
GAM511 GABRE	AGAACTTTGGACAACATTTC	8141	TGA C _ G	TTC
	GAC TTG A AACATTTC			
	TTG AAC T TTGTAAAGG			
	_____ A C G CGI			
GAM511 GPC5	AGACATTCAGA-CATTTCCTTC	8142	_ C G A	I
	GAC TT AGA CATTTCCTT			
	CTG AA TCT GTAAAGGAA			
	T T G _ I			
GAM511 GPC5	AGACATTCAGA-CATTTCCTTC	8142	TGAG C G A	
	AC TT AGA CATTTCCTTC			

	TG AA TCT GTAAAGGAAG		
	____ T G _		
GAM511 PINX1	TGAGAGCCACGATTGAGAACATT 8144	_ ____	TCCTTCI
	TGAGA CC TTGAGAACATT		
	ACTCT GG AACTCTTGTA		
	C TGCT IIICTTC		
GAM511 PINX1	TGAGAGCCACGATTGAGAACATT 8144	_ ____	IIIA
	TGAGA CC TTGAGAACAT		
	ACTCT GG AACTCTTGTA		
	C TGCT AIII		
GAM511 PKD2L1	TGAATCCT-GAGTTCATTTCTT 8148	A T AA	C
	TGAG CCT GAG CATTTCTT		
	ACTT GGA CTC GTAAAGGAA		
	A _ AA I		
GAM511 PKD2L1	TGAATCCT-GAGTTCATTTCTT 8148	_ A T AA	I
	GAG CCT GAG CATTTCTT		
	CTT GGA CTC GTAAAGGA		
	A A _ AA I		
GAM511 RNGTT	ACCTTGAGAA-TTTTCCCTC 8139	_ CA	I
	CCTTGAGAA TTTCTT		
	GGAACTCTT AAAGGGA		
	T A_ I		
GAM511 RNGTT	ACCTTGAGAA-TTTTCCCTC 8139	TGAGACCT	CA
	TGAGAA TTTCTT		
	ACTCTT AAGGGAG		
	____ AA		
GAM511 ST7	TGAGACCTTGATATAATTT 8147	GAACATTII	
	TGAGACCTTGA		
	ACTCTGGA		
	ATATTAAAI		
GAM511 ST7	TGAGACCTTGATATAATTT 8147	GAACATTTCTT	
	TGAGACCTTGA		
	ACTCTGGA		
	ATATTAAAIIC		
GAM511 TEM7R	TGAGACATCAGAGAACATTT 8146	CTT_	CCTT
	TGAGAC GAGAACATTT		
	ACTCTG CTCTTGTA		
	TAGT IIIC		
GAM511 TEM7R	TGAGACATCAGAGAACATTT 8146	CTT_	II
	TGAGAC GAGAACATT		

	ACTCTG CTCTTGTA			
	TAGT AI			
GAM511 TGFBI	TGAGACACATTTGACAGAACATTTTC 8145	C___	CTTCII	
	TGAGAC TTGA GAACATTTTC			
	ACTCTG AACT CTTGTAAAG			
	TGTA GT CTT			
GAM511 TGFBI	TGAGACACATTTGACAGAACATTTTC 8145	GA___	CTTG	I
	GAC AGAACATTT			
	CTG TCTTGTA			
	TGTAA ___ I			
GAM511 UBE4A	ACCTTTA--ACATTTCCCTTC 8140	GAG	I	
	ACCTT AACATTTCCCT			
	TGGAA TTGTAAAGGA			
	A___ A			
GAM511 ZNF264	ACCTTGA-AACATTTCCCTTC 8138	A	I	
	CCTTGAGA CATTTCCCTT			
	GGAACCTT GTAAAGGGA			
	___ A			
GAM511 ZNF264	ACCTTGA-AACATTTCCCTTC 8138	TGAGACCT	A	
	TGAGA CATTTCCCTT			
	ACTTT GTAAAGGGA			

GAM512 ACAD8	TGAATAGCA-CTCCTGGACCAC 8160	A T _	CA	
	TGAA AGC GCTC TGGACCAC			
	ACTT TCG TGAG ACCTGGTG			
	A _ G II			
GAM512 GABRB1	AAGAGCTGATAACCTGGACCAC 8151	TGAAA	C___	CAI
	AGCTG TCTGGACCAC			
	TCGAC GGACCTGGTG			
	C___ TATT CCI			
GAM512 HOXD4	GAAAAGCTGCTCTATGTCACCA 8157	TG	GAC	I
	AAAAGCTGCTCTG CACCA			
	TTTTCGACGAGAT GTGGT			
	___ ACA C			
GAM512 LEF1	GAAAAGCTGCTCAGCTGCCCCAC 8154	TG	___ GA	CAI
	AAAAGCTGCTC TG CCAC			
	TTTTCGACGAG AC GGTG			
	___ TCG GG TII			
GAM512 LNK	TGTAAAGCTGCTGTAAACCA 8161	A	C	CCA
	TG AAAGCTGCT TGGACCA			

	AC TTTTCGACGA ATTTGGT	
	A C III	
GAM512 NCOA3	GAAAAGCTGTGGTGCCTACC 8155 TG CTC G C A	
	AAAAGCTG TG AC ACC	
	II	
	TTTTCGAC AC TG TGG	
	___ ACC G A G	
GAM512 P2RY2	GAACAGTTGACTCTGGACCAC 8153 TGAAA C _ CA	
	AG TG CTCTGGACCAC	
	TC AC GAGACCTGGTG	
	TTG___ A T TI	
GAM512 PIP5K1B	AAAAGCTGCTTAGTAGCAACA 8152 TGAA C ACCACCA	
	AAGCTGCT TGG	
	TTCGACGA ATC	
	___ _ ATCGTTG	
GAM512 PRKG1	TGAAAGGCTTTGCTTCAGGACCACCA 8158 A _ _ T III	
	TGAAA GCT GCT C GGACCACCA	
	ACTTT CGA CGA G CCTGGTGGT	
	C AA A T III	
GAM512 PYGB	GAAAAGCAG---GGACCACCA 8156 TG TGCTCT	
	AAAAGC GGACCACC	
	TTTTCG CCTGGTGG	
	___ TC___	
GAM512 REQ	TGAAAAGCTCCTTGTGGAC 8159 G C_ CACC	
	TGAAAAGCT CT TGGAC	
	ACTTTTCGA GA ACCTG	
	G AC IIIA	
GAM513 AGRN	ACAAAGAAGATCCTGGTGTCC 8168 TGAC C A_ _ T	
	AAAGAAG TTC GT TCTCC	
	TTTCTTC AGG CA AGGGG	
	___ T AC C I	
GAM513 ATP8A2	TGACAAAGAA--TTCAATT 8184 GC CTC	
	TGACAAAGAA TTCAGTT	
	ACTGTTTCTT AAGTTAA	
	___ III	
GAM513 BCAT1	ACAAAGAAGGTACACTTCT 8167 TGAC CTT G CC	
	AAAGAAG CA TTCT	
	TTTCTTC GT AAGA	
	___ CAT G TA	
GAM513 CLECSF5	AAAGAAGC-TCAGTT-TCC 8164 TGACAAAG T CT	
	AAGCT CAGTT C	
	I	

		TTCGA GTCAA G		
		_____ _ AG		
GAM513 EYA1		GACAAAGAAACAGCAGAATCTC 8179 TG	TT T_ CT	
		ACAAAGAAGC CAG TCTC		
		TGTTTCTTTG GTC AGAG		
		_____ TC TT TI		
GAM513 FBXL7		CACAGAA---TCAGTTCTCCT 8174 TGACAAAGA CT		
		AG TCAGTTCTC		
		TC AGTCAAGAG		
		_____ TT		
GAM513 FER		GACAAAGAAGATACTTGAG 8177 TG	___ C TTCTCC	
		ACAAAGAAG CTT AG		
		TGTTTCTTC GAA TC		
		_____ TAT C TIIITC		
GAM513 GALNT1		CATAGAAGGTACAGTTCTCC 8172 TGACAA CTT		
		AGAAG CAGTTCTCC		
		TCTTC GTCAAGAGG		
		_____ CAT		
GAM513 GPR85		AACAA-CTTCCCAGTTCTCCT 8165 TGACAAAGAAGC		
		TTCAGTTCTCC		
		GGGTCAAGAGG		
		GAA_____		
GAM513 KMO		TGACAAAGAGGAGTTTCAG 8180	___ C TTCTCC	
		TGACAAAGA AG TTCAG		
		ACTGTTTCT TC AAGTC		
		CC A IIITCC		
GAM513 LFG		CAAAGAAGC--CATTTCTC 8170 TGACAA TCAG		
		AGAAGCT TTCTC		
		TCTTCGG AAGAG		
		_____ TA_		
GAM513 MEST		TGACAAAGAGGACTCAGCTCT 8185	A_ T CCT	
		TGACAAAGA GCT CAGTTCT		
		ACTGTTTCT TGA GTCGAGA		
		CC _ III		
GAM513 NAV2		CACAGCAACTTGAGTTCTCCT 8176 TGACAA A C		
		AG AGCTT AGTTCTCCT		
		TC TTGAA TCAAGAGGA		
		_____ G C		
GAM513 NUP155		TGA-AAAGAAGCTGCTTGCTGTTCTCC8183 C	TCA_____ TII	
		TGA AAAGAAGCT GTTCTCC		

	ACT TTTCTTCGA CAAGAGG	
	CGAACGA III	
GAM513 NXF2	GACAAAGAAGACATCGGAGGGCTCCT 8178 TG	_ T _ TT II
	ACAAAGAAG C TC AG CTCCT	
	I I I	
	TGTTTCTTC G AG TC GAGGA	
	T T CC CC AI	
GAM513 OLR1	TGACAAAGAATAGCTTAAATTC 8181	_ C TCCT
	TGACAAAGA AGCTT AGTTC	
	ACTGTTTCT TCGAA TTAAG	
	TA T IIIT	
GAM513 PCDHB16	CACAGAAGCTTCATGTATCC 8171 TGACAA	_ _
	AGAAGCTTCA GT TCTCC	
	TCTTCGAAGT CA AGGGG	
	A T	
GAM513 SAS	CACAGAAGCTTCCCATATCCT 8175 TGACAA	A _ CT
	AGAAGCTTC GTTCTC	
	TCTTCGAAG TAGGAG	
	GGTA AA	
GAM513 SHMT1	AGAAGCTAATTCAGTTCTCCT 8169 TGACAAAGAAGC	
	TTCAGTTCTCCT	
	AAGTCAAGAGGA	
	ATT	
GAM513 SMARCA3	CAAAGAAGC--AAGCTGTCCT 8173 TGACAA	TTCA _
	AGAAGC GTTCTCC	
	TCTTCG CAGGAGG	
	TTCGA	
GAM513 TIM3	TGAAAAATATAGCTTCAGTT 8182 C GA _	CTCC
	TGA AAA AGCTTCAGTT	
	ACT TTT TCGAAGTCAA	
	T ATA IIIT	
GAM513 TLL1	TGAAAGAGACCTTTTCAGTTCTC 8186 TG C AG _	CT
	A AAAGA CT TCAGTTCTC	
	I	
	A TTTCT GG AGTCAAGAG	
	_ C CT AA II	
GAM513 TXK	ACACAACAGTCTTCAGTTCTTCT 8166 TG AGAAG	C I
	ACAA CTTTCAGTTCT CT	
	TGTT GAAGTCAAGA GA	
	_ GTCA _ A C	
GAM514 AIRE	TCTCAGCTCACTGCAACCTC 8194	G A GGC
	TCTCAGCTCA TG AACCTC	

	AGAGTCGAGT AC TTGGAG		
	G G III		
GAM514 AIRE	TCTCAGCTCACTGCAACCTC 8194	G A I	
	CTCAGCTCA TG AACCT		
	II		
	GAGTCGAGT AC TTGGA		
	G G I		
GAM514 CARKL	TCTCAGCTCACTGCAACCTCTGCC 8202	G A G I	
	CTCAGCTCA TG AACCTC GC		
	II II		
	GAGTCGAGT AC TTGGAG CG		
	G G A I		
GAM514 CARKL	TCTCAGCTCACTGCAACCTCTGCC 8202	G A G I	
	TCTCAGCTCA TG AACCTC GCC		
	II III		
	AGAGTCGAGT AC TTGGAG CGG		
	G G A I		
GAM514 CKAP1	AGC-CA-TGAAACCTCTGC 8189	CA GGI	
	AGCT GTGAAACCTC		
	TCGG TACTTTGGAG		
	— ACG		
GAM514 CPT2	TCTCAGCTCACTGCAACCTC 8194	G A GGC	
	TCTCAGCTCA TG AACCTC		
	II		
	AGAGTCGAGT AC TTGGAG		
	G G III		
GAM514 CPT2	TCTCAGCTCACTGCAACCTC 8194	G A I	
	CTCAGCTCA TG AACCT		
	II		
	GAGTCGAGT AC TTGGA		
	G G I		
GAM514 CYP4F3	TCTCGGCTCACTGAAACCTC 8195	A G GGC	
	TCTC GCTCA TGAAACCTC		
	AGAG CGAGT ACTTTGGAG		
	C G III		
GAM514 CYP4F3	TCTCGGCTCACTGAAACCTC 8195	A G I	
	CTC GCTCA TGAAACCT		
	GAG CGAGT ACTTTGGA		
	C G I		
GAM514 DDOST	TCTCAGCTCACTGCAAGCTCTGCC 8204	G AAAC G I	
	TCTCAGCTCA TG CTC GCC		
	II		
	AGAGTCGAGT AC GAG CGG		
	G GTTC A I		
GAM514 DDOST	TCTCAGCTCACTGCAAGCTCTGCC 8204	G AAAC G I	
	CTCAGCTCA TG CTC GC		
	II		

	GAGTCGAGT AC GAG CG	
	G GTTC A I	
GAM514 DGKI	TCTCAGCTCACTGCCAGCTCCGCC 8206	G AAAC G I
	TCTCAGCTCA TG CTC GCC	
	AGAGTCGAGT AC GAG CGG	
	G GGTC G I	
GAM514 DGKI	TCTCAGCTCACTGCCAGCTCCGCC 8206	G AAAC G I
	CTCAGCTCA TG CTC GC	
	GAGTCGAGT AC GAG CG	
	G GGTC G I	
GAM514 DSCAM	TCAGCTCAGTGGGCCCCCGGC 8192	AAA I
	CAGCTCAGTG CCTCGG	
	GTCGAGTCAC GGGGCC	
	CCG I	
GAM514 DSCAM	TCAGCTCAGTGGGCCCCCGGC 8192 TCTC	AAA C
	AGCTCAGTG CCTCGGC	
	TCGAGTCAC GGGGCCG	
	____ CCG T	
GAM514 FGFR1	TCTCAGCTCACTGCAACCTCTGCC 8202	G A G I
	TCTCAGCTCA TG AACCTC GCC	
	AGAGTCGAGT AC TTGGAG CGG	
	G G A I	
GAM514 FGFR1	TCTCAGCTCACTGCAACCTCTGCC 8202	G A G I
	CTCAGCTCA TG AACCTC GC	
	GAGTCGAGT AC TTGGAG CG	
	G G A I	
GAM514 GALNT7	TCTCAGCTCACTGCAACCTCTGCC 8202	G A G I
	CTCAGCTCA TG AACCTC GC	
	GAGTCGAGT AC TTGGAG CG	
	G G A I	
GAM514 GALNT7	TCTCAGCTCACTGCAACCTCTGCC 8202	G A G I
	TCTCAGCTCA TG AACCTC GCC	
	AGAGTCGAGT AC TTGGAG CGG	
	G G A I	
GAM514 HIP1	TCTCAGCTCACTGCAACCTCTGCC 8202	G A G I
	TCTCAGCTCA TG AACCTC GCC	
	AGAGTCGAGT AC TTGGAG CGG	
	G G A I	
GAM514 HIP1	TCTCAGCTCACTGCAACCTCTGCC 8202	G A G I
	CTCAGCTCA TG AACCTC GC	

	GAGTCGAGT AC TTGGAG CG		
	G G A I		
GAM514 IRAK4	TCTCAGCTCACTGCAACCTC 8194	G A	GGC
	TCTCAGCTCA TG AACCTC		
	AGAGTCGAGT AC TTGGAG		
	G G III		
GAM514 IRAK4	TCTCAGCTCACTGCAACCTC 8194	G A	I
	CTCAGCTCA TG AACCT		
	GAGTCGAGT AC TTGGA		
	G G I		
GAM514 IRS1	CAGCTCAGTCGCAGAGACCGCGGC 8190 AGCT	___	A T I
	CAGT GA ACC CGG		
	GTCA CT TGG GCC		
	___ GCGT C C I		
GAM514 IRS1	CAGCTCAGTCGCAGAGACCGCGGC 8190 T	C A _	A T CI
	CTCAG TC GT GA ACC CGGC		
	GAGTC AG CG CT TGG GCCG		
	_ _ _ T C C CG		
GAM514 KAI1	TCTCAGCTCACTGCAACCTCCGC 8197	G A	G CI
	TCTCAGCTCA TG AACCTC GC		
	AGAGTCGAGT AC TTGGAG CG		
	G G G II		
GAM514 KAI1	TCTCAGCTCACTGCAACCTCCGC 8197	G A	GGI
	CTCAGCTCA TG AACCTC		
	GAGTCGAGT AC TTGGAG		
	G G GCI		
GAM514 MAFF	TCTCAGCTCACTACAACCTCTGCC 8200	G A	G I
	TCTCAGCTCA TG AACCTC GCC		
	AGAGTCGAGT AT TTGGAG CGG		
	G G A I		
GAM514 MAFF	TCTCAGCTCACTACAACCTCTGCC 8200	G A	G I
	CTCAGCTCA TG AACCTC GC		
	GAGTCGAGT AT TTGGAG CG		
	G G A I		
GAM514 MOG	TCTCAGCTCACTGCAACCTCTGCC 8202	G A	G I
	TCTCAGCTCA TG AACCTC GCC		
	AGAGTCGAGT AC TTGGAG CGG		
	G G A I		
GAM514 MOG	TCTCAGCTCACTGCAACCTCTGCC 8202	G A	G I
	CTCAGCTCA TG AACCTC GC		

	GAGTCGAGT AC TTGGAG CG		
	G G A I		
GAM514 NPHS1	TCTCAGCTCACTGCAACCTCCGCC 8201	G A	G I
	TCTCAGCTCA TG AACCTC GCC		
	AGAGTCGAGT AC TTGGAG CGG		
	G G G I		
GAM514 NPHS1	TCTCAGCTCACTGCAACCTCCGCC 8201	G A	G I
	CTCAGCTCA TG AACCTC GC		
	GAGTCGAGT AC TTGGAG CG		
	G G G I		
GAM514 PA2G4	TCTCAGCTCACTGCAACCTC 8194	G A	GGC
	TCTCAGCTCA TG AACCTC		
	AGAGTCGAGT AC TTGGAG		
	G G		
GAM514 PA2G4	TCTCAGCTCACTGCAACCTC 8194	G A	I
	CTCAGCTCA TG AACCT		
	GAGTCGAGT AC TTGGA		
	G G I		
GAM514 PCSK1	GCTCAGTGAAGCGCTTCGG 8191	ACCTCG	
	GCTCAGTGAA		
	CGAGTCACTT		
	CGCGAAGCC		
GAM514 PLA2G2D	TCTGGGCTCACTGAAACCTCTGCC 8209	CA G	G I
	TCT GCTCA TGAAACCTC GCC		
	AGA CGAGT ACTTTGGAG CGG		
	CC G A I		
GAM514 PLA2G2D	TCTGGGCTCACTGAAACCTCTGCC 8209	CTCA G	G I
	GCTCA TGAAACCTC GC		
	CGAGT ACTTTGGAG CG		
	GACC G A I		
GAM514 POLH	TCTCAGCTCAATGCAACCTCCGCC 8198	A G I	
	TCTCAGCTCAGTG AACCTC GCC		
	AGAGTCGAGTTAC TTGGAG CGG		
	G G I		
GAM514 POLH	TCTCAGCTCAATGCAACCTCCGCC 8198	A G I	
	CTCAGCTCAGTG AACCTC GC		
	GAGTCGAGTTAC TTGGAG CG		
	G G I		
GAM514 POLH	TCTCAGCTCACCCCAACCTCTGCC 8199	GTGA G I	
	TCTCAGCTCA AACCTC GCC		

	AGAGTCGAGT TTGGAG CGG		
	GGGG A I		
GAM514 POLH	TCTCAGCTCACCCCAACCTCTGCC 8199	GTGA	G I
	CTCAGCTCA AACCTC GC		
	II		
	GAGTCGAGT TTGGAG CG		
	GGGG A I		
GAM514 PSMD5	TCTCAGCTCACTGCAACCTCTGCC 8202	G A	G I
	TCTCAGCTCA TG AACCTC GCC		
	II III		
	AGAGTCGAGT AC TTGGAG CGG		
	G G A I		
GAM514 PSMD5	TCTCAGCTCACTGCAACCTCTGCC 8202	G A	G I
	CTCAGCTCA TG AACCTC GC		
	II II		
	GAGTCGAGT AC TTGGAG CG		
	G G A I		
GAM514 SLC19A1	TCACAGGGCCCTGCAAACCTCGGCC 8193	T _ A G	II
	TC CA GCTC GT AAACCTCGGCC		
	II II II		
	AG GT CGGG CG TTTGGAGCCGG		
	T CC A _ II		
GAM514 SLC19A1	TCACAGGGCCCTGCAAACCTCGGCC 8193	CTCA_ A G	I
	GCTC GT AAACCTCGGC		
	II		
	CGGG CG TTTGGAGCCG		
	TGTCC A _ I		
GAM514 SUDD	TCTCAGCTCACTGCAACCTCTGCC 8202	G A	G I
	TCTCAGCTCA TG AACCTC GCC		
	II III		
	AGAGTCGAGT AC TTGGAG CGG		
	G G A I		
GAM514 SUDD	TCTCAGCTCACTGCAACCTCTGCC 8202	G A	G I
	CTCAGCTCA TG AACCTC GC		
	II II		
	GAGTCGAGT AC TTGGAG CG		
	G G A I		
GAM514 SWAP70	TCTCAGCTCGCTGCAACCTCCGCC 8207	A GA_	G I
	TCTCAGCTC GT AACCTC GCC		
	II III		
	AGAGTCGAG CG TTGGAG CGG		
	_ ACG G I		
GAM514 SWAP70	TCTCAGCTCGCTGCAACCTCCGCC 8207	A GA_	G I
	CTCAGCTC GT AACCTC GC		
	II II		
	GAGTCGAG CG TTGGAG CG		
	_ ACG G I		
GAM514 TADA2L	TCTCAGCTCGCTGCAACCTCTGCC 8208	A GA_	G I
	TCTCAGCTC GT AACCTC GCC		
	II III		

	AGAGTCGAG CG TTGGAG CGG	
	_ ACG A I	
GAM514 TADA2L	TCTCAGCTCGCTGCAACCTCTGCC 8208	A GA_ G I
	CTCAGCTC GT AACCTC GC	
	GAGTCGAG CG TTGGAG CG	
	_ ACG A I	
GAM514 TPMT	TCTCAGCTCACTGCAACCTCCGCC 8201	G A G I
	TCTCAGCTCA TG AACCTC GCC	
	AGAGTCGAGT AC TTGGAG CGG	
	G G G I	
GAM514 TPMT	TCTCAGCTCACTGCAACCTCCGCC 8201	G A G I
	CTCAGCTCA TG AACCTC GC	
	GAGTCGAGT AC TTGGAG CG	
	G G G I	
GAM514 TRIM14	TCTCAGCTCACTGCAATCTCCGCC 8205	G AAAC G I
	TCTCAGCTCA TG CTC GCC	
	AGAGTCGAGT AC GAG CGG	
	G GTTA G I	
GAM514 TRIM14	TCTCAGCTCACTGCAATCTCCGCC 8205	G AAAC G I
	CTCAGCTCA TG CTC GC	
	GAGTCGAGT AC GAG CG	
	G GTTA G I	
GAM514 TSHR	TCTCAGCTC--TG-CACCTCGG 8196	A GAA C
	TCTCAGCTC GT ACCTCGG	
	AGAGTCGAG CG TGGAGCC	
	A _ I	
GAM514 TSHR	TCTCAGCTC--TG-CACCTCGG 8196_	A GAA
	CTCAGCTC GT ACCTCG	
	GAGTCGAG CG TGGAGC	
	A A _	
GAM514 UBE2G2	TCTCAGCTCACTGCAAGCTCCGCC 8203	G AAAC G I
	TCTCAGCTCA TG CTC GCC	
	AGAGTCGAGT AC GAG CGG	
	G GTTC G I	
GAM514 UBE2G2	TCTCAGCTCACTGCAAGCTCCGCC 8203	G AAAC G I
	CTCAGCTCA TG CTC GC	
	GAGTCGAGT AC GAG CG	
	G GTTC G I	
GAM514 UPK1B	TCTCAGCTCACTGCAACCTC 8194	G A I
	CTCAGCTCA TG AACCT	

	GAGTCGAGT AC TTGGA		
	G G I		
GAM514 UPK1B	TCTCAGCTCACTGCAACCTC 8194	G A	GGC
	TCTCAGCTCA TG AACCTC		
	AGAGTCGAGT AC TTGGAG		
	G G III		
GAM514 VDR	TCTCAGCTCACTGCAACCTC 8194	G A	GGC
	TCTCAGCTCA TG AACCTC		
	AGAGTCGAGT AC TTGGAG		
	G G III		
GAM514 VDR	TCTCAGCTCACTGCAACCTC 8194	G A	I
	CTCAGCTCA TG AACCT		
	GAGTCGAGT AC TTGGA		
	G G I		
GAM514 XRCC2	TCTCAGCTCACTGCAACCTC 8194	G A	GGC
	TCTCAGCTCA TG AACCTC		
	AGAGTCGAGT AC TTGGAG		
	G G III		
GAM514 XRCC2	TCTCAGCTCACTGCAACCTC 8194	G A	I
	CTCAGCTCA TG AACCT		
	GAGTCGAGT AC TTGGA		
	G G I		
GAM514 ZNF14	TCTCAGCTCACTGCAACCTC 8194	G A	GGC
	TCTCAGCTCA TG AACCTC		
	AGAGTCGAGT AC TTGGAG		
	G G III		
GAM514 ZNF14	TCTCAGCTCACTGCAACCTC 8194	G A	I
	CTCAGCTCA TG AACCT		
	GAGTCGAGT AC TTGGA		
	G G I		
GAM514 ZNF264	TCTCAGCTCACTGCAACCTCCGCC 8201	G A	G I
	TCTCAGCTCA TG AACCTC GCC		
	AGAGTCGAGT AC TTGGAG CGG		
	G G G I		
GAM514 ZNF264	TCTCAGCTCACTGCAACCTCCGCC 8201	G A	G I
	CTCAGCTCA TG AACCTC GC		
	GAGTCGAGT AC TTGGAG CG		
	G G G I		
GAM515 CLCN7	CTGTGAGGGCTAAGCAGGG 8215 T	—	III
	CT TGAGGGCTA CAGG		

	GA ACTCCCGAT GTCC			
	C TC CII			
GAM515 CYP8B1	CCAGACTTTGAAG---ACAGG	8214	TACI	
	CCAGACTTTGAGGGC			
	GGTCTGAAACTTCTG			
	TCCI			
GAM515 CYP8B1	CCAGACTTTGAAG---ACAGG	8214 GTCC	GCT	
	AGACTTTGAGG ACAG			
	TCTGAAACTTC TGTC			
GAM515 HAP1	CCAGACTTTG-GGGTTTCTGG	8213 _	A CTACAGI	
	CAGACTTTG GGG			
	GTCTGAAAC CCC			
	G _ AAAGACI			
GAM515 HAP1	CCAGACTTTG-GGGTTTCTGG	8213 GTCC	A CTACA	
	AGACTTTG GGG GG			
	TCTGAAAC CCC CC			
	_ _ AAAGA			
GAM515 PYGO2	GTCCAGACTTTCAGG---ACAG	8216	G TACAGG	
	GTCCAGACTTT AGGGC			
	CAGGTCTGAAA TCCTG			
	G TCIIG			
GAM515 PYGO2	GTCCAGACTTTCAGG---ACAG	8216	G TAI	
	GTCCAGACTTT AGGGC			
	CAGGTCTGAAA TCCTG			
	G TCI			
GAM515 TCP10	CCAAATATTGAGGGCTACA	8212 CT	II	
	CCAGA TTGAGGGCTAC			
	GGTTT AACTCCCGATG			
	AT TI			
GAM515 TCP10	CCAAATATTGAGGGCTACA	8212 GTCC CT	G	
	AGA TTGAGGGCTACAG			
	TTT AACTCCCGATGTT			
	_ AT A			
GAM515 UBE2V1	TCCGGTACTTTGAGGTCTACA	8217 CCAG	G I	
	ACTTTGAGG CTAC			
	TGAAACTCC GATG			
	GCCA A I			
GAM515 UBE2V1	TCCGGTACTTTGAGGTCTACA	8217 GT AG_	G GG	
	CC ACTTTGAGG CTACAG			

	GG TGAAACTCC GATGTT		
	__ CCA A II		
GAM516 ADD3	TGTGAATAAA---ATTCCAAATGAAT 8235	GCAA __ I	
	TGTGAATAAAG TCCA TGAAT		
	ACACTTATTTT AGGT ACTTA		
	A__ TT I		
GAM516 ADD3	TGTGAATAAA---ATTCCAAATGAAT 8235 _	GCAA __ I	
	GTGAATAAAG TCCA TGAA		
	CACTTATTTT AGGT ACTT		
	A A__ TT I		
GAM516 APPL	AAGAAAAGCATATCCATGAAT 8220 AT _ I		
	AAAGGCA ATCCATGAA		
	TTTTCGT TAGGTACTT		
	C_ A I		
GAM516 APPL	AAGAAAAGCATATCCATGAAT 8220 TGTGAATA _		
	AAGGCA ATCCATGAAT		
	TTTCGT TAGGTACTTA		
	_____ A		
GAM516 ARHGEF6	TGTGAACTGAAGGCAATC--TGAA 8232 A_ CA T		
	TGTGAAT AAGGCAATC TGAA		
	ACACTTG TTCCGTTAG ACTT		
	AC __ I		
GAM516 ARHGEF6	TGTGAACTGAAGGCAATC--TGAA 8232 _ A_ CA I		
	GTGAAT AAGGCAATC TGA		
	CACTTG TTCCGTTAG ACT		
	A AC __ I		
GAM516 B4GALT5	GTGGATACAATCAATCCATG 8227 A AAGG I		
	TG ATA CAATCCAT		
	AC TAT GTTAGGTA		
	C GTTA I		
GAM516 B4GALT5	GTGGATACAATCAATCCATG 8227 TG A AAGG AA		
	TG ATA CAATCCATG		
	AC TAT GTTAGGTAC		
	_ C GTTA AI		
GAM516 IL2RB	ATAAAGGCAA--CAGGAAT 8223 CCATGAAI		
	ATAAAGGCAAT		
	TATTTCCGTTG		
	TCCTTAII		
GAM516 IL2RB	ATAAAGGCAA--CAGGAAT 8223 TGTGAATAA C A		
	AGG AATCC TGA		

		TCC TTAGG ACT		
		CCGTTG___ _ _		
GAM516 KIF3C	GTGAATAAAGG--ATCTAT	8225	CA CAI	
	GTGAATAAAGG ATC			
	CACTTATTTCC TAG			
	___ ATA			
GAM516 KIF3C	GTGAATAAAGG--ATCTAT	8225 TG	CA C GA	
	TGAATAAAGG ATC AT			
	ACTTATTTCC TAG TA			
	___ _ A AI			
GAM516 KIT	ATAAAGGCAACATACCTGAAT	8222	___ A	
	ATAAAGGCAAT CC TGAA			
	TATTTCCGTTG GG ACTT			
	TAT _ AII			
GAM516 NCOA6IP	GTGAATAAAGG-AAGACATG	8226 _	C TC I	
	TGAATAAAGG AA CAT			
	ACTTATTTCC TT GTA			
	C _ CT I			
GAM516 NCOA6IP	GTGAATAAAGG-AAGACATG	8226 TG	C TC AA	
	TGAATAAAGG AA CATG			
	ACTTATTTCC TT GTAC			
	___ _ CT GI			
GAM516 ODC1	GTGAATAAA---AATCCAT	8224	GGC	
	GTGAATAAA AATCCA			
	CACTTATTT TTAGGT			

GAM516 ODC1	GTGAATAAA---AATCCAT	8224 TG	GGC	
	TGAATAAA AATCCATG			
	ACTTATTT TTAGGTAT			

GAM516 PACE4	TGAATAAAGGGGAAAACATG	8230	C TC II	
	TGAATAAAGG AA CAT			
	ACTTATTTCC TT GTA			
	C TT CI			
GAM516 PACE4	TGAATAAAGGGGAAAACATG	8230 TGTG	C TC AA	
	AATAAAGG AA CATG			
	TTATTTCC TT GTAC			
	___ C TT CA			
GAM516 PARK2	TGAACTGAAATCCAATCCATG	8228	___ GG	
	TGAAT AAA CAATCCAT			

	ACTTG TTT GTTAGGTA		
	AC AG CII		
GAM516 PARK2	TGAACTGAAATCCAATCCATG	8228 TG_ TAAAGG	AAT
	TGAA CAATCCATG		
	ACTT GTTAGGTAC		
	TTG TAG_ AGI		
GAM516 PRKY	AATAATGCCAGTTCCATGAAT	8221 ATAAAG AA_	I
	GC TCCATGAA		
	CG AGGTACTT		
	ATTA_ GTCA I		
GAM516 PSCDBP	TGTGAATAAAGATCACTCCA	8234 _ A TGAA	
	TGTGAATAAAGG CA TCCA		
	ACACTTATTTCT GT AGGT		
	A G IIIT		
GAM516 PSCDBP	TGTGAATAAAGATCACTCCA	8234 _ A II	
	TGTGAATAAAGG CA TCC		
	ACACTTATTTCT GT AGG		
	A G TI		
GAM516 TMP21	TGAAAGAGGGCAATCCAAATGAA	8229 TGAATAAA	TI
	GGCAATCCA		
	CCGTTAGGT		
	CTC_ TT		
GAM516 TMP21	TGAAAGAGGGCAATCCAAATGAA	8229 TGTGAATAAA	_ TI
	GGCAATCCA TGAA		
	CCGTTAGGT ACTT		
	TTTCTC_ TT CA		
GAM516 TOX	TGTACAAAG-CAATCCATG	8231 TGAATA	I
	AAGGCAATCCAT		
	TTTCGTTAGGTA		
	ACATG_ C		
GAM516 TOX	TGTACAAAG-CAATCCATG	8231 TGTGAATA	A
	AAGGCAATCCATG		
	TTTCGTTAGGTAC		
	ATG_ C		
GAM516 TRIM	TGTGAATAAGAGGTAAGCCA	8233 _ C T TGAA	
	TGTGAATAA AGG AA CCA		
	ACACTTATT TCC TT GGT		
	C A C IIIT		
GAM516 TRIM	TGTGAATAAGAGGTAAGCCA	8233 _ C T II	
	TGTGAATAA AGG AA CC		

	ACACTTATT TCC TT GG			
	C A C TI			
GAM517 AGTR1	CCGGCAGAGCTGCTAGCGGCGC	8244 CG	___	AGI
	GCAGAGC CTGGTGG			
	CGTCTCG GATCGCC			
	___ AC GCI			
GAM517 AGTR1	CCGGCAGAGCTGCTAGCGGCGC	8244 TCACCG	___	A T
	GCAGAGC CTGGTGG GC			
	CGTCTCG GATCGCC CG			
	_____ AC G C			
GAM517 ARHGEF7	CCGGCAGAG--GGGCGGAG	8246	CCT	I
	CCGGCAGAG GGTGGA			
	GGCCGTCTC CCGCCT			
	C___ C			
GAM517 ARHGEF7	CCGGCAGAG--GGGCGGAG	8246 TCACCG	CCT	
	GCAGAG GGTGGAG			
	CGTCTC CCGCCTC			
	_____ C___			
GAM517 BAG1	CGGCAGAG-CTGGTGGCGC	8249	C	AGI
	CGGCAGAGC TGGTGG			
	GCCGTCTCG ACCACC			
	___ GCG			
GAM517 BAG1	CGGCAGAG-CTGGTGGCGC	8249 TCACCGGC	C	A
	AGAGC TGGTGG G			
	TCTCG ACCACC C			
	_____ _ G			
GAM517 CCT3	ACCGGCAGAACCTTCTGGAG	8239	GG	I
	CCGGCAGAGCCT TGGA			
	GGCCGTCTTGGA ACCT			
	AG I			
GAM517 CCT3	ACCGGCAGAACCTTCTGGAG	8239 TCAC	GG	C
	CGGCAGAGCCT TGGAG			
	GCCGTCTTGGA ACCTC			
	_____ AG T			
GAM517 DLEC1	CACC--CAG---CTGGTGGAG	8242 A___	AGAGCC	
	CCGGC TGGTGG			
	GGTCG ACCACC			
	GTG _____			
GAM517 DLEC1	CACC--CAG---CTGGTGGAG	8242 TCA	AGAGCC	
	CCGGC TGGTGA			

	GGTCG ACCACCT			
	TG_ _____			
GAM517 GALC	CCGGCGTCACCTGGTGGAGC	8247	AGA	I
	CGGC GCCTGGTGGAG			
	GCCG TGGACCACCTC			
	CAG I			
GAM517 GALC	CCGGCGTCACCTGGTGGAGC	8247	TCACCG AGA	
	GC GCCTGGTGGAGC			
	CG TGGACCACCTCG			
	_____ CAG			
GAM517 HCS	ACCAGGCAGGGCCTGGTGG	8238	_ A	II
	ACC GGCAG GCCTGGTG			
	TGG CCGTC CGGACCAC			
	T C CI			
GAM517 HCS	ACCAGGCAGGGCCTGGTGG	8238	TCACC A	AGC
	GGCAG GCCTGGTGG			
	CCGTC CGGACCACC			
	GT_ C GAI			
GAM517 MYBL2	CCGGCAGAGCCCGGAGCGGGAGC	8245	CGG	T_ I
	CAGAGCCTGG GGAG			
	GTCTCGGGCC CCTC			
	_____ TCGC I			
GAM517 MYBL2	CCGGCAGAGCCCGGAGCGGGAGC	8245	TCACCG	T_ I
	GCAGAGCCTGG GGAGCT			
	CGTCTCGGGCC CCTCGG			
	_____ TCGC C			
GAM517 PAX2	GCAGCAGCCTGGTGG-GCT	8250	_ A	II
	GCAG AGCCTGGTGG GC			
	CGTC TCGGACCACC CG			
	G _ AI			
GAM517 SH3GL1	GCAGAGCCTGGGGTCCGGAGCT	8251	_____	IIIA
	GCAGAGCCTGG TGGAGC			
	CGTCTCGGACC GCCTCG			
	CCAG AIII			
GAM517 SIGLEC11	CCAGCAGGAAGCCTGGTGGAG	8243	_____	III
	CCGGCAG AGCCTGGTGA			
	GGTCGTC TCGGACCACCT			
	CT CII			
GAM517 SIGLEC11	CCAGCAGGAAGCCTGGTGGAG	8243	TCACCG	_____ CT
	GCAG AGCCTGGTGGAG			

	CGTC TCGGACCACCTC	
	_____ CT CC	
GAM517 SMP1	CACAGG--GAGCCTGGTGG 8241 C CA I	
	CAC GG GAGCCTGGTG	
	GTG CC CTCGGACCAC	
	T _ C	
GAM517 SMP1	CACAGG--GAGCCTGGTGG 8241 TCAC CA AG	
	CGG GAGCCTGGTGG	
	GTC CTCGGACCACC	
	T _ C _ GI	
GAM517 STK4	TCACC--CAAAGCCTGGGTGGAGCT 8253 GG _ I	
	TCACC CAGAGCCTGG TGGAGCT	
	AGTGG GTTTCGGACC ACCTCGA	
	_ C I	
GAM517 STK4	TCACC--CAAAGCCTGGGTGGAGCT 8253 _ GG _ I	
	CACC CAGAGCCTGG TGGAGC	
	GTGG GTTTCGGACC ACCTCG	
	A _ C I	
GAM517 TEAD3	CGGCTGAGCCTGGTCCGAGCT 8248 G A G _ I	
	GC GAGCCTGGT GAGC	
	CG CTCGGACCA CTCG	
	_ A GG I	
GAM517 TEAD3	CGGCTGAGCCTGGTCCGAGCT 8248 TCACCGGCA G _	
	GAGCCTGGT GAGCT	
	CTCGGACCA CTCGA	
	A _ GG	
GAM517 TNFAIP2	GCAGAGCCTTAGGGGGAGC 8252 _ T	
	GCAGAGCCT GG GGAG	
	CGTCTCGGA CC CCTC	
	AT C G	
GAM517 TNP1	CACCAGGGCAGAGCCCGCTGG 8240 _ G	
	CACC GGCAGAGCCTG TG	
	GTGG CCGTCTCGGGC AC	
	TC G C	
GAM517 TNP1	CACCAGGGCAGAGCCCGCTGG 8240 TC _ G AGCT	
	ACC GGCAGAGCCTG TGG	
	TGG CCGTCTCGGGC ACC	
	_ TC G C	
GAM518 CHST5	TCCTGGTAGGCAGCAACAAT 8268 CAGC TA GGC	
	TCC AG AGCAACAAT	

	AGG TC TCGTTGTTA		
	ACCA CG III		
GAM518 CHST5	TCCTGGTAGGCAGCAACAAT	8268	CCCAGC TA I
	AG AGCAACAA		
	II IIIIIII		
	TC TCGTTGTT		
	GGACCA CG I		
GAM518 DNASE1	GCAG-AA--AACAATGGCT	8264	TAAGC
	GCAG AACAATGGC		
	IIII IIIIIII		
	CGTC TTGTTACCG		
	TT__		
GAM518 ITGA1	CAGCATTAACAGCAACAAT	8257	GTA__ III
	CAGCA AGCAACAA		
	IIII IIIIIII		
	GTCGT TCGTTGTT		
	AATTG AII		
GAM518 ITGA1	CAGCATTAACAGCAACAAT	8257	TCCCAGCAGTA GGC
	AGCAACAAT		
	IIIIIIII		
	TCGTTGTTA		
	GTAATTG__ GGC		
GAM518 LAIR1	TCCCAGCAGT--GCAGC-CTGGC	8270	A_ AACAATI
	TCCCAGCAGT AGC		
	IIIIIIII III		
	AGGGTCGTCA TCG		
	CG GACCGII		
GAM518 LAIR1	TCCCAGCAGT--GCAGC-CTGGC	8270	AA ACAA
	TCCCAGCAGT GCA TGGC		
	IIIIIIII III III		
	AGGGTCGTCA CGT ACCG		
	_ CGG_		
GAM518 LENG4	CCCAGCAGTGGGAAACACTGGC	8262	AAGC A I
	CCAGCAGT AACA TGG		
	IIIIII III III		
	GGTCGTCA TTGT ACC		
	CCCT G I		
GAM518 LENG4	CCCAGCAGTGGGAAACACTGGC	8262	TC AAGC A
	CCAGCAGT AACA TGGCT		
	IIIIII III IIIII		
	GGTCGTCA TTGT ACCGG		
	_ CCCT G		
GAM518 MASP1	TCCCAGCAGTCAGC-ACAA	8267	A A TGG
	TCCCAGCAGT AGCA CAA		
	IIIIIIII III III		
	AGGGTCGTCA TCGT GTT		
	G _ III		
GAM518 MASP1	TCCCAGCAGTCAGC-ACAA	8267	A ACAI
	TCCCAGCAGT AGCA		
	IIIIIIII III		

	AGGGTCGTCA TCGT		
	G GTTI		
GAM518 MOX2	AGCAGTAAGCAGGAAGTGG	8256	ACAATGII
	AGCAGTAAGCA		
	TCGTCATTTCGT		
	CCTTGACC		
GAM518 MYCN	TCCCAGCAGAACCCCACACTGG	8269	TAAGCA A CT
	TCCCAGCAG ACA TGG		
	AGGGTCGTC TGT ACC		
	TTGGGG G II		
GAM518 MYCN	TCCCAGCAGAACCCCACACTGG	8269	TA AA ATGI
	CCCAGCAG AGC CA		
	II		
	GGGTCGTC TTG GT		
	— GG GTGA		
GAM518 PCTP	TCCTAATAGTAAGCAAGCAAAGG	8266	C C _ T CTI
	TCC AG AGTAAGCAA CAA GG		
	AGG TT TCATTCGTT GTT CC		
	A A C T		
GAM518 PCTP	TCCTAATAGTAAGCAAGCAAAGG	8266	CCCAGC _ TI
	AGTAAGCAA CAA		
	TCATTCGTT GTT		
	ATTA_ C TC		
GAM518 PDCL	CCAGGTCAGTAAGCATCAA	8258	_ ACA
	CCAG CAGTAAGCA		
	GGTC GTCATTTCGT		
	CA AGTTII		
GAM518 PDCL	CCAGGTCAGTAAGCATCAA	8258	TCCCAG A GGC
	CAGTAAGCA CAAT		
	GTCATTTCGT GTTG		
	TCCA_ A GII		
GAM518 POLG	CCCAACA---AGCAACAATG	8261	GTA I
	CCCAGCA AGCAACAA		
	GGGTTGT TCGTTGTT		
	_ A		
GAM518 POLG	CCCAACA---AGCAACAATG	8261	TC GTA G
	CCAGCA AGCAACAATG		
	GGTTGT TCGTTGTTAC		
	_ _ G		
GAM518 PPP1CB	TCCCAGCAG-CGGGAACAAGGGCT	8271	AAGC T I
	TCCCAGCAGT AACAA GGCT		

	AGGGTCGTCG TTGTT CCGA	
	CCC_ C I	
GAM518 PPP1CB	TCCCAGCAG-CGGGAACAAGGGCT 8271 _	AAGC T I
	CCCAGCAGT AACAA GGC	
	GGGTCGTCG TTGTT CCG	
	A CCC_ C I	
GAM518 SOX11	CCAGCAGTAAGTAA-AATGG 8260 _	CAACAATGI
	CAGCAGTAAG	
	GTCGTCATTC	
	G ATTTTACII	
GAM518 SOX11	CCAGCAGTAAGTAA-AATGG 8260 TCCC	C C C
	AGCAGTAAG AA AATGG	
	TCGTCATTC TT TTACC	
	_____ A _ T	
GAM518 SQSTM1	TCCCAGCAGGAAGCCCACAACACTGGC8265	T A_ ____ TIII
	TCCCAGCAG AAGC ACAA TGGC	
	AGGGTCGTC TTCG TGTT ACCG	
	C GG GTG IIIT	
GAM518 SQSTM1	TCCCAGCAGGAAGCCCACAACACTGGC8265 CC C_ AA	A I
	CAG AGT GCAACA TGG	
	GTC TCG TGTTGT ACC	
	C_ CT GG G I	
GAM518 UBE2L3	CCAGCAGATCTTCTACAATGGCT 8259 C	TAAGCA_ I
	AGCAG ACAATGGC	
	TCGTC TGTTACCG	
	_ TAGAAGA I	
GAM518 UBE2L3	CCAGCAGATCTTCTACAATGGCT 8259 TCCC	TAAGCA_ I
	AGCAG ACAATGGCT	
	TCGTC TGTTACCGA	
	_____ TAGAAGA C	
GAM518 WHSC1	CCCAGCAGT---CAACA--GGCT 8263 _	AAG AT
	CCAGCAGT CAACA GG	
	GGTCGTCA GTTGT CC	
	G _____	
GAM518 WHSC1	CCCAGCAGT---CAACA--GGCT 8263 TC	AAG AT
	CCAGCAGT CAACA GG	
	GGTCGTCA GTTGT CC	

GAM519 CUBN	GGTTTGGTGAAAAACCATACA 8277 _____	GCTA I
	GGTGG AAAACCATGC	

	CCACT TTTTGGTATG	
	CAAA _____ I	
GAM519 CUBN	GGTTTGGTGAAAAACCATACA 8277 TAG GCTA	
	GGTGG AAAACCATGCA	
	CCACT TTTTGGTATGT	
	AAA _____	
GAM519 ERBB2IP	TGGTCCAAATAACCATGCA 8282 G _ II	
	TGG CTAAA AACCATGC	
	ACC GGTTT TTGGTACG	
	A A TI	
GAM519 ERBB2IP	TGGTCCAAATAACCATGCA 8282 TAGGGTGGGCTAAA	
	AACCATGC	
	TTGGTACG	
	GTTTA_____	
GAM519 FOSB	GGGTGGGAGAGCCAAAACCATG 8276 ____ T A III	
	GGG GGGCTAAAA CCAT	
	CCC CTCGGTTTT GGTA	
	CCCA T _ CII	
GAM519 FOSB	GGGTGGGAGAGCCAAAACCATG 8276 TA T A CAI	
	GGG GGGCTAAAA CCATG	
	CCC CTCGGTTTT GTTAC	
	CA T _ CAI	
GAM519 GPC4	AGGGTGGGCTAGCTAACC-TGC 8275 AA_ ATGI	
	GGGTGGGCTA AACC	
	CCCACCCGAT TTGG	
	CGA ACII	
GAM519 GPC4	AGGGTGGGCTAGCTAACC-TGC 8275 TA AA_ A A	
	GGGTGGGCTA AACC TGC	
	CCCACCCGAT TTGG ACG	
	____ CGA _ G	
GAM519 HNF3G	AGGGTGGGCTTCAGAGAAAACCA 8274 A_____ IIIT	
	AGGGTGGGCT AAAACC	
	TCCACCCGA TTTTGG	
	AGTCTC TIII	
GAM519 HNF3G	AGGGTGGGCTTCAGAGAAAACCA 8274 TA A_____ TGCAI	
	GGGTGGGCT AAAACCA	
	CCCACCCGA TTTTGGT	
	____ AGTCTC TIIIA	
GAM519 HNF3G	GGTGGCCATCAAACCATGCA 8278 GTG A_ I	
	GGCTA AAACCATGC	

	CCGGT TTTGGTACG		
	CA_ AG I		
GAM519 HNF3G	GGTGGCCATCAAACCATGCA	8278	TAGGGTG A_
	GGCTA AAACCATGCA		
	CCGGT TTTGGTACGT		
	_____ AG		
GAM519 MAX	TAGGGTGGGCAGGACACTATG	8281	TAAAA C CA
	TAGGGTGGGC AC ATG		
	ATCCACCCG TG TAC		
	TCCTG A II		
GAM519 MAX	TAGGGTGGGCAGGACACTATG	8281	TAAAA CATI
	AGGGTGGGC AC		
	TCCACCCG TG		
	TCCTG ATAI		
GAM519 PXN	TAGGGTGGGTCACTATAAAC	8279	___ A CATGCA
	TAGGGTGGG CTA AAAC		
	ATCCACCC GAT TTTG		
	AGT A IIIACG		
GAM519 PXN	TAGGGTGGGTCACTATAAAC	8279	CTAAAAAIII
	TAGGGTGGG		
	ATCCACCC		
	AGTGATATTT		
GAM519 TMPRSS3	TAGGGTGGGCCCTAATCCA	8280	AA A TGC
	TAGGGTGGGCT AA CCA		
	ATCCACCCGG TT GGT		
	GA A III		
GAM519 TMPRSS3	TAGGGTGGGCCCTAATCCA	8280	AA A II
	TAGGGTGGGCT AA CC		
	ATCCACCCGG TT GG		
	GA A TI		
GAM520 CACNA1C	GGGCCGGCGGCTGGCCGGA	8296	AT___ III
	GGGCCGGCGG TCGGG		
	CCCGGCCGCC GGCC		
	GACC TII		
GAM520 CACNA1C	GGGCCGGCGGCTGGCCGGA	8296	TGAGAAG C GA G
	GGCCGG G TTCGG		
	CCGGCC C GAGCC		
	CGCCGA_ _TC I		
GAM520 CD44	GGGCCGGCGGAGGACGGGA	8295	TT_ II
	GGGCCGGCGGA CGGG		

	CCCGGCCGCCT GCCC		
	CCT TI		
GAM520 CSH2	GAGAAGGGCCTGGAGGATT 8289	_ C II	
	GAGAAGGGCC GG GGAT		
	II		
	CTCTTCCCGG CC CCTA		
	A T AI		
GAM520 CSH2	GAGAAGGGCCTGGAGGATT 8289 TG	_ C CGGG	
	AGAAGGGCC GG GGATT		
	II		
	TCTTCCCGG CC CCTAA		
	— A T TIII		
GAM520 CYP4A11	GAGAAGGGCAGGCAGACTGGGG 8293	C C I	
	AGAAGGGC GGCGGATT GG		
	II		
	TCTTCCCG CCGTCTGA CC		
	T C I		
GAM520 CYP4A11	GAGAAGGGCAGGCAGACTGGGG 8293 TG	C C A	
	AGAAGGGC GGCGGATT GGG		
	III		
	TCTTCCCG CCGTCTGA CCC		
	— T C C		
GAM520 ETS2	AGGGCCGGCGCTTGTCGGGA 8285	GAT_ III	
	AGGGCCGGCG TCGGG		
	TCCCGGCCGC AGCCC		
	GAACC TII		
GAM520 FAAH	GAGAAGGGCTG--TGATTCTGGA 8294	CGGCG _ I	
	GAGAAGGGC GATTC GG		
	II		
	CTCTTCCCG CTAAG CC		
	ACA_ A T		
GAM520 FAAH	GAGAAGGGCTG--TGATTCTGGA 8294 TG	CGGCG G	
	AGAAGGGC GATTC GGA		
	III		
	TCTTCCCG CTAAG CCT		
	— ACA_ A		
GAM520 LMO1	GAGAAGGGC--GCCGACTCGGG 8292 _	CG G I	
	AGAAGGGC GC GATTCGG		
	II		
	TCTTCCCG CG CTGAGCC		
	C _ G I		
GAM520 LMO1	GAGAAGGGC--GCCGACTCGGG 8292 TG	CG G	
	AGAAGGGC GC GATTCGGG		
	II		
	TCTTCCCG CG CTGAGCCC		
	— _ G		
GAM520 MBTPS1	AGGGCCGGCGGGCCCGGA 8287	AT II	
	AGGGCCGGCGG TCGGG		

	TCCCGGCCGCC GGCCC		
	CG TI		
GAM520 MEF2D	TGAGAAGGGAAGGC-CATTC 8297	CC GG GGG	
	TGAGAAGGG GGC ATTC		
	ACTCTTCCC CCG TAAG		
	TT G_		
GAM520 MEF2D	TGAGAAGGGAAGGC-CATTC 8297 _	CC GGATTI	
	GAGAAGGG GGC		
	CTCTTCCC CCG		
	A TT GTA		
GAM520 NR3C1	TGAGAAGGGTGGTCAGAAT-GGGA 8299	CC _ TTC I	
	TGAGAAGGG GG CGGA GGGA		
	ACTCTTCCC CC GTCT CCCT		
	A_ A TA_ I		
GAM520 NR3C1	TGAGAAGGGTGGTCAGAAT-GGGA 8299 _	CC _ TTC I	
	GAGAAGGG GG CGGA GGG		
	CTCTTCCC CC GTCT CCC		
	A A_ A TA_ I		
GAM520 PTGS1	TGAGAAGGGCAG--GGATCCAGG 8298	C C A	
	TGAGAAGGGC GG GGATTCGGG		
	ACTCTTCCCG TC CCTAGGTCC		
	_ _ I		
GAM520 PTGS1	TGAGAAGGGCAG--GGATCCAGG 8298 _	C C I	
	GAGAAGGGC GG GGATTCGG		
	CTCTTCCCG TC CCTAGGTC		
	A _ _ I		
GAM520 RET	AGGGCCGGCGG-GTCTGGA 8286	A TC I	
	AGGGCCGGCGG T GGG		
	TCCCGGCCGCC A CCT		
	C GA I		
GAM520 SMARCA5	GAGAAGGG-CGGAGGGTTGGGG 8291 _	C C A C I	
	AGAAGGGC GG GG TT GG		
	TCTTCCCG CC CC AA CC		
	C _ T C C I		
GAM520 SMARCA5	GAGAAGGG-CGGAGGGTTGGGG 8291 TG	C C A C A	
	AGAAGGGC GG GG TT GGG		
	TCTTCCCG CC CC AA CCC		
	_ _ T C C C		
GAM520 SOX12	GAAGGGCCGGTGCGCTCAGGGA 8288 A	CGGA I	
	AGGGCCGG TTCGGG		

		TCCCGGCC GAGTCC			
		— ACGC C			
GAM520 SOX12		GAAGGGCCGGTGCCTCAGGGA	8288	TGAGAA	CGGA A
		GGGCCGG TTCGGG			
		CCCGGCC GAGTCC			
		— ACGC C			
GAM520 TPM4		GAGAAGGGCC--AGGATTC	8290	GC	I
		GAGAAGGGCCG GGATT			
		CTCTTCCCGGT CCTAA			
		— G			
GAM520 TPM4		GAGAAGGGCC--AGGATTC	8290	TG	GC GG
		AGAAGGGCCG GGATTC			
		TCTTCCCGGT CCTAAG			
		— — AI			
GAM521 COL1A1		GAGGGTTTCAGAGGAG-AGA	8306	G	— AGCAI
		AGGGTTTCAG GGA			
		TCCCAAAGTC CCT			
		— T CTCTI			
GAM521 COL1A1		GAGGGTTTCAGAGGAG-AGA	8306	TG	A C AA
		AGGGTTTCAGGG AG AGA			
		TCCCAAAGTCTC TC TCT			
		— C — CI			
GAM521 CYP1B1		TGAGGGTTTCTGATTAAAGCAGTAA	8313	AGG—	AAAAII
		TGAGGGTTTC GAAGCAG			
		ACTCCCAAAG TTTCGTC			
		ACTAA ATTII			
GAM521 CYP1B1		TGAGGGTTTCTGATTAAAGCAGTAA	8313	A	AGG— AAI
		GGGTTTC GAAGCAG			
		CCCAAAG TTTCGTC			
		— ACTAA AII			
GAM521 FE65L2		GAGGGTTTCAGCCGGAAGGCATCAAGAAAA	8304	— T	CAI
		GAGGGT TCAGGGAAG			
		CTTCCG AGTTCTTTT			
		GC T III			
GAM521 FE65L2		GAGGGTTTCAGCCGGAAGGCATCAAGAAAA	8304	TG	— — GA AIIC
		AGGGTTTCAG GGAAG CA AA			
		TCCCAAAGTC CCTTC GT TT			
		— GG C AG CTTTT			
GAM521 FLG		TGATGGTTTCTG-GAAGCAGA	8317	G	AG AA
		TGA GGTTC GGAAGCAGA			

	ACT CCAAAG CCTTCGTCT		
	A A_ II		
GAM521 FLG	TGATGGTTTCTG-GAAGCAGA 8317_ G	AG	I
	GA GGTTTC GGAAGCAG		
	II IIIII IIIIIII		
	CT CCAAAG CCTTCGTC		
	A A A_ I		
GAM521 GABRB2	TGAGGGTTTCACTGAAG-AGA 8316	GG	C AA
	TGAGGGTTTCA GAAG AGA		
	IIIIIIII III III		
	ACTCCCAAAGT CTTC TCT		
	GA _ II		
GAM521 GABRB2	TGAGGGTTTCACTGAAG-AGA 8316_	GG	C I
	GAGGGTTTCA GAAG AG		
	IIIIIIII III II		
	CTCCCAAAGT CTTC TC		
	A GA _ I		
GAM521 GATA2	GGGTTGAAGGGTTAGCAGAAAA 8308 G	TC	A_ I
	GTT AGGG AGCAGAAA		
	III III IIIIIII		
	CAA TCCC TCGTCTTT		
	_ CT AA I		
GAM521 GATA2	GGGTTGAAGGGTTAGCAGAAAA 8308 T__	TCAGGGA	
	GAGGGTT AGCAGAAAA		
	IIIIII IIIIIII		
	TTCCCAA TCGTCTTTT		
	AAC _____		
GAM521 KLK13	TGAGATGTTTCAGGGATGCA 8311 _	A	GAAA
	TGAGG GTTTCAGGGA GCA		
	IIII IIIIIII III		
	ACTCT CAAAGTCCCT CGT		
	A A IIIA		
GAM521 KLK13	TGAGATGTTTCAGGGATGCA 8311 _	A	II
	TGAGG GTTTCAGGGA GC		
	IIII IIIIIII II		
	ACTCT CAAAGTCCCT CG		
	A A TI		
GAM521 LOXL2	GAGGGTTTCATTGGAAG-AGA 8303	G_	C I
	AGGGTTTCA GGAAG AG		
	IIIIII III II		
	TCCCAAAGT CCTTC TC		
	AA _ I		
GAM521 LOXL2	GAGGGTTTCATTGGAAG-AGA 8303 TG	G_	C AA
	AGGGTTTCA GGAAG AGA		
	IIIIII III III		
	TCCCAAAGT CCTTC TCT		
	_ AA _ CI		
GAM521 MRPL49	TGAGGGTTTCCATGGAAGC 8312	AG_	AGAAA
	TGAGGGTTTC GGAAGC		
	IIIIII IIIII		

	ACTCCCAAAG CCTTCG			
	GTA IIIAA			
GAM521 MRPL49	TGAGGGTTTCCATGGAAGC	8312	AG_	II
	TGAGGGTTTC GGAAG			
	ACTCCCAAAG CCTTC			
	GTA GI			
GAM521 MVK	TGGGAGCTTCAGGGAAGCAG	8315 A		AAA
	TG GGGTTTCAGGGAAGCAG			
	AC CTCGAAGTCCCTTCGTC			
	C III			
GAM521 MVK	TGGGAGCTTCAGGGAAGCAG	8315 GA		I
	GGGTTTCAGGGAAGCA			
	CTCGAAGTCCCTTCGT			
	CC I			
GAM521 PTP4A2	GTTTCAC---AGCAGAAAA	8310	GGGA	
	GTTTCA AGCAGAAA			
	CAAAGT TCGTCTTT			
	G_			
GAM521 PTPRF	TGAGGGTTT---GAAGCAGAA	8318	CAGG	
	TGAGGGTTT GAAGCAGAA			
	ACTCCCAA CTTCGTCTT			

GAM521 PTPRF	TGAGGGTTT---GAAGCAGAA	8318 _	CAGG	
	GAGGGTTT GAAGCAGA			
	CTCCCAA CTTCGTCT			
	A _____			
GAM521 RBP5	TGAAGGTTTCAGGAGAATGCAG	8314	_ _	AAAA
	TGAGGGTTTCAGG GAA GCAG			
	ACTTCCAAAGTCC CTT CGTC			
	T A IIIA			
GAM521 RBP5	TGAAGGTTTCAGGAGAATGCAG	8314 GA	_ _	I
	GGGTTTCAGG GAA GCA			
	TCCAAAGTCC CTT CGT			
	_____ T A I			
GAM521 RFX5	AGGGTGAGAGGGAAGCAGGAA	8302	TTC	AAI
	GGGT AGGGAAGCAG			
	CCCA TCCCTTCGTC			
	CTC CTI			
GAM521 RFX5	AGGGTGAGAGGGAAGCAGGAA	8302 TGAG	TTC	AAAA
	GGT AGGGAAGCAG			

		CCA TCCCTTCGTC			
		____ CTC CTTA			
GAM521 SCA2		GAGGGGT-CAGACGGAAGCAGAA	8305 A	TCAG	I
		GGGTT GGAAGCAGA			
		CCCAG CCTTCGTCT			
		C TCTG I			
GAM521 SCA2		GAGGGGT-CAGACGGAAGCAGAA	8305 TG	TT ____	AA
		AGGG TCAG GGAAGCAGAA			
		TCCC AGTC CCTTCGTCTT			
		__ C_ TG GI			
GAM521 SIGLEC5		GGCTGTCAGGGAAG--GAAA	8309 G	_ C I	
		GGTT TCAGGGAAG AGA			
		CCGA AGTCCCTTC TTT			
		_ C C I			
GAM521 SIGLEC5		GGCTGTCAGGGAAG--GAAA	8309 TGAGGGTT		CA
		TCAGGGAAG GAA			
		AGTCCCTTC CTT			
		AC_____			
GAM521 THPO		GGGTTTCAGGAGAAAGTAGGAAA	8307 G	_ CAGAAAI	
		TTTCAGG GAAG			
		AAAGTCC CTTT			
		_ T CATCCTI			
GAM521 THPO		GGGTTTCAGGAGAAAGTAGGAAA	8307 TGAGGG	_ CA__ AI	
		TTTCAGG GAAG GAAA			
		AAAGTCC CTTT CTTT			
		_____ T CATC AG			
GAM522 ADAM19		AGGATGGGAGGAGGCCCCA	8322	TGTAT	II
		AGGGT GAGGCCCC			
		TCCTA CTCCGGGG			
		CCCTC TI			
GAM522 ADAM19		AGGATGGGAGGAGGCCCCA	8322 TGAA	TTGTAT	T
		GGG GAGGCCCCA			
		CCC CTCCGGGGT			
		TA__ TC__ C			
GAM522 CD209L		GAAGAGGTTGTATGGAGCCTCCAT	8323 AA	AG _ I	
		GGGTTGTATG GCC CCA			
		TCCAACATAC CGG GGT			
		C_ CT A I			
GAM522 CD209L		GAAGAGGTTGTATGGAGCCTCCAT	8323 TG	_ AG _ CI	
		AAG GGTGTATG GCC CCAT			

	TTC CCAACATAC CGG GGTA		
	__ T CT A CI		
GAM522 CDKN2D	GGGTCTCGTCTGAGGCCCA 8326	GTA__ III	
	GGGTT TGAGGCCCC		
	CCCAG ACTCCGGGG		
	AGCAG TII		
GAM522 CDKN2D	GGGTCTCGTCTGAGGCCCA 8326	TGAAGGG A T	
	TTGT TGAGGCCCA		
	AGCA ACTCCGGGGT		
	G____ G C		
GAM522 CNP	GGGTTCTGGCTGTGGCCCCATC 8327	____ ATGA I	
	GGTTGT GGCCCCAT		
	CCGACA CCGGGGTA		
	AAGA ____ I		
GAM522 CNP	GGGTTCTGGCTGTGGCCCCATC 8327	TGAAG ATGA	
	GGTTGT GGCCCCATC		
	CCGACA CCGGGGTAG		
	AGA__ ____		
GAM522 GABRA2	AAGGGTTGTA-CAGGATCCCCAT 8321	A G __ I	
	GGGTTGTAT AGG CCCCA		
	CCCAACATG TCC GGGGT		
	_ _ TA I		
GAM522 GABRA2	AAGGGTTGTA-CAGGATCCCCAT 8321	TGAA G __ C	
	GGGTTGTAT AGG CCCCAT		
	CCCAACATG TCC GGGGTA		
	____ _ TA A		
GAM522 GRIA1	TGAAGGGTTTGGGATGGGGC 8331	GT__ A CCCAT	
	TGAAGGGTT ATG GGC		
	ACTTCCCAA TAC CCG		
	ACCC C IICT		
GAM522 GRIA1	TGAAGGGTTTGGGATGGGGC 8331	GT__ A III	
	TGAAGGGTT ATG GG		
	ACTTCCCAA TAC CC		
	ACCC C GII		
GAM522 MAP1B	GAAGGGTTG-ATCAGGACC 8325	T G _ I	
	GAAGGGTTG AT AGG CC		
	CTTCCCAAC TA TCC GG		
	_ G T I		
GAM522 MAP1B	GAAGGGTTG-ATCAGGACC 8325	TG T G _ CCA	
	AAGGGTTG AT AGG CC		

	TTCCCAAC TA TCC GG		
	___ _ G T TII		
GAM522 NR1D1	GAAGGGTTGGACGTTGAGGC 8324	TA___ III	
	GAAGGGTTG TGAGG		
	CTTCCCAAC ACTCC		
	CTGCA GII		
GAM522 NR1D1	GAAGGGTTGGACGTTGAGGC 8324 TG	TA___ CCCAT	
	AAGGGTTG TGAGGC		
	TTCCCAAC ACTCCG		
	___ CTGCA TIIIC		
GAM522 OTP	TGCAGGGTTGTA-GATGTCC 8332 A	T GG_ CCAT	
	TG AGGGTTGTA GA CC		
	AC TCCCAACAT CT GG		
	G _ ACA IIIC		
GAM522 OTP	TGCAGGGTTGTA-GATGTCC 8332 _A	T GGCCI	
	G AGGGTTGTA GA		
	C TCCCAACAT CT		
	A G _ ACAGI		
GAM522 PBX3	GGTTTGTATGAGTTCGCAT 8328 G	GCCCCAI	
	GG TTGTATGAG		
	CC AACATACTC		
	A AAGCGTAI		
GAM522 PBX3	GGTTTGTATGAGTTCGCAT 8328 TGAA_ _	CCCCAT	
	GGGTT GTATGAGG		
	CTCAA CGTACTCC		
	ACATA G IIICTA		
GAM522 RAB1A	TGAAGGGTTGTGCGCCCGCCCCAT 8334	ATGAG CI	
	TGAAGGGTTGT GCCCCAT		
	ACTTCCCAACA CGGGGTA		
	GCGGG II		
GAM522 RAB1A	TGAAGGGTTGTGCGCCCGCCCCAT 8334	ATGAG I	
	GAAGGGTTGT GCCCCA		
	CTTCCCAACA CGGGGT		
	GCGGG I		
GAM522 SDPR	TGAGGGTGTAGGATGAGGCC 8330 A T _	CATC	
	TGA GGGT GTA TGAGGCC		
	ACT CCA CAT ACTCCGGG		
	_ _ CCT IIIC		
GAM522 SDPR	TGAGGGTGTAGGATGAGGCC 8330 GA T _	I	
	AGGGT GTA TGAGGCC		

	TCCCA CAT ACTCCGG			
	__ _ CCT I			
GAM522 TAL1	GGCTGAATTAGGGCCCCATC	8329	T GA_ II	
	GGTTG AT GGCCCCAT			
	CCGAC TA CCGGGGTA			
	T ATC GI			
GAM522 TAL1	GGCTGAATTAGGGCCCCATC	8329	TGAAGGGTTGTATGA	
	GGCCCCAT			
	CCGGGGTA			
	TTAATC_____			
GAM522 XRCC3	TGAGGGG--GTCTGAGGCCCA	8333	A_ GTA T	
	TGA GGGTT TGAGGCCCA			
	ACT CCCAG ACTCCGGGGT			
	CC ____ I			
GAM522 XRCC3	TGAGGGG--GTCTGAGGCCCA	8333	_ A_ GTA I	
	GA GGGTT TGAGGCCCA			
	CT CCCAG ACTCCGGGG			
	A CC ____ I			
GAM523 AR	TGGCTGGCA-CAGAGTAGT	8343	A A CTC	
	TG CTGGTA CAGAGTAGT			
	AC GACCGT GTCTCATCA			
	C _			
GAM523 CYP1A2	CTGGCAACAGAGTAAGACTC	8338	TGACTG _ T G	
	GTAACAGAGTA G CTC			
	CGTTGTCTCAT C GAG			
	_____ T T A			
GAM523 EGFL4	TGCCTG---ACAGAGTAGGTA	8341	TGA GTA T__ I	
	CTG ACAGAGTAG CTCGA			
	GAC TGTCTCATC GAGCT			
	ACG ____ CAT I			
GAM523 FGA	TGACGTGTAACAGAG-AGT	8342	TG T CTC	
	TGAC GTAACAGAG AGT			
	ACTG CATTGTCTC TCA			
	CA _			
GAM523 GALNT7	CTGGATAACAGAGTA-TCT	8337	TGACT G C	
	GGTAACAGAGTA TCT			
	CTATTGTCTCAT AGA			
	_____ _ A			
GAM523 NDUFB3	TGACTGAGGTAACAGA-TACTGTAGA	8339	____ TCTCGAII	
	TGACT GGTAACAGA GTAG			

	ACTGA CCATTGTCT CATC		
	CT ATGA TIIIAGCT		
GAM523 RFP	TGACTGGTAAGGGATCTAGT 8340	CA G_	CTCG
	TGACTGGTAA GA TAGT		
	ACTGACCATT CT ATCA		
	CC AG IIIA		
GAM524 ASNS	TCAGC-AAGT-CACTTGATG 8350	TGTCACCTAAATG	
	CACTTGATG		
	GTGAACTAC		
	TCGTTCA_____		
GAM524 GOLGA5	TGTCACCTAACATACA---GATGGT 8352	_	CTT
	TGTCACCTAA ATGCA GATGGT		
	ACAGTGGATT TATGT CTACCA		
	G _____		
GAM524 MRE11A	TGTCAGA-AAATGCACTCGAT 8353	CCT	GG
	TGTCA AAATGCACTTGAT		
	ACAGT TTTACGTGAGCTA		
	CT_ II		
GAM524 MTCP1	GTCACCTAAGGGAACCTGA 8348	TG ATGC	TGG
	TCACCTAA ACTTGA		
	AGTGGATT TGGACT		
	___ CCCT TII		
GAM524 MYB	TCAACTAAATGCACTTGATG 8349	TGTCAC	A G
	CTAAATGCACTTG TG		
	GATTTACGTGAAC AC		
	TT_____ C G		
GAM524 NARS	ACCTTAATATCACTTGATG 8346	TGTCACCTA _	G
	AATG CACTTGATG		
	TTAT GTGAACTAC		
	A_____ A A		
GAM524 RGS9	TGTCACCCAAATGCACTT--TGGT 8354		GA
	TGTCACCTAAATGCACTT TGGT		
	ACAGTGGGTTTACGTGAA ACCA		

GAM524 TCEB1L	GTCACCTAAAGTTAACTTG 8347	TG TGC_	ATGG
	TCACCTAAA ACTTG		
	AGTGGATTT TGAAC		
	___ CAAT CIII		
GAM524 TMOD	TGTCACACATTTTAAATGCACTTGA 8351	C_____	TGGTII
	TGTCAC TAAATGCACTTGA		

	ACAGTG	ATTTACGTGAACT		
	TGTAAA	IIITGG		
GAM525 ABCB9	AAGGGGAGAGGCCTAGTCTC	8357 TGGAA	A	A AT
	GGGGAG CTTAGT TC			
	CCTCTC GGATCA AG			
	C_____ C G AC			
GAM525 EDAR	AAGGGGAGACTCACTCATCAT	8358 TGGAAG	G_	A
	GGGAGACTTA TATCAT			
	CCCTCTGAGT GTAGTA			
	_____ GA G			
GAM525 GLTSCR1	TGGCAGGGGAGACGTTTTCAT	8365 A		TTAGTATCATA
	TGG AGGGGAGAC			
	ACC TCCCCTCTG			
	G CAAAATGTAT			
GAM525 ITGA2	TGGAAGGGGAGCCGTGGTAT	8362	_ A TA_	CATA
	TGGAAGGGG AG CT GTAT			
	ACCTTCCCC TC GG CATA			
	G _ CAC A			
GAM525 JUNB	TGGAAGGGGGGGCTT-GTA	8364	AGA A TCA	
	TGGAAGGGG CTT GTA			
	ACCTTCCCC GAA CAT			
	CCC _			
GAM525 KIF5A	GGGGAGGGAGTTAGTATCA	8361 TGGAAG	AC	T
	GGGAG TTAGTATCA			
	CCCTC AATCATAGT			
	_____ _ C			
GAM525 NR3C1	TGCAAGGGGAGATTGAGTA	8363 G	CTT	TCAT
	TG AAGGGGAGA AGTA			
	AC TTCCCCTCT TCAT			
	G AAC A			
GAM525 SCNN1A	GGAAGGGGAATTGCCTAAGTAACA	8359 TG	A_ _	T TAI
	GAAGGGGAG CTTA GTA CA			
	CTTCCCCTT GGAT CAT GT			
	_ AAC T T T			
GAM525 SON	GGAAGGGGAG--TTA-CATCATA	8360 TG	AC	G
	GAAGGGGAG TTA TATCAT			
	CTTCCCCTC AAT GTAGTA			
	_____ _ _			
GAM526 BAALC	GAAAGCTATGCAAAATTGCAATGTC	6909 AAAG	TG C	I
	GTG AA TTGCAATGT			

	TAC TT AACGTTACA		
	TCGA GT T I		
GAM526 BAALC	GAAAGCTATGCAAATTGCAATGTC 6909 TGAAAG TG C	II	
	GTG AA TTGCAATGTC		
	TAC TT AACGTTACAG		
	TTTCGA GT T AI		
GAM526 CALCRL	GAAAGA-GTGAAAGCTTTGCAATGT 6910 AAA T C__	I	
	GG GTGAA TTGCAATG		
	TC CACTT AACGTTAC		
	__ T TCGA I		
GAM526 CALCRL	GAAAGA-GTGAAAGCTTTGCAATGT 6910 TGA T C__	CI	
	AAGG GTGAA TTGCAATGT		
	TTTC CACTT AACGTTACA		
	__ T TCGA CI		
GAM526 DCX	TGAAAGGTGTCAGACCTGAAA 6912 GA_ CAATGTC		
	TGAAAGGTGT ACTTG		
	ACTTTCCACA TGGAC		
	GTC TTTIIC		
GAM526 DCX	TGAAAGGTGTCAGACCTGAAA 6912 G GA_ CAI		
	AAAGGTGT ACTTG		
	TTTCCACA TGGAC		
	_ GTC TTI		
GAM526 DRD2	TGCAGGGTGTGAACTGTCCATCTC 6915 AAA TGCA G I		
	TG GGTGTGAACT AT TC		
	AC CCACACTTGA TA AG		
	GTC CAGG G I		
GAM526 DRD2	TGCAGGGTGTGAACTGTCCATCTC 6915 AAA TGCAAI		
	GGTGTGAACT		
	CCACACTTGA		
	C_ CAGGTA		
GAM526 GRB10	GGTGT-AACT-GCAATGTC 8379 AC I		
	GGTGTGA TTGCAATGT		
	CCACATT GACGTTACA		
	_ G		
GAM526 ITK	TGAAAGGTGGTGCACCTTG 6911 _ A III		
	TGAAAGGTG TG ACTT		
	ACTTTCCAC AC TGGA		
	C G ACI		
GAM526 ITK	TGAAAGGTGGTGCACCTTG 6911 _ AA_ CAATGT		
	TGAAAGGTG TG CTTG		

	ACTTTCCAC AC GAAC		
	C GTG IIICTG		
GAM526 MTF1	TGAAAGGTGAGGA-TTTCAA	6914	T_ ACTTGCAATGT
	TGAAAGGTG GA		
	II		
	ACTTTCCAC CT		
	TC AAAGTTIIICT		
GAM526 MTF1	TGAAAGGTGAGGA-TTTCAA	6914_	T_ ACTTGCAI
	GAAAGGTG GA		
	II		
	CTTTCCAC CT		
	A TC AAAGTIII		
GAM526 NDRG3	AAGGA-TGGACTTGCAATG	6908	T A I
	AAGG GTG ACTTGCAAT		
	III		
	TTCC TAC TGAACGTTA		
	_ C C		
GAM526 NDRG3	AAGGA-TGGACTTGCAATG	6908	TGAAA T A
	GGTG GA CTTGCAATG		
	II		
	CTAC CT GAACGTTAC		
	_____ - -		
GAM526 OCRL	TGAAAGG-GAGA-CTAATGCAATGTC	6913	TGT ACT_ I
	TGAAAGG GA TGCAATGTC		
	II		
	ACTTTCC CT ACGTTACAG		
	CT_ GATT I		
GAM526 OCRL	TGAAAGG-GAGA-CTAATGCAATGTC	6913	TGT ACT_ I
	GAAAGG GA TGCAATGT		
	II		
	CTTTCC CT ACGTTACA		
	CT_ GATT I		
GAM526 RORB	AAAAGTCTTGACCTTGCAATGT	6905	AAGG_ T A I
	TG GA CTTGCAATG		
	AC CT GAACGTTAC		
	TCAGA _ G I		
GAM526 RORB	AAAAGTCTTGACCTTGCAATGT	6905	TGAAAGG T A CI
	TG GA CTTGCAATGT		
	AC CT GAACGTTACA		
	TTCAGA_ _ G AT		
GAM526 SRD5A2	AAACATGAGAGTTTGCAATGTC	6906	G T AC I
	AA GTG GA TTGCAATGT		
	TT TAC CT AACGTTACA		
	G T CA I		
GAM526 SRD5A2	AAACATGAGAGTTTGCAATGTC	6906	TGAAAG T AC
	GTG GA TTGCAATGTC		

	TAC CT AACGTTACAG	
	TG____ T CA	
GAM526 ZNF215	AAGGTGTGACGTGAC-TGCAA 6907 AC____ III	
	AAGGTGTGA TTGCA	
	TTCCACACT GACGT	
	GCACT TII	
GAM526 ZNF215	AAGGTGTGACGTGAC-TGCAA 6907 TGAAA GT AC T	
	G GTGA TTGCAA GT	
	C CACT GACGTT CA	
	CACA_TG ____ _	
GAM527 MUC3B	TACTG-ATATCAGTGGGTA 8393 AT G G CT	
	ACTG ATG CAGTGGGTA	
	TGAC TAT GTCACCCAT	
	____ _ A AI	
GAM527 MX1	CTGGATGGC-G-GCGTTCTTC 8392 ATACTG A GGTA	
	GATGGC GTG CTT	
	CTACCG CGC GAA	
	____ C AA__	
GAM528 BCRP2	AGAGCCTTGCGCGGCACAC 8398 _ T II	
	AGA CCTT TGCGGCACA	
	TCT GGAA GCGCCGTGT	
	C C GI	
GAM528 BCRP2	AGAGCCTTGCGCGGCACAC 8398 TGAAGA T CT	
	CCTT TGCGGCACAC	
	GGAA GCGCCGTGTG	
	C____ C AT	
GAM528 COX7C	AAGACCTTTTTTTTCACGACCT 8397 A GCGG _ I	
	GACCTTTT CAC ACC	
	CTGGAAAA GTG TGG	
	_ AAAA C I	
GAM528 COX7C	AAGACCTTTTTTTTCACGACCT 8397 TGAA GCGG _ G	
	GACCTTTT CAC ACCT	
	CTGGAAAA GTG TGGA	
	____ AAAA C A	
GAM528 HUNK	AAGAC-TTTTGTAGGCACACCT 8396 C C_ I	
	AGAC TTTTG GGCACACC	
	TCTG AAAAC CCGTGTGG	
	_ AT I	
GAM528 HUNK	AAGAC-TTTTGTAGGCACACCT 8396 TGAA C C_	
	GAC TTTTG GGCACACCTG	

		CTG AAAAC CCGTGTGGAT		
		_____ AT		
GAM528 IL16		CCTTCTGTGCGGCACACCTG 8401 _ II		
		CCTTTTG CGGCACACCT		
		GGAAGAC GCCGTGTGGA		
		A CI		
GAM528 SIRPB2		TGAAGACCTTGCTCTGGGGCA 8402 _ C CACCTG		
		TGAAGACCT TTTG GGCA		
		ACTTCTGGA AGAC CCGT		
		ACG C GTC		
GAM528 SIRPB2		TGAAGACCTTGCTCTGGGGCA 8402 _ C		
		TGAAGACCT TTTG GGC		
		ACTTCTGGA AGAC CCG		
		ACG C T		
GAM528 TCF2		AGCCCTGTGTCACGGCACACC 8400 AGA T TG II		
		CCT T CGGCACAC		
		GGA A GCCGTGTG		
		TCG C GT GI		
GAM528 TCF2		AGCCCTGTGTCACGGCACACC 8400 TGAAGA T TG T		
		CCT T CGGCACACC		
		GGA A GCCGTGTGG		
		_____ C GT C		
GAM528 WT1		AGACCAACTCTTCCAGGCACACCTG 8399 TGAA _ TT C II		
		GAC CTT G GGCACACCTG		
		TTG GAA T CCGTGTGGAC		
		GG_ A GG_ CA		
GAM528 WT1		AGACCAACTCTTCCAGGCACACCTG 8399 _ TT C I		
		GAC CTT G GGCACACCT		
		TTG GAA T CCGTGTGGA		
		A GG_ I		
GAM529 BACE		TCT-TGGAGATGAGGTCTAA 8418 G _ TATA		
		TCT TGGAGA GAGGTCTAA		
		AGA ACCTCT CTCCAGATT		
		_ A A		
GAM529 BACE		TCT-TGGAGATGAGGTCTAA 8418 G _ II		
		TCT TGGAGA GAGGTCTA		
		AGA ACCTCT CTCCAGAT		
		_ A TI		
GAM529 BACH1		TGTAATGCTATGCAATATACAGAA 8425 G AC _ II		
		TGTAA GC TGT TATACAGAA		

	ACATT CG ACG ATATGTCTT		
	A AT TT II		
GAM529 BAZ2A	TGTAAGGCAGTGATGGACCCAGAA 8427	C TTATA__ II	
	TGTAAGGCA TG CAGAA		
	II		
	ACATTCCGT AC GTCTT		
	C TACCTGG II		
GAM529 BPAG1	AAGGTCACTAT-ATACAGAA 8405 TGTAAGG T		
	CACTGT ATACAGAA		
	GTGATA TATGTCTT		
	CA_____ _		
GAM529 DHCR24	TGTAAGGCACTGAAATTA ACTACAG 8424	TTA_____ AAIII	
	TGTAAGGCACTG TACAG		
	ACATTCCGTGAC ATGTC		
	TTTAATTG IIIAA		
GAM529 DIRC1	TGTGGAGAGAAATTCAATA 8431	C II	
	TGTGGAGAGAGGT TAAT		
	ACACCTCTCTTTA GTTA		
	A TI		
GAM529 DIRC1	TGTGGAGAGAAATTCAATA 8431 TCTG	C TA	
	TGGAGAGAGGT TAATA		
	ACCTCTCTTTA GTTAT		
	_____ A CA		
GAM529 ENAM	AAGACAGTTTTATACAGAA 8407 TGTAAG CTG		
	GCA TTATACAGAA		
	TGT AATATGTCTT		
	_____ CAA		
GAM529 HSPA4	AGGCACTCTGTTATACAGAA 8409 TGTAAG A		
	GC CTGTTATACAGAA		
	TG GACAATATGTCTT		
	_____ A		
GAM529 IRF1	AAGGCACTG-TATAAATAA 8408 TGTAAG T CAGA		
	GCACTGT ATA		
	CGTGACA TAT		
	_____ _ TTAT		
GAM529 KCNK2	TAAGGCACTG---ACAGAA 8417 TGTA TTAT		
	AGGCACTG ACAG		
	TCCGTGAC TGTC		
	_____ _		
GAM529 LOXL2	TGGAAGAGAGGTCTAGATAT 8422 _ ATAIII		
	TGGA GAGAGGTCTA		

	ACCT CTCTCCAGAT			
	T CTATAI			
GAM529 LOXL2	TGGAAGAGAGGTCTAGATAT	8422	TCTGTGG	_ A
	AGAGAGGTCTA ATAT			
	TCTCTCCAGAT TATA			
	_____ C A			
GAM529 LZTFL1	TGGAGAGAGTGTGTC-AATTTA	8423	_ T ATII	
	TGGAGAGAG GTC AAT			
	ACCTCTCTC CAG TTA			
	A _ AATI			
GAM529 MST1R	TCTGTGGAGTGAGGGACCTAAT	8420	A _ ATAA	
	TCTGTGGAG GAGG TCTAAT			
	AGACACCTC CTCC GGATTA			
	A CT IIIA			
GAM529 MST1R	TCTGTGGAGTGAGGGACCTAAT	8420	CT A _ I	
	GTGGAG GAGG TCTAA			
	CACCTC CTCC GGATT			
	_ A CT I			
GAM529 MX1	TCTTTGCAAAGTAAGCTCTAATATA	8419	C TG A G I	
	TG GAG GAG TCTAATAT			
	AC TTC TTC AGATTATA			
	A GT A G I			
GAM529 MX1	TCTTTGCAAAGTAAGCTCTAATATA	8419	TC_ TG A G AII	
	TG GAG GAG TCTAATATA			
	AC TTC TTC AGATTATAT			
	AGAA GT A G III			
GAM529 OAS3	TGTGGAGAGTCAGGCTGTCTAA	8430	_ CTAIIT	
	TGTGGAGAG AGGT			
	ACACCTCTC TCCG			
	AG ACAGATT			
GAM529 OAS3	TGTGGAGAGTCAGGCTGTCTAA	8430	TCTG _ _ TATAA	
	TGGAGAG AGGT CTAA			
	ACCTCTC TCCG GATT			
	_____ AG ACA CTIII			
GAM529 PITX2	TGTACGAAA-TGTTATACA	8428	A CAC GA	
	TGTA GG TGTTATACA			
	ACAT CT ACAATATGT			
	G TT_ II			
GAM529 PLAG1	GTAGAGCCACTGTTATTAGACAAAA	8414	TGTA G _ III	
	AG CACTGTTAT ACAGAA			

	TC GTGACAATA TGTTTT		
	ATC_ G ATC TII		
GAM529 PMCHL1	GTAAGTCATAATTATACAGAA 8415 TG G CT I		
	TAAG CA GTTATACAGAA		
	ATTC GT TAATATGTCTT		
	_ A AT A		
GAM529 PNUTL1	CTGTGGAGAAGGGGTGTAA 8412 A_ CTAII		
	CTGTGGAGAG GGT		
	GACACCTCTT CCA		
	CC CATTI		
GAM529 PNUTL1	CTGTGGAGAAGGGGTGTAA 8412 TC A_ C TATA		
	TGTGGAGAG GGT TAA		
	ACACCTCTT CCA ATT		
	_ CC C CIII		
GAM529 PPP1R11	TCTGTCGCT-GAGGTCTAAGAGAA 8421 GGAGA TATAAI		
	TCTGT GAGGTCTAA		
	AGACA CTCCAGATT		
	GCGA_ CTCTTI		
GAM529 PPP1R11	TCTGTCGCT-GAGGTCTAAGAGAA 8421 _ GGAGA TATAI		
	CTGT GAGGTCTAA		
	GACA CTCCAGATT		
	A GCGA_ CTCTI		
GAM529 PRKY	TGTAATGCTTTTTATATACAGAA 8426 G ACTGT_ II		
	TGTAA GC TATACAGAA		
	ACATT CG ATATGTCTT		
	A AAAAAT II		
GAM529 PTGFR	AAAGAAATCTTATACAGAA 8406 TGTAAGGCACTG		
	TTATACAGAA		
	AATATGTCTT		
	CTTTAG_____		
GAM529 RABIF	CTGTAGCAGTGAGGAGCTAATATAA 8411 T_ TG A AG T I		
	G G GAG G CTAATATA		
	C C CTC C GATTATAT		
	AT GT A CT_ I		
GAM529 RABIF	CTGTAGCAGTGAGGAGCTAATATAA 8411 TC _ A T_ II		
	TGTGG AG GAGG CTAATATAA		
	ACATC TC CTCC GATTATATT		
	_ G A TC TI		
GAM529 TCFL4	GTAGAGAGAGGT-TGCTATAA 8416 _ ATATI		
	TGGAGAGAGGT CTA		

	ATCTCTCTCCA GAT		
	AC ATIII		
GAM529 TCFL4	GTAGAGAGAGGT-TGCTATAA 8416 TCTGTG	CTAA	
	GAGAGAGGT TATA		
	CTCTCTCCA ATAT		
	_____ ACG_		
GAM529 TGFA	CTGATTGATAGAGGTCTAA 8410 TG_ G	II	
	CTG GA AGAGGTCTA		
	GAC CT TCTCCAGAT		
	TAA A TI		
GAM529 TGFA	CTGATTGATAGAGGTCTAA 8410 TCTGTG G	TATA	
	GA AGAGGTCTAA		
	CT TCTCCAGATT		
	ACTAA_ A TIII		
GAM529 TGFB1	TGTAAGGCACT-TCA-ACAG 8429	GTTAT A	
	TGTAAGGCACT ACAG		
	ACATTCCGTGA TGTC		
	AGT_ I		
GAM529 ZNF256	CTGTGGAGAAGTGCTCTGCTGATAA 8413	AG_ AATATAI	
	TGGAGAG G TCT		
	ACCTCTT C AGA		
	CA G CGACTII		
GAM529 ZNF256	CTGTGGAGAAGTGCTCTGCTGATAA 8413 TC	AG_ AATATAAII	
	TGTGGAGAG G TCT		
	ACACCTCTT C AGA		
	_____ CA G CGACTATTC		
GAM530 ANK1	TCACTGTTTACTCT-CTCT 8438	TCGTA AGA	
	TCACTGTT TGCTCT		
	AGTGACAA ATGAGA		
	_____ GAG		
GAM530 HMGN3	CACTGATTA-T-TGCTCTAGA 8434 TC	TTTCGTA	
	ACTG TGCTCTAGA		
	TGAC ACGAGATCT		
	_____ TAATA_		
GAM530 MTMR8	CTGTCTCCTTGACTGCTCTAGA 8435 TCA G	CGTA I	
	CT TTT TGCTCTAGAG		
	GA GAA ACGAGATCTT		
	A_ G CTG_ A		
GAM530 NPEPPS	TCACAGTTTCGTTATGCTCTA 8437 T	_ GAG	
	TCAC GTTTCGT ATGCTCTA		

AGTG CAAAGCA TACGAGAT
 T A III
 GAM530 SFRP4 TCACTGTTTCTGGTGCTGCTTAAGAG 8436 GTA___ CT III
 TCACTGTTTC TGCT AGAG
 ||||| ||| |||
 AGTGACAAAG ACGA TCTC
 ACCACG AT III
 GAM530 ZNF36 TCACTGTTTAGAAAG-TCTA 8439 CGTATGC GA
 TCACTGTTT TCTA
 ||||| |||
 AGTGACAAA AGAT
 TCTTTC_ II
 GAM531 COX15 ATAGGAAGCATGGCGCTGGCATC 8443 CATTGT _ AI
 AGGC TGGCGCTGGCATC
 ||| |||||
 TTCG ACCGCGACCGTAG
 ATCC_ T AI
 GAM531 EML1 GTAGGCTGGTGATGTCATCA 8447 CATTGTAG CGC G
 GCTGG TG CATC
 ||| |||
 CGACC AC GTAG
 _____ ACT A
 GAM531 EP300 AGGCTGGCGCCGCCGCTCA 8442 CATTGTAG G G_
 GCTG CGCT GCATC
 ||| ||| |||
 CGGC GCGG TGTAG
 CG_____ G AG
 GAM531 ETF1 TTGTAGGCTGCTGCGCTGACACCA 8448 CATT _ I
 GTAGGCTG GCGCTGGCATCA
 ||||| |||||
 CATCCGAC CGCGACTGTGGT
 _____ GA A
 GAM531 PCDHB9 ATTGTAGGCTGGGTGCGGTGGC-TCA 8445 CA _ C A II
 TTGTAGGCTG GCG TGGC TCA
 ||||| ||| ||| |||
 AACATCCGAC CGC ACCG AGT
 _____ CCA C _ AI
 GAM531 PPP1R12B ATGGTAGGCTGGGCGTGCGC 8444 CATT _ CT ATC
 GTAGGCTGG CG GGC
 ||||| || |||
 CATCCGACC GC CCG
 AC_ C AC GII
 GAM531 TCL1A CATTGTAGGCTGGC-CAGGC-TCA 8446 GCT A
 CATTGTAGGCTGGC GGC TCA
 ||||| ||| |||
 GTAACATCCGACCG CCG AGT
 GT_ _
 GAM532 AP1M1 AGGCTGGCGTCTCTCACCA 8450 _ GG II
 AGGCTGGCG CT CATC
 ||||| || |||

	TCCGACCGC GA GTGG		
	A GA TI		
GAM532 COX15	ATAGGAAGCATGGCGCTGGCATC	8443 CATTGT	_ AI
	AGGC TGGCGCTGGCATC		
	TTCG ACCGCGACCGTAG		
	ATCC_ T AI		
GAM532 COX15	ATAGGAAGCATGGCGCTGGCATC	8443 TTGT	_ I
	AGGC TGGCGCTGGCAT		
	TTCG ACCGCGACCGTA		
	TCC_ T I		
GAM532 EML1	GTAGGCTGGTGTATGTCATCA	8447 CGC G	I
	TAGGCTGG TG CATC		
	ATCCGACC AC GTAG		
	ACT A I		
GAM532 EML1	GTAGGCTGGTGTATGTCATCA	8447 CATTGTAG	CGC G
	GCTGG TG CATC		
	CGACC AC GTAG		
	_____ ACT A		
GAM532 EP300	AGGCTGGCGCCGCCGCCTCA	8442	___ ATC
	AGGCTGGCGCTG GC		
	TCCGACCGCGGC CG		
	GG GAGT		
GAM532 EP300	AGGCTGGCGCCGCCGCCTCA	8442 CATTGTAG	G G_
	GCTG CGCT GCATC		
	CGGC GCGG TG TAG		
	CG_____ G AG		
GAM532 ETF1	TTGTAGGCTGCTGCGCTGACACCA	8448 CATT	_ I
	GTAGGCTG GCGCTGGCATCA		
	CATCCGAC CGCGACTGTGGT		
	_____ GA A		
GAM532 ETF1	TTGTAGGCTGCTGCGCTGACACCA	8448 TG	_ I
	TAGGCTG GCGCTGGCATC		
	ATCCGAC CGCGACTGTGG		
	_____ GA I		
GAM532 LNK	TGTAGGCTGGGCGCGGTGGC	8464	_ T
	TGTAGGCTGG CGC GG		
	ACATCCGACC GCG CC		
	C _ ACC		
GAM532 PCDHB9	ATTGTAGGCTGGGTGCGGTGGC-TCA	8445	___ C ATCI
	GTAGGCTG GCG TGGC		

	CATCCGAC CGC ACCG		
	CCA C III C		
GAM532 PCDHB9	ATTGTAGGCTGGGTGCGGTGGC-TCA 8445 CA	___ C A II	
	TTGTAGGCTG GCG TGGC TCA		
	AACATCCGAC CGC ACCG AGT		
	___ CCA C _ AI		
GAM532 PPP1R12B	ATGGTAGGCTGGGCGTGGGC 8444 ATT	C _ II	
	GTAGGCTGG GC TGG		
	CATCCGACC CG ACC		
	TAC _ C CG		
GAM532 PPP1R12B	ATGGTAGGCTGGGCGTGGGC 8444 CATT	_ CT ATC	
	GTAGGCTGG CG GGC		
	CATCCGACC GC CCG		
	AC___ C AC GII		
GAM532 TCL1A	CATTGTAGGCTGGC-CAGGC-TCA 8446	GCT A	
	CATTGTAGGCTGGC GGC TCA		
	GTAACATCCGACCG CCG AGT		
	GT_ _		
GAM532 TCL1A	CATTGTAGGCTGGC-CAGGC-TCA 8446	GCT ATI	
	CATTGTAGGCTGGC GGC		
	GTAACATCCGACCG CCG		
	GT_ AGT		
GAM532 YES1	TGTAGGCTGGGCGCGGTGGC-TCA 8466 T	_ _ ATCI	
	AGGCTGG CGC TGGC		
	TCCGACC GCG ACCG		
	_ C CC AIII		
GAM533 ACTN1	GAGATGGGCGACGGCGGAGGTGCAA 8474 TG	_ _ A _ AII	
	AGATGGGC ACG TGGA GT CAA		
	TCTACCCG TGC GCCT CA GTT		
	_ C C C C CII		
GAM533 ADORA3	TGAGATGGGCCAAGAGGAAGT 8483	ACGT_ CAAA	
	TGAGATGGGC GGAAGT		
	ACTCTACCCG CCTTCA		
	GTTCT IIIA		
GAM533 ARHGDIB	TGAGATGGAGACGTGGAAG 8486	C TCAA	
	TGAGATGGG ACGTGGAAG		
	ACTCTACCT TGCACCTTC		
	C IIIA		
GAM533 BMP1	TGTGAGGCCACGTGGAAG 8488 TGA T G_	TCAA	
	GA GG CACGTGGAAG		

	CT CC GTGCACCTTC			
	ACA _ GG IIIA			
GAM533 CALM3	TGGGATCTGCACGTGGAA-TCA	8490	A GG G AA	
	TG GAT GCACGTGGAA TCA			
	AC CTA CGTGCACCTT AGT			
	C GA _ II			
GAM533 CCBL1	TGTGATCGGTACATGGTGGAAAGTC	8484	TGA G C ____	AAAI
	GAT GG AC GTGGAAGTC			
	CTA CC TG CACCTTCAG			
	ACA G A TAC IIIA			
GAM533 CDC25B	TGAGATGGG--CGT-AAAGTCAAA	8491	ACGTG	
	TGAGATGGGC GAAGTCAAA			
	ACTCTACCCG TTTCAGTTT			
	CA____			
GAM533 EPB72	ATGAGTCA-GTGGAAAGTCAAA	8473	TGAGATGGG C	
	CA GTGGAAGTCAA			
	GT CACCTTCAGTT			
	CA_____			
GAM533 FOXD2	GAGATGGGCGC-TGGACGT	8475	TG ACG A CA	
	AGATGGGC TGGA GT			
	TCTACCCG ACCT CA			
	_ CG_ G CI			
GAM533 GPC5	TGAGCTGCAGACGTGGAAG	8487	A _ C TCAA	
	TGAG TG GG ACGTGGAAAG			
	ACTC AC TC TGCACCTTC			
	G G _ IIIA			
GAM533 GPX3	TGGGCAGAGAGGTGGAAGTCA	8492	TG T CAC AA	
	AGA GGG GTGGAAGTCA			
	TCT CTC CACCTTCAGT			
	_ _ _ CC			
GAM533 HTR2C	TGAAATGGGCACGTATGGAA	8485	_ GTCAA	
	TGAGATGGGCACGT GGAA			
	ACTTTACCCGTGCA CCTT			
	TA IIIAA			
GAM533 MAPK9	AGATGGGCAAGTCCAAG-CAA	8472	TGAG C GG T	
	ATGGGCA GT AAG CAA			
	TACCCGT CA TTC GTT			
	_ _ T GG _			
GAM533 MSR1	GAGAAGGCCATGTGGAAGTCA	8476	TG T G C AA	
	AGA GG CA GTGGAAGTCA			

	TCT CC GT CACCTTCAGT		
	___ T G A CI		
GAM533 NEBL	TGGGAGGGAAGCACGTGGAA	8482 T___ AT	GTCAA
	GAG GGGCACGTGGAA		
	CTC TTCGTGCACCTT		
	ACC CC IIIAA		
GAM533 NOLA1	TGACGCTGAGC-CGTGGAAGT	8480 GA_ A	CAA
	TGA TGGGC CGTGGAAGT		
	ACT ACTCG GCACCTTCA		
	GCG _ III		
GAM533 NRXN3	AGATGGGCAGTTTGAATTC	8471 TGAG	CG_ AG A
	ATGGGCA TGGA TCA		
	TACCCGT ACTT GGT		
	_____ CAA AA I		
GAM533 RNF26	GGGCACGTGGCCCCAAAGTCA	8479 TGAGATG	ACGTG AA
	GGC GAAGTCA		
	CCG TTTCAGT		
	CA_____ GGG_ CC		
GAM533 RPA3	GAGATGGGC-CGCGG-GGTCA	8477 TG	A AA A
	AGATGGGC CGTGG GTCA		
	TCTACCCG GCGCC CAGT		
	_ _ C_ A		
GAM533 RPH3AL	TGAGATGGG-GGTTGGGAGTCA	8489	CACG A AA
	TGAGATGGG TGG AGTCA		
	ACTCTACCC ACC TCAGT		
	CCA_ C II		
GAM533 SDS	GATGGGCACAGAGCAGTCA	8478 TGAGAT	T A A
	GGGCACG GG AGTCA		
	CCCGTGT TC TCAGT		
	_____ C G G		
GAM533 SELL	TGAGATGCTAGGT--GTGGAAGTCA	8481	___ CAC AAI
	TGAGATG GG GTGGAAGTCA		
	ACTCTAC CC CACCTTCAGT		
	GAT A_ III		
GAM534 ARHGAP6	TAAGAGTAGCAT---GTTTTA	8503	TAGGTAI
	TAAGAGTAGCAT		
	ATTCTCATCGTA		
	CAAATI		
GAM534 ARHGAP6	TAAGAGTAGCAT---GTTTTA	8503	TAGGTATTAG
	TAAGAGTAGCAT		

	ATTCTCATCGTA			
	CAAATIIIG			
GAM534 ATRN	TAGCATTAGCTTAAGTTAGTG	8506	G_ _	III
	TAGCATTAG TA TTAGT			
	II			
	ATCGTAATC AT AATCA			
	GA TC CII			
GAM534 ATRN	TAGCATTAGCTTAAGTTAGTG	8506	TAAGAG A	AT
	TAGC TTAGGT TAGTG			
	ATCG AATTCA ATCAC			
	_____ _			
GAM534 CD34	TAA-AGTAGCATTATCTGGTA	8500	TA _	TTAGT
	AGAGTAGCATT GGT			
	TTTCATCGTAAT CCAT			
	A_ AGA IIIGT			
GAM534 CD34	TAA-AGTAGCATTATCTGGTA	8500	TA _	III
	AGAGTAGCATT GGT			
	TTTCATCGTAAT CCA			
	A_ AGA TII			
GAM534 DEC1	AAGAGTAGC-TCTGGGATT	8496	A A	TATI
	AAGAGTAGC TT GG			
	II II			
	TTCTCATCG AG CC			
	_ A CTAA			
GAM534 DEC1	AAGAGTAGC-TCTGGGATT	8496	TA A A T	AG
	AGAGTAGC TT GG ATT			
	II II			
	TCTCATCG AG CC TAA			
	_ _ A C GI			
GAM534 EEF1A1	TAAGAGTGGGGTGGCAGGTATTAG	8499	AGCAT_	TGI
	TAAGAGT TAGGTATTAG			
	ATTCTCA GTCCATAATC			
	CCCCACC III			
GAM534 EEF1A1	TAAGAGTGGGGTGGCAGGTATTAG	8499	AA AGCAT_	I
	GAGT TAGGTATTA			
	CTCA GTCCATAAT			
	_ CCCCACC I			
GAM534 FMR2	TAAGAGTAGCATT-GCTAT	8502	AGGTAI	
	TAAGAGTAGCATT			
	ATTCTCATCGTAA			
	CGATAI			
GAM534 FMR2	TAAGAGTAGCATT-GCTAT	8502	AGGTATTAG	
	TAAGAGTAGCATT			

	ATTCTCATCGTAA		
	CGATAIIIG		
GAM534 MADH4	AACAGTGAGACATTAGGTA-GAGTG 8495 A TA	TTI	
	GAG GCATTAGGTA		
	CTC TGTAATCCAT		
	A _ CTC		
GAM534 MADH4	AACAGTGAGACATTAGGTA-GAGTG 8495 TAA_ TA	TT I	
	GAG GCATTAGGTA AGTG		
	CTC TGTAATCCAT TCAC		
	TGTCA _ C_ T		
GAM534 MAPK14	TAGCATTAGTTATTGGGAGTG 8507	G AGTIII	
	TAGCATTAG TATT		
	ATCGTAATC ATAA		
	A CCCTCA		
GAM534 P4HA1	TAAGAG--GCA--AGGTATTAG 8504 TA TT		
	TAAGAG GCA AGGTATTAG		
	ATTCTC CGT TCCATAATC		
	_ _		
GAM534 P4HA1	TAAGAG--GCA--AGGTATTAG 8504 _ TA TT		
	AAGAG GCA AGGTATTA		
	TTCTC CGT TCCATAAT		
	A _ _		
GAM534 RASAL1	AGGAGCA--AG-TATTAGTG 8497 _ T TTA		
	G AGCA GGTATTAGT		
	C TCGT TCATAATCA		
	T C _		
GAM534 RFX5	TAAGAGTAGCCT--GGTGTTAG 8505	ATTA A T	
	TAAGAGTAGC GGT TTAG		
	ATTCTCATCG CCA AATC		
	GA_ C I		
GAM534 RFX5	TAAGAGTAGCCT--GGTGTTAG 8505	ATTA ATTI	
	TAAGAGTAGC GGT		
	ATTCTCATCG CCA		
	GA_ CAAT		
GAM534 SERPINB13	TAAGAG---CATTAGGTAT 8501 TAA T		
	GAG AGCATTAGGTA		
	TTC TCGTAATCCAT		
	A_ _		
GAM534 SERPINB13	TAAGAG---CATTAGGTAT 8501 TAA T	TA	
	GAG AGCATTAGGTAT		

		TTC TCGTAATCCATA			
		A_ _ II			
GAM534	TEX15	TAA-AGAAGCAGCTTAGGTATT	8498	_ A I	
		AAGA GTAGC TTAGGTAT			
		TTCT CGTCG AATCCATA			
		T _ I			
GAM534	TEX15	TAA-AGAAGCAGCTTAGGTATT	8498	T_ _ A AGTG	
		AAGA GTAGC TTAGGTATT			
		TTCT CGTCG AATCCATAA			
		AT T _ IIIG			
GAM535	APBB2	TGTCCATGTGTCAAAGAGCTT	8514	_ _T ACTGA	
		TGTC ATGTGTCAA G GCTT			
		ACAG TACACAGTT C CGAA			
		G T T IIIAG			
GAM535	ARHGEF12	TGTTA-GTGTCAAGTGGCTAC	8517	CAT C TG	
		TGT GTGTCAAGTG TTAC			
		ACA CACAGTTCAC GATG			
		AT_ C II			
GAM535	CARPX	TGT-ATGTG-CAAGTGCTT	8516	C T ACT	
		TGT ATGTG CAAGTGCTT			
		ACA TACAC GTTCACGAA			
		_ _ III			
GAM535	GDA	ATTTGTCAAGTGAATACTG	8510	TGTCATGT CT	
		GTCAAGTG TACTG			
		CAGTTCAC ATGAC			
		_____ TT			
GAM535	OGT	TGTCATGTTTTCAAGTGCT	8515	G_ TACTG	
		TGTCATGT TCAAGTGCT			
		ACAGTACA AGTTCACGA			
		AA IIIAG			
GAM535	POP2	GTGATTTATTGAGTGCTTACT	8511	TGTCATG CA GA	
		TGT AGTGCTTACT			
		ATA TCACGAATGA			
		ACTAA_ AC AI			
GAM535	RAB23	TGTCAGATGAAAAGTCTTACTG	8518	T TC G AI	
		TGTCA GTG AA TGCTTACTG			
		ACAGT TAC TT ACGAATGAC			
		C TT G II			
GAM535	TRIM9	TCATGTGTC--TTGCTTACT	8512	TGTC AAG	
		ATGTGTC TGCTTACT			

	TACACAG ACGAATGA	
	_____ A _____	
GAM535 UBQLN2	TGTACA-GTGCCAATTGTGCTTACTG 8513 _ T _	All
	TGT CA GTGTCAA GTGCTTACTG	
	ACA GT CACGGTT CACGAATGAC	
	T _ AA III	
GAM536 ADCY1	TGAGGCCCGACACGCAGTA 8526 _ A TTATGGAG	
	TGAGGCCCG CAC CA	
	ACTCCGGGC GTG GT	
	T C CATIIIGG	
GAM536 BAZ2A	GGTCCGCACACAGTACAGAG 8525 TGAGGC T	
	CCGCACACA TATGGAG	
	GGCGTGTGT ATGTCTC	
	_____ C	
GAM536 EGLN2	GACGCCTCCCAACACATTAT 8521 _ AGG C GGAG	
	TG CCCG ACACATTAT	
	GC GGGT TGTGTAATA	
	T GGA _ GIII	
GAM536 RAD18	TGAGACTC-CACACATTAT 8527 _ CATTATGGA	
	TGAGGC CCGCACA	
	ACTCTG GGTGTGT	
	A AATAIIIGG	
GAM536 RORB	GAGGCC---ACACATTATG 8523 TG CGC G	
	AGGCC ACACATTATG	
	TCCGG TGTGTAATAC	
	_____ A	
GAM536 TEM8	GAGGCCCGC---TATTAAGGAGG 8524 TG ACAC T	
	AGGCCCGC ATTA GGAG	
	TCCGGGCG TAAT CCTC	
	_____ A_____ T	
GAM536 UBE2I	GAGGCCCGCACTCAGGTTCTGG 8522 TG A TTA__ AGG	
	AGGCCCGCAC CA TGG	
	TCCGGGCGTG GT ACC	
	_____ A CCAAG CII	
GAM537 APG5L	TCAACCAAAGCCAAACCTA 8542 _ A AAAGGT	
	TCAA AAAGCCAAA CTA	
	AGTT TTTCGGTTT GAT	
	GG G IIIC TG	
GAM537 APG5L	TCAACCAAAGCCAAACCTA 8542 _ ACTIII	
	TCAA AAAGCCAAA	

	AGTT TTTCGGTTT			
	GG GGATII			
GAM537 BIG1	CAAAAAGGGCAAACTAAAA	8538	C_	II
	CAAAAAG CAAAACTAAA			
	GTTTTTC GTTTTGATTT			
	CC TI			
GAM537 BIG1	CAAAAAGGGCAAACTAAAA	8538 TC	C_	GT
	AAAAAG CAAAACTAAAAG			
	TTTTTC GTTTTGATTTTT			
	_ CC II			
GAM537 C7	AATAAGGAATAAATAAAAGGTC	8533	TCAAAAAGCCAAAAC	
	TAAAAGGTC			
	ATTTTCCAG			
	ATTCCTTATTT_			
GAM537 CCNT2	AAAAGCCAAGCAACAAAAA	8535	AACTAAAI	
	AAAAGCCAA			
	TTTTCGGTT			
	CGTTGTTTTT			
GAM537 CCNT2	AAAAGCCAAGCAACAAAAA	8535	TCAAAA	_ T
	AGCCAA AAC AAAAGGT			
	TCGGTT TTG TTTTTTA			
	_ CG _			
GAM537 COX15	TCAAAAAG-CAAAACAAAAA	8546	C T	GT
	TCAAAAAGC AAAAC AAAAG			
	AGTTTTTCG TTTTG TTTTT			
	_ _ II			
GAM537 COX15	TCAAAAAG-CAAAACAAAAA	8546	_ C	TAAAI
	CAAAAAGC AAAAC			
	GTTTTTCG TTTTG			
	A _ TTTT			
GAM537 EXT2	TCAAAAAGCCAAACCAAAGAGG	8548	A _	TC
	TCAAAAAGCCAAA CTAAA AGG			
	AGTTTTTCGGTTT GGTTT TCC			
	_ C II			
GAM537 EXT2	TCAAAAAGCCAAACCAAAGAGG	8548	A	AGI
	CAAAAAGCCAAA CTAAA			
	GTTTTTCGGTTT GGTTT			
	_ CTC			
GAM537 GLS	AAAGCCAAAACAAAAAGATC	8536	T	I
	AAGCCAAAAC AAAAGGT			

		TTCGGTTTTG TTTTCTA			
		T I			
GAM537 GLS		AAAGCCAAAACAAAAGATC	8536	TCAAAAAG	T
		CCAAAAC AAAAGGT			
		GGTTTTG TTTTCTA			
		T			
GAM537 GPR85		TCAAAAAG-CAAAACCATAA	8547	C	AAAGGT
		TCAAAAAGC AAAACTA			
		AGTTTTTCG TTTTGGT			
		ATT			
GAM537 GPR85		TCAAAAAG-CAAAACCATAA	8547	C	AAI
		CAAAAAGC AAAACTA			
		GTTTTTCG TTTTGGT			
		A _ ATI			
GAM537 HOXC4		TCCAAAAGCC-AAACAAAA	8544	A	ACTAAAAGG
		TC AAAAGCCAAA			
		AG TTTTCGGTTT			
		G GTTTTIIC			
GAM537 HOXC4		TCCAAAAGCC-AAACAAAA	8544	A	ACTAAI
		TC AAAAGCCAAA			
		AG TTTTCGGTTT			
		G GTTTTI			
GAM537 LTB4R		AAGCCAAAATCCAAATGGTC	8537	_ A II	
		AAGCCAAAA CTAAA GGT			
		TTCGGTTTT GGTTC CCA			
		A A GI			
GAM537 LTB4R		AAAAAG---AAACTAAAAAGTC	8532	_ CCA	
		AAAAG AAACATAAAAGGT			
		TTTTC TTTGATTTTCA			
		T _			
GAM537 LTB4R		AAAAAG---AAACTAAAAAGTC	8532	TCAA CCA	
		AAAG AAACATAAAAGGT			
		TTTC TTTGATTTTCA			

GAM537 PCBP1		CAAAA---CAAACTAAAA	8539	TCAA C	
		AAAGC AAAACTAAAAG			
		TTTTG TTTGATTTT			

GAM537 PRL		TCAAAAGAGATACAACTAAAAG	8543	_ CCAA	GTC
		TCAAAA AG AACTAAAAG			

		AGTTTT TC TTGATTTTC			
		C TATG III			
GAM537 SELL		CAAAACCCCCAAACTAAAA 8540	AG A	II	
		CAAAA CC AA ACTAAA			
		II			
		GTTTT GG TTTGATTT			
		GG G TI			
GAM537 SELL		CAAAACCCCCAAACTAAAA 8540	TCA G A_	GT	
		AAAA CC AA ACTAAAAG			
		II			
		TTTT GG TTTGATTTTT			
		___ G GG II			
GAM537 SH3BP2		TCAAAAACAAAAAACTAAAA 8545	GCC	GGT	
		TCAAAA AA ACTAAAA			
		AGTTTTT TTTTGATTTT			
		GTT III			
GAM537 TPK1		CAGAAAATACTACTAAAAGGT 8541	AA C A	I	
		AAAGC AA ACTAAAAGG			
		II			
		TTTTG TT TGATTTTCC			
		TC A A I			
GAM537 TPK1		CAGAAAATACTACTAAAAGGT 8541	TCAA C A	C	
		AAAGC AA ACTAAAAGGT			
		II			
		TTTTG TT TGATTTTCCA			
		TC_ A A T			
GAM537 UVRAG		AAAAAGCAGACAAATAGCTAAAAGGT 8530	AAA C A_	I	
		AG CAAA CTAAAAGG			
		TC GTTT GATTTTCC			
		G_ T ATC I			
GAM537 UVRAG		AAAAAGCAGACAAATAGCTAAAAGGT 8530	TCAA _ A_	CII	
		AAAGC CAAA CTAAAAGGT			
		TTTCG GTTT GATTTTCCA			
		___ TCT ATC CTI			
GAM537 WASF3		AACAGCAATCAAACTAAAACGGTC 8534	AAAGC _	I	
		CAAACTAAAA GGT			
		GTTTTGATTTT CCA			
		GTTA_ G I			
GAM537 ZIC1		AAAAAGCCAAA--GAAAAGG 8531	ACTAAAAI		
		AAAAAGCCAAA			
		TTTTTCGGTTT			
		CTTTTCCI			
GAM537 ZIC1		AAAAAGCCAAA--GAAAAGG 8531	TCAA ACT		
		AAAGCCAAA AAAAGG			

	TTTCGGTTT TTTTCC		
	_____ C_____		
GAM538 COL19A1	AGCACC--ATTGTAGGTATTGC 8558 AA G T G		
	GCA CT ATTGTAGGTGT GC		
	CGT GG TAACATCCATA CG		
	_____ A		
GAM538 CUBN	CAGCTTATTCT--CTGTGGC 8560 AAGCAG GTAGG		
	CTTATT TGTGG		
	GAATAA ACACC		
	_____ GAG_____		
GAM538 CYLN2	AGCAGCTTA--G-AGGTGTG 8556 AA TTGT G		
	GCAGCTTA AGGTGTG		
	CGTCGAAT TCCACAC		
	_____ C_____ A		
GAM538 EN2	GCAGACACTTATTGTAAGTGTG 8561 AA G G		
	GCA CTTATTGTAGGTGTG CG		
	TGT GAATAACATTCACAC GC		
	TC _ _		
GAM538 GLI2	AGCA--TTATTGTAGGAGT 8555 AA GC T GG		
	GCA TTATTGTAGG GT		
	CGT AATAACATCC CA		
	_____ T GI		
GAM538 KIAA0857	AGCAGCTTAATGGATGGATGG 8557 AA T TA_ T CG		
	GCAGCTTA TG GG GTGG		
	CGTCGAAT AC CC TACC		
	_____ T CTA _ CI		
GAM538 PCDHB9	AAGAAAATTATTGTAGGCTGGGTGCG 8553 C C GTG_ II		
	AAG AG TTATTGTAGGT GCG		
	TTC TT AATAACATCCG CGC		
	T T ACCCA II		
GAM538 PCSK1	AAGCCAGC--ATTGTAGGTG 8551 _ TT TGG		
	AAGC AGC ATTGTAGGTG		
	TTCG TCG TAACATCCAC		
	G _ III		
GAM538 RARB	GCTTATCCTCTAGGTGTGG 8563 AAGCAGCTTA G C		
	TT TAGGTGTGG		
	GA ATCCACACC		
	AG_____ G T		
GAM538 TEM7R	AGCAGCTTAGAGCTTGTGTGTG 8554 AA AG GCGI		
	GCAGCTTA TTGT GTGTG		

	CGTCGAAT AACACACAC	
	CTCG AA AIII	
GAM538 TNKS	AAACAGCTTATTTCTAGGCTGT 8552	G_ GTGGCG
	AAGCAGCTTATT TAGGT	
	TTTGTCTGAATAA ATCCG	
	AG ACAIII	
GAM538 TNNT1	GCGGCCT-TGGTAGGTGTGG 8562 AAGCA ATT C	
	GCTT GTAGGTGTGG	
	CGGA CATCCACACC	
	C_ AC_ A	
GAM538 XT3	CAGCTTATTGGAGG-GTGG 8559 AAGCAG T T	
	CTTATTG AGG GTGG	
	GAATAAC TCC CACC	
	C _	
GAM539 ZNF264	GGAAGGGGTCAGGCTCGTACAAAG 8566 TG CGAC_ C AI	
	GAAG GGC CGTACAAAG	
	CTTC CCG GCATGTTTC	
	_ CCCAGT A CI	
GAM540 BCL6	TGTCCGGCCTTTCTAGAACTTC 8571 _ _ ATACI	
	TGTCCGGCC CTT GAAATTC	
	ACAGGCCGG GGA CTTTGAAG	
	AAA T IIIA	
GAM540 BCL6	TGTCCGGCCTTTCTAGAACTTC 8571 GTCC _ _ I	
	GGCC CTT GAAATTC	
	CCGG GGA CTTTGAA	
	_ AAA T I	
GAM540 PTPRD	TGTCCGATC--TGAAATTTC 8572 CCC TA	
	TGTCCGG TTGAAATTTC	
	ACAGGCT GACTTTAAAGT	
	A_ II	
GAM540 PTPRD	TGTCCGATC--TGAAATTTC 8572_ CCC I	
	GTCCGG TTGAAATTC	
	CAGGCT GACTTTAAAG	
	A A_ I	
GAM540 SAA4	TCCAGC---TGAAATTTC 8570 CCT	
	TCCGGC TGAAATTC	
	AGGTCG ACTTTAAAG	
	_	
GAM540 SAA4	TCCAGC---TGAAATTTC 8570 TGTC CCT	
	CGGC TGAAATTC	

GTCG ACTTTAAAGT

GAM540 WT1	TCCGGCCCTGGAGACGTTCA	8569	T AATTCII
	TCCGGCCCT GA		
	AGGCCGGGA CT		
	C CTGCAAGT		
GAM540 WT1	TCCGGCCCTGGAGACGTTCA	8569 TGTC	T A _ TA
	CGGCCCT GA AT TTCA		
	GCCGGGA CT TG AAGT		
	C C C CG		
GAM541 ANK3	CATTTAAAAAGATCCTCTCAAGCA	8576 TC	_ GG _ AI
	ATTTAAAAA AT TTTCA GCA		
	TAAATTTTT TA AGAGT CGT		
	C GG T GI		
GAM541 EGFL5	TTTAAAAAAAATGTTTCAGGAA	8577 TCATTT	G CAA
	AAAAAATG TTTCAG		
	TTTTTTAC AAAGTC		
	TT _ _ CTT		
GAM541 MBNL	ATTTCCAAGCTGCTTTCAGCAA	8575 TCA	AAAA G
	TTTAA TG TTTCAGCAA		
	AGGTT AC AAAGTCGTT		
	A _ CG _ G		
GAM541 TOX	TTTAAAAAAAAGTGTTTCAGCAA	8578 TCATTT	T _
	AAAAAA GGT TTCAGCAA		
	TTTTTT TCA AAGTCGTT		
	T C		
GAM542 ADCY2	AGCAAGCACAGT--GCAAGTGGC	8590 _	CTAG I
	GCAAGCACA GCAGGTGG		
	CGTTCGTGT CGTTCACC		
	T CA _ I		
GAM542 ADCY2	AGCAAGCACAGT--GCAAGTGGC	8590 CA	CTAG
	GCAAGCACA GCAGGTGGC		
	CGTTCGTGT CGTTCACCG		
	CA _		
GAM542 APBB2	AGCAAGCACCCAAGG-AGGT	8586 _	A C I
	GCAAGCAC CTAGG AGG		
	CGTTCGTG GGTTT TCC		
	T _ C I		
GAM542 APBB2	AGCAAGCACCCAAGG-AGGT	8586 CA	A C GG
	GCAAGCAC CTAGG AGGT		

		CGTTCGTG GGTTC TCCA		
		___ _ C GI		
GAM542 CAPG		AGCAAGCA-----GGCAGGTGG 8588 _	CACTA	
		GCAAGCA GGCAGGT		
		CGTTCGT CCGTCCA		
		T _____		
GAM542 CAPG		AGCAAGCA-----GGCAGGTGG 8588 CA	CACTA	
		GCAAGCA GGCAGGTG		
		CGTTCGT CCGTCCAC		
		___ _____		
GAM542 CYP4A11		CAGGAAG-ACAGGACGGCAGGTGG 8599 C C CTA_	CI	
		CAG AAG ACA GGCAGGTGG		
		GTC TTC TGT CCGTCCACC		
		C _ CCTG II		
GAM542 CYP4A11		CAGGAAG-ACAGGACGGCAGGTGG 8599 C C CTA_	I	
		AG AAG ACA GGCAGGTG		
		TC TTC TGT CCGTCCAC		
		C _ CCTG I		
GAM542 DNASE1L1		ACACTACCTGGCAGGTGGC 8584 _____		
		ACACTA GGCAGGTGG		
		TGTGAT CCGTCCACC		
		GGA GII		
GAM542 DRG2		CAGGGAGACGAGGCAGGTGG 8593 AAGCAC T	I	
		AC AGGCAGGTG		
		TG TCCGTCCAC		
		TCCCTC C I		
GAM542 DRG2		CAGGGAGACGAGGCAGGTGG 8593 CAGCAAGCAC T		
		AC AGGCAGGTGG		
		TG TCCGTCCACC		
		CCTC_____ C		
GAM542 FBXW1B		GCAAGCACACGTATAAAGGTG 8606 C _ GGC	I	
		AAGCACAC TA AGGT		
		TTCGTGTG AT TCCA		
		_ C ATT I		
GAM542 FBXW1B		GCAAGCACACGTATAAAGGTG 8606 CAGC _ GGC	GC	
		AAGCACAC TA AGGTG		
		TTCGTGTG AT TCCAC		
		_____ C ATT AA		
GAM542 FZD7		CAAGCACAC--CGCAGGAGGC 8594 _	AG T I	
		AAGCACACT GCAGG GG		

	TTCGTGTGG CGTCC CC	
	G _ T I	
GAM542 FZD7	CAAGCACAC--CGCAGGAGGC 8594 CAGCAA AG T	
	GCACACT GCAGG GG	
	CGTGTGG CGTCC CC	
	_____ T	
GAM542 GPR44	CAAGTCCAC--GGCAGGTGG 8592_ CA TA I	
	AAG CAC GGCAGGTG	
	TTC GTG CCGTCCAC	
	G AG _ I	
GAM542 GPR44	CAAGTCCAC--GGCAGGTGG 8592 CAGCAAGCA TA	
	CAC GGCAGGTG	
	GTG CCGTCCAC	
	CAG_____	
GAM542 LOXL2	AGCAAGCAC-CAAGCGTAGGTAGC 8585 AC _ I	
	GCAAGCAC TAGGC AGGTGG	
	CGTTCGTG GTTCG TCCATC	
	_ CA I	
GAM542 LOXL2	AGCAAGCAC-CAAGCGTAGGTAGC 8585 CA AC _ I	
	GCAAGCAC TAGGC AGGTGGC	
	CGTTCGTG GTTCG TCCATCG	
	_ _ CA G	
GAM542 LPIN1	CAG-AAGC-CAGAAGGCAGGTG 8600 C A CT G	
	CAG AAGC CA AGGCAGGTG	
	GTC TTCG GT TCCGTCCAC	
	_ _ CT I	
GAM542 LPIN1	CAG-AAGC-CAGAAGGCAGGTG 8600 C A CT I	
	CAG AAGC CA AGGCAGG	
	GTC TTCG GT TCCGTCC	
	_ _ CT A	
GAM542 MATK	CAG-AGGGAAACTGAGGCAGGTG 8598 CAAGCAC _ GC	
	CAG ACT AGGCAGGTG	
	GTC TGA TCCGTCCAC	
	TCCCTT_ C II	
GAM542 MATK	CAG-AGGGAAACTGAGGCAGGTG 8598 AGCAAGCAC _ I	
	ACT AGGCAGGT	
	TGA TCCGTCCA	
	TCTCCCTT_ C I	
GAM542 MFAP4	CAGCTTAGCACACTAG---GGTGGC 8595 A_ CA GI	
	CAGC AGCACACTAGG GGT	

	GTCG TCGTGTGATCC CCG AA CA II
GAM542 MFAP4	CAGCTTAGCACACTAG---GGTGGC 8595 A_ CAG CAGC AGCACACTAGG GTGGC GTCG TCGTGTGATCC CACCG AA ____
GAM542 MGAT1	CAGGAAGGACA---GGCAGGTG 8601 C C CTA G CAG AAG ACA GGCAGGTG GTC TTC TGT CCGTCCAC C C ____ I
GAM542 MGAT1	CAGGAAGGACA---GGCAGGTG 8601 C C CTA I CAG AAG ACA GGCAGG GTC TTC TGT CCGTCC C C ____ A
GAM542 MYD88	AAGCTCTCT--GCAGGTGGC 8583_ ACA AG I AGC CT GCAGGTGG TCG GA CGTCCACC T A_ GA I
GAM542 NTS	CAG-AAGCACACT--GAAGGGGGC 8602 C ____ CA GI CAG AAGCACACT AGG GGT GTC TTCGTGTGA TCC CCG _ CT C_ II
GAM542 NTS	CAG-AAGCACACT--GAAGGGGGC 8602 C A C T CAG AAGCACACT GG AGG GGC GTC TTCGTGTGA CT TCC CCG _ _ _ C
GAM542 PAK4	CAG-AAGTGCCCTCAGGCAGGTG 8597 C CACA _ GC CAG AAG CT AGGCAGGTG GTC TTC GA TCCGTCCAC _ ACGG G II
GAM542 PAK4	CAG-AAGTGCCCTCAGGCAGGTG 8597 AGCAA_ ACAC I GC TAGGCAGGT CG GTCCGTCCA TCTTCA GGA_ I
GAM542 PCMT1	AAGCACACTCGGAGCAGGT 8581 A_ AAGCACACT GGCAGG TTCGTGTGA TCGTCC GCC AII
GAM542 PIGR	AGGAAAAAC-CTAGGCAGGTG 8587 CAGCAAGCACA G CTAGGCAGGTG

		GATCCGTCCAC		
		CCTTTTGT_____A		
GAM542 PIGR	AGGAAAAAC-CTAGGCAGGTG	8587 GCAAGCACA	I	
	CTAGGCAGGT			
	GATCCGTCCA			
	TCCTTTTGT_____I			
GAM542 PTK2B	AAG-ACGC-AGGCAGGTGGC	8582 AGCAC _	I	
	AC TAGGCAGGTGG			
	TG GTCCGTCCACC			
	TTC_ C_____I			
GAM542 SCN2B	CAAGCAC--TGGGCAGGTGG	8591 _ ACTA	I	
	AAGCAC GGCAGGTG			
	TTCGT CCGTCCAC			
	G AC_ I			
GAM542 SCN2B	CAAGCAC--TGGGCAGGTGG	8591 CAGCAAGCA	A	
	CACT GGCAGGTG			
	GTGA CCGTCCAC			
	C_____ C			
GAM542 SEMG1	AGGAAGCA---TGGGCAGGTGG	8589 _ C CACTA		
	G AAGCA GGCAGGTG			
	C TTCGT CCGTCCAC			
	T C AC_			
GAM542 SEMG1	AGGAAGCA---TGGGCAGGTGG	8589 CAGC CACTA		
	AAGCA GGCAGGTGG			
	TTCGT CCGTCCACC			
	CC_ AC_			
GAM542 SLC12A4	GCAAGCAGGGCT-GGCAGGTGG	8605 CA_ A	I	
	CAAGCA CT GGCAGGTG			
	GTTTGT GA CCGTCCAC			
	CCC _ I			
GAM542 SLC12A4	GCAAGCAGGGCT-GGCAGGTGG	8605 CAGC CA_ A	C	
	AAGCA CT GGCAGGTGG			
	TTCGT GA CCGTCCACC			
	_____ CCC _ C			
GAM542 SLC7A5	CAGCAATGCAC-C-AGGCAGGTGG	8596 GCA	C	
	CAGCAA CACTAGGCAGGTGG			
	GTCGTT GTGGTCCGTCCACC			
	AC_ I			
GAM542 SLC7A5	CAGCAATGCAC-C-AGGCAGGTGG	8596 _ GCA	I	
	AGCAA CACTAGGCAGGTG			

	TCGTT GTGGTCCGTCCAC	
	G AC_ I	
GAM542 TEM8	CAGCAATGTCACT--GCAGGTGGC 8603	GCA AG
	CAGCAA CACT GCAGGTGGC	
	GTCGTT GTGA CGTCCACCG	
	ACA _	
GAM542 TEM8	CAGCAATGTCACT--GCAGGTGGC 8603_	GCA AG I
	AGCAA CACT GCAGGTGG	
	TCGTT GTGA CGTCCACC	
	G ACA _ I	
GAM542 TMEM1	GCAAGCACAGTGCTGGGCAGG 8604	_ A III
	GCAAGCACA CT GGCAG	
	CGTTCGTGT GA CCGTC	
	CAC C CII	
GAM542 TMEM1	GCAAGCACAGTGCTGGGCAGG 8604 CAGC	_ A TGGC
	AAGCACA CT GGCAGG	
	TTCGTGT GA CCGTCC	
	_ CAC C TTII	
GAM542 UNC13	GCAGGGAGACTCCCAGGCAGGTGGC 8607 A C A_	I
	C AG AC CTAGGCAGGTGG	
	I	
	C TC TG GGTCCGTCCACC	
	C _ AG I	
GAM542 UNC13	GCAGGGAGACTCCCAGGCAGGTGGC 8607 C CA C A_	II
	AG AG AC CTAGGCAGGTGGC	
	TC TC TG GGTCCGTCCACCG	
	_ CC _ AG GG	
GAM543 ARSF	GAGTGGTGGTTACGCTGTAATCCC 8614 TAGA	C _ AG_ II
	GTGGTGG TC CC AATCCC	
	CACCACC AG GG TTAGGG	
	_ A TGC ACA TC	
GAM543 ATP5B	GATTGGTG-CACC-AGAATCC 8616 TAGAG	G TC
	TGGTG C CCAGAATCC	
	ACCAC G GGTCTTAGG	
	A _ _ T_	
GAM543 CD1A	TAAAGTGAAATGGCTCCCAG 8619	_ AATCC
	TAGAGTG GTGGCTCCCAG	
	ATTTCAC TACCGAGGGTC	
	TT IIIIC	
GAM543 CRY2	TAGGGAGGCAGATGCCAGAATCCC 8620 TAG T T TC_	I
	AG GG GGC CCAGAATCCC	

	TC CC CCG GGTCTTAGGG		
	A__ _ T TCTAC I		
GAM543 ENAM	GAGTGGTGGCTCATTGAGCATCC 8615 TAGA	C__ A CI	
	GTGGTGGCTC CAG ATCC		
	CACCACCGAG GTC TAGG		
	_____ TAA G AT		
GAM543 KIFC3	GAGGGCGTGGCTCCCAGGTTCC 8612 TAGAGTG	AA C	
	GTGGCTCCAG TCC		
	CACCGAGGGTC AGG		
	CCCG_____ CA T		
GAM543 NRXN1	GTGGCTGCTCCAGATTTCC 8617 TAGAGTGGTG	A_	
	GCTCCAGA TCC		
	CGAGGGTCT AGG		
	GA_____ AA		
GAM543 PRSS8	AGAGGGAAGGATCCCAGAATCC 8611 TA T T_ C	C	
	GAG GG GG TCCCAGAATCC		
	CTC CC CC AGGGTCTTAGG		
	__ _ TT T C		
GAM543 RPP30	GTGGTGGCTCATGTAATCCC 8618 TAGAGTGG	CCAG	
	TGGCTC AATCC		
	ACCGAG TTAGG		
	_____ TACA		
GAM543 SMAC	GAGTGGTGGCAGCTCCTGTAATCCC 8613 TAGA	_____ CAG II	
	GTGGTGGC TCC AATCCC		
	CACCACCG AGG TTAGGG		
	_____ TGCG ACA TC		
GAM543 TBXAS1	AGAGTGGTGGTCTTCCAGA 8610 TA	_ C ATCC	
	GAGTGGTGG CT CCAGA		
	CTCACCACC GA GGTCT		
	_____ A A A		
GAM544 ADAMTS4	GTGGTGGCTCACACCTGTAATCCC 8629 TGGT	_____ AA_ I	
	GGCTC CC AATCC		
	CCGAG GG TTAGG		
	_____ TGT ACA I		
GAM544 ADCY6	GTGGTGGCTCACGTCCGTAATCCC 8628 TGGT	_____ AA I	
	GGCTC CC AATCC		
	CCGAG GG TTAGG		
	_____ TGCA CA I		
GAM544 ALDH1B1	GTTGTGGCTCCCACCTGTAATCCC 8632 TGGT	A_____ I	
	GGCTCCCA AATCC		

	CCGAGGGT TTAGG		
	____ GGACA I		
GAM544 ARAF1	GAGATGGAGGAGCTCCCAAAT 8624	_ T__	III
	GAG TGG GGCTCCCAAAA		
	CTC ACC TCGAGGGTTTT		
	T TCC AII		
GAM544 ARAF1	GAGATGGAGGAGCTCCCAAAT 8624	TAGA T__	CCC
	GTGG GGCTCCCAAAT		
	TACC TCGAGGGTTTTA		
	C__ TCC AAI		
GAM544 CD1A	TAAAGTGAAATGGCTCCCA 8634	__	AAATCC
	TAGAGTG GTGGCTCCCA		
	ATTTAC TACCGAGGGT		
	TT IIICC		
GAM544 CD1A	TAAAGTGAAATGGCTCCCA 8634	__	III
	TAGAGTG GTGGCTCCC		
	ATTTAC TACCGAGGG		
	TT TII		
GAM544 CDC6	TGGTGGCTCACGCCTATAATCCC 8638	__ AA_	IIIG
	TGGTGGCTC CC AATCC		
	ACCACCGAG GG TTAGG		
	TGC ATA GIII		
GAM544 CLECSF12	GTGGTGGCTCACATCTGTAATCCC 8631	TGGT C A__	I
	GGCTC CA AATCC		
	CCGAG GT TTAGG		
	____ T AGACA I		
GAM544 CYP1A2	GTGGTGGCTCACACCTGTAATCCC 8629	TGGT __ AA_	I
	GGCTC CC AATCC		
	CCGAG GG TTAGG		
	____ TGT ACA I		
GAM544 DSCR3	GTGGTGGCTCACACCTGTAATCCC 8629	TGGT __ AA_	I
	GGCTC CC AATCC		
	CCGAG GG TTAGG		
	____ TGT ACA I		
GAM544 FZD4	GTGGTGGCTCACACTTGTAATCCC 8630	TGGT C A__	I
	GGCTC CA AATCC		
	CCGAG GT TTAGG		
	____ T GAACA I		
GAM544 GABPB1	TGGTCGGCGCCCAAATCCC 8636	_ T	II
	TGGT GGC CCCAAATCC		

	ACCA CCG GGGTTTTAGG		
	G C GI		
GAM544 IL11	GTGGTGGCTCACACCTGTAATCCC	8629 TGGT	___ AA_ I
	GGCTC CC AATCC		
	II		
	CCGAG GG TTAGG		
	___ TGT ACA I		
GAM544 IL17E	GAGTGGTGGCCTCCAGAAAT	8626	TC AAAlI
	GAGTGGTGGC CCA		
	III		
	CTCACCACCG GGT		
	GA CTTTA		
GAM544 IL17E	GAGTGGTGGCCTCCAGAAAT	8626 TAGA	TC AAATCC
	GTGGTGGC CCA		
	III		
	CACCACCG GGT		
	___ GA CTTTAC		
GAM544 KRT9	GAGTGCTACCGGCTCCCAA	8625 G___	III
	GAGTG TGGCTCCCA		
	CTCAC GCCGAGGGT		
	GATG TII		
GAM544 KRT9	GAGTGCTACCGGCTCCCAA	8625 TAGA GG_	AATCC
	GT TGGCTCCCAA		
	II		
	CG GCCGAGGGTT		
	CA_ ATG CAIII		
GAM544 PCDH11X	AGAGTGGTGGGTAATAAAA	8623	CTCCCAAAlI
	AGAGTGGTGG		
	TCTCACCACC		
	CATTATTTTI		
GAM544 PCDH11X	AGAGTGGTGGGTAATAAAA	8623 TA	CTCCCAAAlATCC
	GAGTGGTGG		
	CTCACCACC		
	___ CATTATTTTII		
GAM544 PCDH11Y	AGAGTGGTGGGTAATAAAA	8623	CTCCCAAAlI
	AGAGTGGTGG		
	TCTCACCACC		
	CATTATTTTI		
GAM544 PCDH11Y	AGAGTGGTGGGTAATAAAA	8623 TA	CTCCCAAAlATCC
	GAGTGGTGG		
	CTCACCACC		
	___ CATTATTTTII		
GAM544 PDE4D	GTGGCTCCAGAGGATCCC	8627	AA_ III
	GTGGCTCCCA ATCC		
	III		

	CACCGAGGGT TAGG		
	CTCC GII		
GAM544 PDE4D	GTGGCTCCCAGAGGATCCC	8627	TAGAGT T C ATCC
	GG GG TCCCAA		
	II II IIIII		
	TC CC AGGGTTT		
	GG___ T T GTTT		
GAM544 RPP30	GTGGTGGCTCATGTAATCCC	8618	CCAA I
	TGGTGGCTC AATCC		
	IIIIII II		
	ACCACCGAG TTAGG		
	TACA I		
GAM544 RPP30	GTGGTGGCTCATGTAATCCC	8618	TAGAGTGG CCAA
	TGGCTC AATCC		
	IIII II		
	ACCGAG TTAGG		
	_____ TACA		
GAM544 SAS	TATAGTC-TGGCTCCCACTAAAAT	8635	TAGA ___ AAATCCCI
	GTGGT GGCTCCCA		
	IIII IIIII		
	TATCA CCGAGGGT		
	A___ GA GATTTTAI		
GAM544 SAS	TATAGTC-TGGCTCCCACTAAAAT	8635	TAGAGTGG AI
	TGGCTCCCA		
	IIIIII		
	ACCGAGGGT		
	AG_____ GA		
GAM544 SORCS1	TGGTCACTTCCCAAAATGCC	8637	G _ _ II
	TGGT GCT CCCAAAT CC		
	IIII III IIIII II		
	ACCA TGA GGGTTTTA GG		
	G A C II		
GAM544 TP53	GTGGTGGCTCACAATTGTAATCCC	8633	TGGT C ___ I
	GGCTC CAA AATCC		
	IIII III II		
	CCGAG GTT TTAGG		
	_____ T AACA I		
GAM544 UGDH	GTGGTGGCTCACACCTGTAATCCC	8629	TGGT ___ AA_ I
	GGCTC CC AATCC		
	IIII II III		
	CCGAG GG TTAGG		
	_____ TGT ACA I		
GAM545 ADAMTS4	GTGGTGGCTCACACCTGTAATCCC	8629	TGGT ___ AA_ I
	GGCTC CC AATCC		
	IIII II III		
	CCGAG GG TTAGG		
	_____ TGT ACA I		
GAM545 ADCY6	GTGGTGGCTCACGTCCGTAATCCC	8628	TGGT ___ AA I
	GGCTC CC AATCC		
	IIII II III		

	CCGAG GG TTAGG		
	____ TGCA CA I		
GAM545 ALDH1B1	GTTGTGGCTCCCACCTGTAATCCC 8632 TGGT	A____	I
	GGCTCCCA AATCC		
	CCGAGGGT TTAGG		
	____ GGACA I		
GAM545 ARAF1	GAGATGGAGGAGCTCCCAAAT 8624 _ T__	III	
	GAG TGG GGCTCCCAAAA		
	CTC ACC TCGAGGGTTTT		
	T TCC AII		
GAM545 ARAF1	GAGATGGAGGAGCTCCCAAAT 8624 TAGA T__	CCC	
	GTGG GGCTCCCAAAT		
	TACC TCGAGGGTTTTA		
	C__ TCC AAI		
GAM545 CD1A	TAAAGTGAAATGGCTCCCA 8634 __	AAATCC	
	TAGAGTG GTGGCTCCCA		
	ATTTCAC TACCGAGGGT		
	TT IIICC		
GAM545 CD1A	TAAAGTGAAATGGCTCCCA 8634 __	III	
	TAGAGTG GTGGCTCCC		
	ATTTCAC TACCGAGGG		
	TT TII		
GAM545 CDC6	TGGTGGCTCACGCCTATAATCCC 8638 __	AA_ IIIG	
	TGGTGGCTC CC AATCC		
	ACCACCGAG GG TTAGG		
	TGC ATA GIII		
GAM545 CLECSF12	GTGGTGGCTCACATCTGTAATCCC 8631 TGGT	C A____	I
	GGCTC CA AATCC		
	CCGAG GT TTAGG		
	____ T AGACA I		
GAM545 CYP1A2	GTGGTGGCTCACACCTGTAATCCC 8629 TGGT	__ AA_	I
	GGCTC CC AATCC		
	CCGAG GG TTAGG		
	____ TGT ACA I		
GAM545 DSCR3	GTGGTGGCTCACACCTGTAATCCC 8629 TGGT	__ AA_	I
	GGCTC CC AATCC		
	CCGAG GG TTAGG		
	____ TGT ACA I		
GAM545 FZD4	GTGGTGGCTCACACTTGTAATCCC 8630 TGGT	C A____	I
	GGCTC CA AATCC		

	CCGAG GT TTAGG		
	____ T GAACA I		
GAM545 GABPB1	TGGTCGGCGCCCAAAATCCC	8636	_ T II
	TGGT GGC CCCAAAATCC		
	ACCA CCG GGGTTTTAGG		
	G C GI		
GAM545 IL11	GTGGTGGCTCACACCTGTAATCCC	8629	TGGT ____ AA_ I
	GGCTC CC AATCC		
	CCGAG GG TTAGG		
	____ TGT ACA I		
GAM545 IL17E	GAGTGGTGGCCTCCAGAAAT	8626	TC AAII
	GAGTGGTGGC CCA		
	CTCACCACCG GGT		
	GA CTTTA		
GAM545 IL17E	GAGTGGTGGCCTCCAGAAAT	8626	TAGA TC AAATCC
	GTGGTGGC CCA		
	CACCACCG GGT		
	____ GA CTTTAC		
GAM545 KRT9	GAGTGCTACCGGCTCCCAA	8625	G____
	GAGTG TGGCTCCCA		
	CTCAC GCCGAGGGT		
	GATG TII		
GAM545 KRT9	GAGTGCTACCGGCTCCCAA	8625	TAGA GG_ AATCC
	GT TGGCTCCCAA		
	CG GCCGAGGGTT		
	CA_ ATG CAII		
GAM545 PCDH11X	AGAGTGGTGGGTAATAAAA	8623	CTCCCAAII
	AGAGTGGTGG		
	TCTCACCACC		
	CATTATTTI		
GAM545 PCDH11X	AGAGTGGTGGGTAATAAAA	8623	TA CTCCCAAATCC
	GAGTGGTGG		
	CTCACCACC		
	____ CATTATTTTII		
GAM545 PCDH11Y	AGAGTGGTGGGTAATAAAA	8623	CTCCCAAII
	AGAGTGGTGG		
	TCTCACCACC		
	CATTATTTI		
GAM545 PCDH11Y	AGAGTGGTGGGTAATAAAA	8623	TA CTCCCAAATCC
	GAGTGGTGG		

	CTCACCACC			
	___ CATTATTTTTII			
GAM545 PDE4D	GTGGCTCCCAGAGGATCCC	8627	AA___ III	
	GTGGCTCCCA ATCC			
	CACCGAGGGT TAGG			
	CTCC GII			
GAM545 PDE4D	GTGGCTCCCAGAGGATCCC	8627	TAGAGT T C	ATCC
	GG GG TCCCAA			
	TC CC AGGGTTT			
	GG___ T T GTTT			
GAM545 RPP30	GTGGTGGCTCATGTAATCCC	8618	CCAA I	
	TGGTGGCTC AATCC			
	ACCACCGAG TTAGG			
	TACA I			
GAM545 RPP30	GTGGTGGCTCATGTAATCCC	8618	TAGAGTGG	CCAA
	TGGCTC AATCC			
	ACCGAG TTAGG			
	_____ TACA			
GAM545 SAS	TATAGTC-TGGCTCCCACTAAAAT	8635	TAGA ___	AAATCCCI
	GTGGT GGCTCCCA			
	TATCA CCGAGGGT			
	A___ GA GATTTTAI			
GAM545 SAS	TATAGTC-TGGCTCCCACTAAAAT	8635	TAGAGTGG	AI
	TGGCTCCCA			
	ACCGAGGGT			
	AG_____ GA			
GAM545 SORCS1	TGGTCACTTCCCAAAATGCC	8637	G _ _ II	
	TGGT GCT CCCAAAAT CC			
	ACCA TGA GGGTTTTA GG			
	G A C II			
GAM545 TP53	GTGGTGGCTCACAATTGTAATCCC	8633	TGGT C _____	I
	GGCTC CAA AATCC			
	CCGAG GTT TTAGG			
	_____ T AACA I			
GAM545 UGDH	GTGGTGGCTCACACCTGTAATCCC	8629	TGGT ___ AA_	I
	GGCTC CC AATCC			
	CCGAG GG TTAGG			
	_____ TGT ACA I			
GAM546 A1BG	GTGGTGGCTCACCCCTGTAATCCC	8688	TGGT _ AG___	I
	GGCTC CC AATCC			

	CCGAG GG TTAGG	
	____ T GGACA I	
GAM546 ADCY6	GTGGTGGCTCACGTCCGTAATCCC 8628 TGGT ____ AG I	
	GGCTC CC AATCC	
	CCGAG GG TTAGG	
	____ TGCA CA I	
GAM546 ARSF	GAGTGGTGGTTCACGCCTGTAATCCC 8614 A G_ T CAG I	
	GTGGT GC CC AATCC	
	CACCA TG GG TTAGG	
	_ AG C ACA I	
GAM546 ARSF	GAGTGGTGGTTCACGCCTGTAATCCC 8614 TAGA C ____ AG_ II	
	GTGGTGG TC CC AATCCC	
	CACCACC AG GG TTAGGG	
	____ A TGC ACA TC	
GAM546 ATP5B	GATTGGTG-CACC-AGAATCC 8616 AG_ G TC I	
	TGGTG C CCAGAATC	
	ACCAC G GGTCTTAG	
	CTA _ T_ I	
GAM546 ATP5B	GATTGGTG-CACC-AGAATCC 8616 TAGAG G TC	
	TGGTG C CCAGAATCC	
	ACCAC G GGTCTTAGG	
	A ____ _ T_	
GAM546 CCNF	TGCTGGCTCCCAGGCTCCC 8714 G AA II	
	TG TGGCTCCCAG TCC	
	AC ACCGAGGGTC AGG	
	G CG GI	
GAM546 CD1A	TAAAGTGAAATGGCTCCCAG 8619 ____ AATCC	
	TAGAGTG GTGGCTCCCAG	
	ATTTCAC TACCGAGGGTC	
	TT CC	
GAM546 CD1A	TAAAGTGAAATGGCTCCCAG 8619 ____	
	TAGAGTG GTGGCTCCCA	
	ATTTCAC TACCGAGGGT	
	TT C	
GAM546 CLECSF12	GTGGTGGCTCACATCTGTAATCCC 8631 TGGT C G ____ I	
	GGCTC CA AATCC	
	CCGAG GT TTAGG	
	____ T AGACA I	
GAM546 CRY2	TAGGGAGGCAGATGCCAGAATCCC 8620 AG T T TC ____ I	
	AG GG GGC CCAGAATCC	

	TC CC CCG GGTCTTAGG	
	__ _ T TCTAC I	
GAM546 CRY2	TAGGGAGGCAGATGCCAGAATCCC 8620 TAG T T TC__ I	
	AG GG GGC CCAGAATCCC	
	TC CC CCG GGTCTTAGGG	
	A__ _ T TCTAC I	
GAM546 CRY2	TGGCTGCCTCC-AGAATCCC 8708 G TC II	
	TGGT GC CCAGAATCC	
	ACCG CG GGTCTTAGG	
	A GA GI	
GAM546 CYP1A2	GTGGTGGCTCACACCTGTAATCCC 8629 TGGT __ AG_ I	
	GGCTC CC AATCC	
	CCGAG GG TTAGG	
	__ TGT ACA I	
GAM546 DNASE1L1	GTGGTGGCTCATGCCTGTAATCCC 8694 TGGT __ AG_ I	
	GGCTC CC AATCC	
	CCGAG GG TTAGG	
	__ TAC ACA I	
GAM546 DSCR3	GTGGTGGCTCACACCTGTAATCCC 8629 TGGT __ AG_ I	
	GGCTC CC AATCC	
	CCGAG GG TTAGG	
	__ TGT ACA I	
GAM546 ENAM	GAGTGGTGGCTCATTGAGCATCC 8615 TAGA C__ A CI	
	GTGGTGGCTC CAG ATCC	
	CACCACCGAG GTC TAGG	
	__ TAA G AT	
GAM546 ENAM	GAGTGGTGGCTCATTGAGCATCC 8615 AG C__ A I	
	TGGTGGCTC CAG ATC	
	ACCACCGAG GTC TAG	
	__ TAA G I	
GAM546 FZD4	GTGGTGGCTCACACTTGTAATCCC 8630 TGGT C G__ I	
	GGCTC CA AATCC	
	CCGAG GT TTAGG	
	__ T GAACA I	
GAM546 HCS	TGGTGGCTCACGCCTGCAATCCC 8712 __ AG_ IIIG	
	TGGTGGCTC CC AATCC	
	ACCACCGAG GG TTAGG	
	TGC ACG GIII	
GAM546 IGF1	GTGGTGGCTCATGCCTGTAATCCC 8694 TGGT __ AG_ I	
	GGCTC CC AATCC	

	CCGAG GG TTAGG		
	____ TAC ACA I		
GAM546 IL11	GTGGTGGCTCACACCTGTAATCCC	8629 TGGT	___ AG_ I
	GGCTC CC AATCC		
	II		
	CCGAG GG TTAGG		
	____ TGT ACA I		
GAM546 KIFC3	GAGGGCGTGGCTCCCAGGTTCC	8612 GAGTG	AAI
	GTGGCTCCCAG		
	CACCGAGGGTC		
	CG____ CAA		
GAM546 KIFC3	GAGGGCGTGGCTCCCAGGTTCC	8612 TAGAGTG	AA C
	GTGGCTCCCAG TCC		
	III		
	CACCGAGGGTC AGG		
	CCCG____ CA T		
GAM546 NRXN1	GTGGCTGCTCCAGATTTCC	8617 G	ATCCI
	TGGT GCTCCCAGA		
	ACCG CGAGGGTCT		
	A AAAGI		
GAM546 NRXN1	GTGGCTGCTCCAGATTTCC	8617 TAGAGTGGTG	A_
	GCTCCCAGA TCC		
	III		
	CGAGGGTCT AGG		
	GA_____ AA		
GAM546 PDE4D	GTGGCTCCCAGAGGATCCC	8627	___ III
	GTGGCTCCCAGA ATCC		
	CACCGAGGGTCT TAGG		
	CC GII		
GAM546 PRSS8	AGAGGGAAGGATCCCAGAATCC	8611 T T_ C	I
	GAG GG GG TCCCAGAATC		
	II		
	CTC CC CC AGGGTCTTAG		
	_ TT T I		
GAM546 PRSS8	AGAGGGAAGGATCCCAGAATCC	8611 TA T T_ C	C
	GAG GG GG TCCCAGAATCC		
	II		
	CTC CC CC AGGGTCTTAGG		
	_ _ TT T C		
GAM546 RPP30	GTGGTGGCTCATGTAATCCC	8618	CCAG I
	TGGTGGCTC AATCC		
	ACCACCGAG TTAGG		
	TACA I		
GAM546 RPP30	GTGGTGGCTCATGTAATCCC	8618 TAGAGTGG	CCAG
	TGGCTC AATCC		

	ACCGAG TTAGG		
	_____ TACA		
GAM546 SMAC	TGGTGGCTCACGCCTGTAATCC 8710	___ AG_ III	
	TGGTGGCTC CC AATC		
	ACCACCGAG GG TTAG		
	TGC ACA GII		
GAM546 SMAC	GAGTGGTGGCACGCTCCTGTAATCCC 8613 A	_ CAG I	
	GTGGTG GCTCC AATCC		
	CACCGT CGAGG TTAGG		
	_ G ACA I		
GAM546 SMAC	GAGTGGTGGCACGCTCCTGTAATCCC 8613 TAGA	___ CAG II	
	GTGGTGGC TCC AATCCC		
	CACCACCG AGG TTAGGG		
	_____ TGCG ACA TC		
GAM546 TBXAS1	AGAGTGGTGGTCTTCCAGA 8610	_ C II	
	AGAGTGGTGG CT CCAG		
	TCTCACCACC GA GGTC		
	A A TI		
GAM546 TBXAS1	AGAGTGGTGGTCTTCCAGA 8610 TA	_ C ATCC	
	GAGTGGTGG CT CCAGA		
	CTCACCACC GA GGTC		
	_ A A AII		
GAM546 TFCP2	AGTGGTGGCTTGCTGCTTCCC 8675	CCCAGAA I	
	GTGGTGGCT TCC		
	CACCACCGA AGG		
	ACGACGA I		
GAM546 TP53	GTGGTGGCTCACAAATTGTAATCCC 8633 TGGT	C ___ I	
	GGCTC CAG AATCC		
	CCGAG GTT TTAGG		
	_____ T AACA I		
GAM547 ARNTL	TGACTTGATCAATGGCT-CTGAG 8722	A G AAGI	
	TGACTTGTA TGATGGCT CT		
	ACTGAACAT GTTACCGA GA		
	A _ CTCI		
GAM547 COX11	GACTTGTAATGGTGATGCTTTGGCTAA8720 TG	A C AAGIII	
	ACTTGTAATG TGG TGCT		
	TGAACATTAC ACT ACGA		
	_ C _ AACCGA		
GAM547 FBN1	ACTTGTAAT-TTGGTTTCTAAG 8717 TGAC	GA CTG	
	TTGTAAT TGG CTAAG		

		AACATTA ACC GATTC	
		_____ A_ AAA	
GAM547 GOLGA4		CTTAGTGATGAAATGGCTGCT	8718 TGA CTT A _ AAG
		GT ATGA TGGCTGCT	
		CA TACT ACCGACGA	
		T_____ C TT AGA	
GAM547 MAP1A		TTATAAGCTGATGAGCTGCTAAG	8723 TGA CTTGTAA _ I
		TGATG GCTGCTAAG	
		ACTAC CGACGATTC	
		TTCG_____ T T	
GAM547 PCDHA11		CTTGTTACTTTGGCTGCTA	8719 TGA CTTGTAATGA A
		TGGCTGCTA	
		ACCGACGAT	
		CAATGAA_____ C	
GAM547 PHKG1		TGA CTTGTATTTCCATGGCT	8721 ATG_ GCTAA
		TGA CTTGTA ATGGCT	
		ACTGAACAT TACCGA	
		AAAGG IIIGA	
GAM548 ARHGAP6		ACCTGGACGTGGGGCGTGC	8726 TGTACG C A_ _ GA
		AC TGG CG GC CGGG	
		TG ACC GC CG GTCC	
		_____ C CC A AC	
GAM548 SLC2A1		GTACG--CGGGT-GGCGACGGGC	8727 TG ACC AC
		TACG TGG GGCGACGGG	
		ATGC GCC CCGCTGCCC	
		_____ CA	
GAM549 ASPA		GGAGTATAT--TTTAAT--TTTC	8741 AG CA
		GGAGTATAT TTTAGT TTTC	
		CCTCATATA AAATTA AAAG	

GAM549 ASPA		GGAGTATAT--TTTAAT--TTTC	8741 AG CAI
		GGAGTATAT TTTAGT	
		CCTCATATA AAATTA	
		_____ AAA	
GAM549 ATP6V1A1		ATAGAAATTGAGTCATTTC	8733 _ T T III
		A AGTT AGTCATTTC	
		C TTAA TCAGTAAAG	
		TAT T C TII	
GAM549 CCRL1		GTATATAGTTCTGTGTCATT	8742 A_ III
		GTATATAGTTT GTCATT	

	CATATATCAAG CAGTAA			
	ACA AII			
GAM549 CCRL1	GTATATAGTTCTGTGTCATTT 8742 GGAGTA	A__	CA	
	TATAGTTT GTCATTT			
	ATATCAAG CAGTAAA			
	_____ ACA AT			
GAM549 CDH19	GAGGA-ATATTTTAGTCAT 8736_	ATAG	TT	
	GGAGTAT TTTAGTCAT			
	CCTTATA AAATCAGTA			
	T _____ TI			
GAM549 CDH19	GAGGA-ATATTTTAGTCAT 8736__	ATAG	I	
	GAGTAT TTTAGTCA			
	CTTATA AAATCAGT			
	CTC _____ A			
GAM549 FBXW7	GGAGTATATCGTCTACACAATT 8740	A	GT TTTCA	
	GGAGTATAT GTTTA CA			
	CCTCATATA CAGAT GT			
	G GT TAAII			
GAM549 FBXW7	GGAGTATATCGTCTACACAATT 8740	A	GT TTI	
	GAGTATAT GTTTA CA			
	CTCATATA CAGAT GT			
	G GT TAI			
GAM549 GRM6	GAGAATA-AGTTTAGTCCCTTTC 8734	TAT	A_ A	
	GGAGTA AGTTTAGTC TTTC			
	TCTTAT TCAAATCAG AAAG			
	_____ GG A			
GAM549 GRM6	GAGAATA-AGTTTAGTCCCTTTC 8734	TAT	ATTI	
	GAGTA AGTTTAGTC			
	CTTAT TCAAATCAG			
	_____ GGAA			
GAM549 HIVEP2	GAGTATATAGATCA-ACATGTTCA 8737	T T	TTCI	
	AGTATATAG TTAG CAT			
	TCATATATC AGTT GTA			
	T _ CAAG			
GAM549 HIVEP2	GAGTATATAGATCA-ACATGTTCA 8737 GG	T T _	I	
	AGTATATAG TTAG CAT TTCA			
	TCATATATC AGTT GTA AAGT			
	_____ T _ C G			
GAM549 HNRPH1	AGT-TATAGTTTACTCAGCTTCA 8732 GGAGTA	G _		
	TATAGTTTA TCA TTTC			

	ATATCAAAT AGT GAAGT		
	A_____ G C		
GAM549 HNRPH1	AGT-TATAGTTTACTCAGCTTCA 8732 GTA	G _ I	
	TATAGTTTA TCA TTTC		
	ATATCAAAT AGT GAAG		
	CA_ G C I		
GAM549 LZTFL1	GAATTTATAGTTTA-TCAT 8735 A	G I	
	GAGT TATAGTTTA TCA		
	CTTA ATATCAAAT AGT		
	A _ A		
GAM549 LZTFL1	GAATTTATAGTTTA-TCAT 8735 GGAGTA	G T	
	TATAGTTTA TCATT		
	ATATCAAAT AGTAG		
	TTAA_ _ I		
GAM549 MAP3K13	TATATAGTTCACTCTTTGCA 8743	G ATTTCI	
	ATATAGTTTA TC		
	TATATCAAGT AG		
	G AAACGI		
GAM549 MAP4K5	GGAGTATATTCATTTTCCTGTCATTT 8738	A_ A_ CAII	
	GGAGTATAT GTTT GTCATTT		
	CCTCATATA TAAA CAGTAAA		
	AG AGGA IIIA		
GAM549 RB1CC1	AGTATATAGTTAAAGAACATTT 8730 GGAG	T_ T_ CA	
	TATATAGTT AG CATTT		
	ATATATCAA TC GTAAA		
	_____ TT TT AA		
GAM549 SLC6A12	GGAG-ATAAGGTTTTAGTCATATC 8739	T TAG_ T AI	
	GGAG ATA TTTAGTCAT TC		
	CCTC TAT AAATCAGTA AG		
	_ TCCA T II		
GAM549 SLC6A12	GGAG-ATAAGGTTTTAGTCATATC 8739	T TAG_ TTI	
	GAG ATA TTTAGTCAT		
	CTC TAT AAATCAGTA		
	_ TCCA TAI		
GAM549 TCF2	AGTTTATAGTTTACAGCCATT 8731 A	_ III	
	AGT TATAGTT TAGTCAT		
	TCA ATATCAA GTCGGTA		
	A AT AII		
GAM549 TCF2	AGTTTATAGTTTACAGCCATT 8731 GGAGTA	_ TCA	
	TATAGTT TAGTCATT		

	ATATCAA GTCGGTAA	
	AA_____ AT CCI	
GAM550 ACP5	AACTATTCTTTTATTGAACATCA 8746 TGAACATG	CCAI
	TTTTTATTGAACA	
	GAAAATAACTTGT	
	GATAA_____ AGTC	
GAM550 AR	TTCAGGAACATGTTTCATG-ACA 8776 TT	_ GGT TT
	TCAGGAACAT TTCA ACA	
	AGTCCTTGTA AAGT TGT	
	_____ C AC_ CI	
GAM550 BAZ1A	TTAAGGAACATTTTCCAGGTA 8777 TTTC	_____ CATT
	AGGAACAT TTCAGGTA	
	TCCTTGTA AGGTCCAT	
	AT_____ AA AII	
GAM550 CASP10	GAACGTGGTTTT--TGAACACCA 8762 TGAAC	TT A
	ATGT TT TTGAACACCA	
	TGCA AA AACTTGTGGT	
	T_____ CC A	
GAM550 CDC23	ACAT-TTTTTATTGAATTCCA 8752 TGAACATG	CA
	TTTTTATTGAA CC	
	AAAAATAACTT GG	
	A_____ AA	
GAM550 CDKN2B	TGAACATGTATTT-TTAAAC 8770	T A ACC
	TGAACATGT TTT TTGAAC	
	ACTTGTACA AAA AATTTG	
	T _	
GAM550 CEACAM5	GAGCAGATTTTTATTGAAC 8759 TGAA T	ACC
	CA GTTTTTATTGAAC	
	GT TAAAAATAACTTG	
	TC_ C AII	
GAM550 COPG2	CAGGAGC-TTTCAGGTACA 8755 TTTCAGGAACA	
	TTTCAGGTACA	
	AAAGTCCATGT	
	CTCG_____	
GAM550 DDX11	CAGGATCTGCTTCAGGTACAT 8754 TTTCAGGAACA	
	TTTCAGGTACATT	
	GAAGTCCATGTAG	
	CTAGAC_____	
GAM550 DIAPH2	TCAGGGTTAACATTTCAAGATCATT 8764 TTTC	_____ TA
	AGG AACATTTTCAGG CATT	

	TCC TTGTAAAGTTC GTAA	
	____ CAA TA GA	
GAM550 DSG2	TCATGAAAAAT-CAGGTACATT 8766 TTTCA CATT	
	GGAA TCAGGTACATT	
	CTTT AGTCCATGTAA	
	TA____ TT__	
GAM550 ED1	AGGAAACACATTTTCAGGAACA 8753 TTTCAGGA T TT	
	ACATTTTCAGG ACA	
	TGTAAAGTCC TGT	
	TTG____ T TC	
GAM550 EIF2C1	TCAGAGAACAAATCAGGTACA 8763 TTTCA TT T	
	GGAACA TCAGGTACAT	
	TCTTGT AGTCCATGTG	
	TC____ TT T	
GAM550 ELMO2	TGAAAGAGTATTTATTGAAAAC 8773 CAT T C CA	
	TGAA GT TTTATTGAA AC	
	ACTT CA AAATAACTT TG	
	TCT T T	
GAM550 EYA1	TTCAGGAAACACATTTTCAG 8775 TT ____ GTACAT	
	TCAGGA ACATTTTCAG	
	AGTCCT TGTAAGTC	
	____ TTG AIIIT	
GAM550 GAS1	TGTACATGTTTAAATAAAAACA 8772 A TATT CCA	
	TG ACATGTTTT GAACA	
	AC TGTACAAAA TTTGT	
	A TTAT	
GAM550 HMGB3	TTCAAAAACATTTTCAG---CATT 8779 TT GTACAT	
	TCAGGAACATTTTCAG	
	AGTTTTTGTAAGTC	
	____ GTAAGI	
GAM550 IDH3B	CATGTTCTTTATTGAACACC 8756 TGAACATG	
	TTTTTATTGAACACC	
	AGAAATAACTTGTGG	
	A_____	
GAM550 IFNA1	GAACATG-TTTTATT--ACAC 8761 TG T GA	
	AACATGTTTT ATT ACAC	
	TTGTACAAAA TAA TGTG	
	____ _	
GAM550 IFNA8	GAACATGTTTTTGTTACACA 8760 TG A A CC	
	AACATGTTTTT TTG ACA	

	TTGTACAAAAA AAT TGT		
	— C G TI		
GAM550 IFNW1	TTTCTG-AACATTTCTCTGTACTTT 8784	AG	AG_ ATTI
	TTTC GAACATTTTC GTAC		
	AAAG CTTGTAAAG CATG		
	A_ AGA AAAl		
GAM550 IFNW1	TGAACATGTTTTGTTATCTTAATAC 8768		TATTGAACACCAII
	TGAACATGTTTT		
	ACTTGTACAAAA		
	CAATAGAATTATGI		
GAM550 JUN	TCAGGTACAT--CAGGTACATT 8765	TTTC A TT	
	AGG ACA TCAGGTACAT		
	TCC TGT AGTCCATGTA		
	— A —		
GAM550 KL	TTTCGAAAGGAACATTCCAG 8780	—	GTACAT
	TTTC AGGAACATTTTCAG		
	AAAG TCCTTGTAAGGTC		
	CTT IIITTA		
GAM550 KTN1	TGAACAA--TTTTATTGAGCA 8771	TGT	ACACC
	TGAACA TTTTATTGA		
	ACTTGT AAAATAACT		
	T_ CGTII		
GAM550 MAB21L1	TTTAAATAACATTTCAAGTATATT 8787	TTTCAGG	CATTI
	AACATTTTCAGGTA		
	TTGTAAAGTTCAT		
	AAATTTA ATAAI		
GAM550 MECP2	TTTTTGAAACGTATACAGGTACATT 8783	TTTCA ATTT_ II	
	GGAAC CAGGTACATT		
	CTTTG GTCCATGTAA		
	AAAAA CATAT II		
GAM550 MKPX	TTTCAGAAAC--TTCAGGTACA 8786	AT	T
	TTTCAGGAAC TTCAGGTACA		
	AAAGTCTTTG AAGTCCATGT		
	— I		
GAM550 MVK	TTCCACAAACCTCTCAGGTACA 8785	G A	TT
	TTTCA GAAC TTTTCAGGTACA		
	AAGGT TTTG AGAGTCCATGT		
	G G II		
GAM550 NCOA3	AACATTTCTGTTTTGAACACCA 8751	TGAACAT	A_
	GTTTTT TTGAACACCA		

	TAAAGA AACTTGTGGT	
	G_____ CAA	
GAM550 NOVA1	GAACAGGTGCTTTTATTGA 8758 TG _____ ACACC	
	AACA TGTTTTTATTGA	
	TTGT ACGAAAATAACT	
	____ CC AIIIA	
GAM550 NSMAF	AACATGTTTTTCCT-AACAC 8749 TGAA ATTG C	
	CATGTTTT AACAC	
	GTACAAAAA TTGTG	
	_____ GGA_ T	
GAM550 PRPS2	TTTAGGATGCAGCATTTTCAGGTA 8781 TTTC A_____ CATTI	
	AGGA CATTTTCAGGTA	
	TCCT GTAAAGTCCAT	
	AAAA ACGTC IIIT	
GAM550 ROBO1	TGAACAAGTTTGGTTTGGTGAACACCA8767 T TTAT_____ III	
	TGAACA GTTT TGAACACCA	
	ACTTGT CAAA ACTTGTGGT	
	T CCAAACC III	
GAM550 SCML1	TGAACATGTTTCCCTTGAA 8769 TA CACC	
	TGAACATGTTTT TTGAA	
	ACTTGTACAAAG AACTT	
	GG IIIA	
GAM550 SPAG11	AACAAATATTTATTGAACACC 8750 TGAA T T A	
	CA GT TTTATTGAACACC	
	GT TA AAATAACTTGTGG	
	_____ T T A	
GAM550 SPTBN1	TTGAGGAACATT--AGGCACA 8778 TTTC TC T	
	AGGAACATT AGGTACA	
	TCCTTGTA TCCGTGT	
	AC_____ C	
GAM550 SSA1	AACATGTTTTTGGTTGATCA 8748 TGAA A_ A CC	
	CATGTTTT TTGA CA	
	GTACAAAAA AACT GT	
	_____ CC A TC	
GAM550 TFAP2C	TTTGGGGAACATTTACAGG 8782 TTTC _ TACAT	
	GGAACATTT CAGG	
	CCTTGTA AAA GTCC	
	AAACC T IIIT	
GAM550 TPTE	TTCAAGGGAACATTT-AGGATAGATT 8774 TT _ C TACATTI	
	TCA GGAACATTT AGG	

	AGT CCTTGTAAG TCC	
	__ TC __ TATCTAAA	
GAM550 VAPA	GAACAGTTTGTGTTTATTG 8757 TG __	AACACC
	AACA TGTTTTTATTG	
	TTGT AAAAAATAAC	
	__ CAA A AC	
GAM550 VIP	AAAATATTTATTATTGAACA 8747 TGAAC _	CC
	ATGTTT TTATTGAACA	
	TATAAA AATAACTTGT	
	T__ T TG	